

## SEQUENCE LISTING

<110> Pompejus, Markus  
Kroger, Burkhard  
Schroder, Hartwig  
Zelder, Oskar  
Haberhauer, Gregor

<120> CORYNEBACTERIUM GLUTAMICUM GENES ENCODING  
REGULATORY PROTEINS

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Ala Arg Glu Ser Ala Ile Lys Ser Arg Glu Val Leu Asp Lys Ile Val			
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Pro His Ala Asp Gly Leu Leu Ala Ala Ser Arg Met Asp Ser Gly			
65	70	75	80
Glu Ile His Lys Val Ala Arg Glu Ile Pro Thr Val Leu Met Ser Arg			
85	90	95	
Glu Val Gln Gly Ile Pro Ser Val Met Val Asp Asn Tyr Asp Gly Ala			
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 Val Glu Thr Gln Ala  
 1 5  
 ttt cag cgc caa aac acc ggc ctc atc gct atg gtt gcc gcc gat gcg 163  
 Phe Gln Arg Gln Asn Thr Gly Leu Ile Ala Met Val Ala Ala Asp Ala  
 10 15 20  
 tcg aat ccc ttc ttc ttg gaa att ttc cgg ggc gcg cag cac gcc gca 211  
 Ser Asn Pro Phe Phe Leu Glu Ile Phe Arg Gly Ala Gln His Ala Ala  
 25 30 35  
 agc act cag ggc tat acg gtt gcg ctt gtc gac gcc cgg gag tcg gcg 259  
 Ser Thr Gln Gly Tyr Thr Val Ala Leu Val Asp Ala Arg Glu Ser Ala  
 40 45 50  
 att aag tcc agg gag gtg ctg gac aag atc gtc ccc cac gcc gat ggc 307  
 Ile Lys Ser Arg Glu Val Leu Asp Lys Ile Val Pro His Ala Asp Gly  
 55 60 65  
 tta ttg ctc gct gct tca agg atg gat tct ggt gag atc cac aaa gtc 355

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Leu Leu Leu Ala Ala Ser Arg Met Asp Ser Gly Glu Ile His Lys Val
 70                               75                               80                               85

gcg cgg gaa att ccc act gta tta atg agc cgt gaa gtg caa ggt att      403
Ala Arg Glu Ile Pro Thr Val Leu Met Ser Arg Glu Val Gln Gly Ile
                               90                               95                               100

ccc agc gtg atg gtg gat aac tac gac ggt gcg ccg aag gct gtg gtg      451
Pro Ser Val Met Val Asp Asn Tyr Asp Gly Ala Pro Lys Ala Val Val
                               105                               110                               115

cat ttg gtg gat cag ggg tgc cgc tcc att acc tat atc gcc ggt cct      499
His Leu Val Asp Gln Gly Cys Arg Ser Ile Thr Tyr Ile Ala Gly Pro
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Asn Lys Ser Trp Ala
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 20                               25                               30

Ala Gln His Ala Ala Ser Thr Gln Gly Tyr Thr Val Ala Leu Val Asp
 35                               40                               45

Ala Arg Glu Ser Ala Ile Lys Ser Arg Glu Val Leu Asp Lys Ile Val
 50                               55                               60

Pro His Ala Asp Gly Leu Leu Leu Ala Ala Ser Arg Met Asp Ser Gly
 65                               70                               75                               80

Glu Ile His Lys Val Ala Arg Glu Ile Pro Thr Val Leu Met Ser Arg
 85                               90                               95

Glu Val Gln Gly Ile Pro Ser Val Met Val Asp Asn Tyr Asp Gly Ala
 100                               105                               110

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Met Lys Leu Asp Ser
1 5

att gat cgc gca att att gcg gag ctt agc gcg aat gcg cgc atc tca 163
Ile Asp Arg Ala Ile Ile Ala Glu Leu Ser Ala Asn Ala Arg Ile Ser
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aat ctc gca ctg gct gac aag gtg cat ctc act ccg gga cct tgc ttg 211
Asn Leu Ala Leu Ala Asp Lys Val His Leu Thr Pro Gly Pro Cys Leu
25 30 35

agg agg gtg cag cgt ttg gaa gcc gaa gga atc att ttg ggc tac agc 259
Arg Arg Val Gln Arg Leu Glu Ala Glu Gly Ile Ile Leu Gly Tyr Ser
40 45 50

gcg gac att cac cct gcg gtg atg aat cgt gga ttt gag gtg acc gtg 307
Ala Asp Ile His Pro Ala Val Met Asn Arg Gly Phe Glu Val Thr Val
55 60 65

gat gtc act ctc agc aac ttc gac cgc tcc act gta gac aat ttt gaa 355
Asp Val Thr Leu Ser Asn Phe Asp Arg Ser Thr Val Asp Asn Phe Glu
70 75 80 85

agc tcc gtt gcg cag cat gat gaa gta ctg gag ttg cac agg ctt ttt 403
Ser Ser Val Ala Gln His Asp Glu Val Leu Glu Leu His Arg Leu Phe
90 95 100

ggt tcg cca gat tat ttt gtc cgc atc gcc gtt gct gat ttg gag gcg 451
Gly Ser Pro Asp Tyr Phe Val Arg Ile Gly Val Ala Asp Leu Glu Ala
105 110 115

tat gag caa ttt tta tcc agt cac att caa acc gtg cca gga att gca 499
Tyr Glu Gln Phe Leu Ser Ser His Ile Gln Thr Val Pro Gly Ile Ala
120 125 130

aag atc tca tca cgt ttt gct atg aaa gtg gtg aaa cca gct cgc ccc 547
Lys Ile Ser Ser Arg Phe Ala Met Lys Val Val Lys Pro Ala Arg Pro
135 140 145

cag gtg tgaagcatgc attttgaagc atg 576
Gln Val
150

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&lt;210&gt; 6

&lt;211&gt; 151

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 6

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Met Lys Leu Asp Ser Ile Asp Arg Ala Ile Ile Ala Glu Leu Ser Ala
1 5 10 15

Asn Ala Arg Ile Ser Asn Leu Ala Leu Ala Asp Lys Val His Leu Thr

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Pro Gly Pro Cys Leu Arg Arg Val Gln Arg Leu Glu Ala Glu Gly Ile					
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Ile Leu Gly Tyr Ser Ala Asp Ile His Pro Ala Val Met Asn Arg Gly					
	50		55		60
Phe Glu Val Thr Val Asp Val Thr Leu Ser Asn Phe Asp Arg Ser Thr					
	65		70		75
Val Asp Asn Phe Glu Ser Ser Val Ala Gln His Asp Glu Val Leu Glu					
		85		90	
Leu His Arg Leu Phe Gly Ser Pro Asp Tyr Phe Val Arg Ile Gly Val					
	100		105		110
Ala Asp Leu Glu Ala Tyr Glu Gln Phe Leu Ser Ser His Ile Gln Thr					
	115		120		125
Val Pro Gly Ile Ala Lys Ile Ser Ser Arg Phe Ala Met Lys Val Val					
	130		135		140
Lys Pro Ala Arg Pro Gln Val					
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 Met Thr Thr Glu Ala  
 1 5  
 ccc att tgg cca gcc gaa ctc ttc gaa gac ctc gac cgc aac gga cca 163  
 Pro Ile Trp Pro Ala Glu Leu Phe Glu Asp Leu Asp Arg Asn Gly Pro  
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 Ile Pro Leu Tyr Phe Gln Val Ala Gln Arg Leu Glu Asp Gly Ile Arg  
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 agc gga gtc ctc cca ccc gga gca cgc cta gaa aac gag atc tcc gtg 259  
 Ser Gly Val Leu Pro Pro Gly Ala Arg Leu Glu Asn Glu Ile Ser Val  
 40 45 50  
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 Ala Lys His Leu Asn Val Ser Arg Pro Thr Val Arg Arg Ala Ile Gln  
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Glu Val Val Asp Lys Gly Leu Leu Val Arg Arg Arg Gly Val Gly Thr  
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 cag gtc gtc caa agc cac gtc acc cgc cca gtc gaa ctg acc agt ttc 403  
 Gln Val Val Gln Ser His Val Thr Arg Pro Val Glu Leu Thr Ser Phe  
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 Phe Asn Asp Leu Lys Asn Ala Asn Leu Asp Pro Lys Thr Arg Val Leu  
 105 110 115  
 gag cac cgc tcc ttg cag caa gtt ccg cca tcg cag aaa aac tcg gag 499  
 Glu His Arg Ser Leu Gln Gln Val Pro Pro Ser Gln Lys Asn Ser Glu  
 120 125 130  
 ttt ccg cag gtg acg aag tcc tcc tca tcc gcc gcc tcc gct cca ccg 547  
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 Glu Thr Ser Pro  
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 Glu Asp Gly Ile Arg Ser Gly Val Leu Pro Pro Gly Ala Arg Leu Glu  
 35 40 45  
 Asn Glu Ile Ser Val Ala Lys His Leu Asn Val Ser Arg Pro Thr Val  
 50 55 60  
 Arg Arg Ala Ile Gln Glu Val Val Asp Lys Gly Leu Leu Val Arg Arg  
 65 70 75 80  
 Arg Gly Val Gly Thr Gln Val Val Gln Ser His Val Thr Arg Pro Val  
 85 90 95  
 Glu Leu Thr Ser Phe Phe Asn Asp Leu Lys Asn Ala Asn Leu Asp Pro  
 100 105 110  
 Lys Thr Arg Val Leu Glu His Arg Ser Leu Gln Gln Val Pro Pro Ser  
 115 120 125  
 Gln Lys Asn Ser Glu Phe Pro Gln Val Thr Lys Ser Ser Ser Ser Ala  
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Arg Glu Thr Ala Gln Thr Thr Ser Thr Val Glu Gln Arg Val Ala Ala	50	55	60
Ala Leu Gln His Leu Asp Ala Lys Leu Gly Gln Ile Arg Gln Asp Gly	65	70	75
Ser Ser Leu Leu Gln Val Arg Leu Arg Arg Asp Asp Val Ala Gly Thr	85	90	95
Thr Val Glu Ser Ala Ser Arg Ala Met Ala Arg Met Lys Lys Thr Gly	100	105	110
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 Val Glu Ile Arg Trp  
 1 5  
 ttg gaa ggc ttt atc gcg gtc gcg gaa gaa ttg cac ttt agt aat gct 163  
 Leu Glu Gly Phe Ile Ala Val Ala Glu Glu Leu His Phe Ser Asn Ala  
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 gcg att cgt ttg ggg atg ccg caa tcg ccg ttg agt cag ttg atc cgg 211  
 Ala Ile Arg Leu Gly Met Pro Gln Ser Pro Leu Ser Gln Leu Ile Arg  
 25 30 35  
 cgg ttg gag tcg gag ttg ggg cag aag ctt ttt gat cgc agt acc cgg 259  
 Arg Leu Glu Ser Glu Leu Gly Gln Lys Leu Phe Asp Arg Ser Thr Arg  
 40 45 50  
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 Ser Val Glu Leu Thr Ala Ala Gly Arg Ala Phe Leu Pro His Ala Arg  
 55 60 65  
 ggg att gtg gcg agc gct gcg gtg gcg agg gaa gct gtg aat gct gcc 355

Gly Ile Val Ala Ser Ala Ala Val Ala Arg Glu Ala Val Asn Ala Ala  
 70 75 80 85  
 gag ggg gag atc gtt ggt gtt gtt cgc att ggt ttt tct ggt gtg ctg 403  
 Glu Gly Glu Ile Val Gly Val Val Arg Ile Gly Phe Ser Gly Val Leu  
 90 95 100  
 aac tat tcc acg ctg ccg ctt ttg acc agt gag gtg cat aaa cgg ctt 451  
 Asn Tyr Ser Thr Leu Pro Leu Leu Thr Ser Glu Val His Lys Arg Leu  
 105 110 115  
 cct aat gtg gag ttg gag ctg gtt ggt cag aag ttg acg agg gaa gcg 499  
 Pro Asn Val Glu Leu Glu Leu Val Gly Gln Lys Leu Thr Arg Glu Ala  
 120 125 130  
 gta agt ttg ctg cgc ttg ggg gcg ttg gat att acg ttg atg ggt ttg 547  
 Val Ser Leu Leu Arg Leu Gly Ala Leu Asp Ile Thr Leu Met Gly Leu  
 135 140 145  
 ccc att gag gat cca gag att gag act cgg ctg att agt ttg gaa gag 595  
 Pro Ile Glu Asp Pro Glu Ile Glu Thr Arg Leu Ile Ser Leu Glu Glu  
 150 155 160 165  
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 Phe Cys Val Val Leu Pro Lys Asp His Arg Leu Ala Gly Glu Gly Val  
 170 175 180  
 gtg gat ttg gtg gat ctg gct aaa gat ggg ttt gtg acg acg ccg gag 691  
 Val Asp Leu Val Asp Leu Ala Lys Asp Gly Phe Val Thr Thr Pro Glu  
 185 190 195  
 ttt gcg ggg tct gtg ttt agg aat tcc acc ttt cag ttg tgt gct gag 739  
 Phe Ala Gly Ser Val Phe Arg Asn Ser Thr Phe Gln Leu Cys Ala Glu  
 200 205 210  
 gct ggt ttt gtg ccg agg atc agc cag caa gtt aat gat cct tac atg 787  
 Ala Gly Phe Val Pro Arg Ile Ser Gln Gln Val Asn Asp Pro Tyr Met  
 215 220 225  
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 Ala Leu Leu Leu Ala Arg  
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&lt;210&gt; 12

&lt;211&gt; 235

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 12

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Ser Gln Leu Ile Arg Arg Leu Glu Ser Glu Leu Gly Gln Lys Leu Phe  
 35 40 45

Asp Arg Ser Thr Arg Ser Val Glu Leu Thr Ala Ala Gly Arg Ala Phe  
 50 55 60

Leu Pro His Ala Arg Gly Ile Val Ala Ser Ala Ala Val Ala Arg Glu  
 65 70 75 80  
 Ala Val Asn Ala Ala Glu Gly Glu Ile Val Gly Val Val Arg Ile Gly  
 85 90 95  
 Phe Ser Gly Val Leu Asn Tyr Ser Thr Leu Pro Leu Leu Thr Ser Glu  
 100 105 110  
 Val His Lys Arg Leu Pro Asn Val Glu Leu Glu Leu Val Gly Gln Lys  
 115 120 125  
 Leu Thr Arg Glu Ala Val Ser Leu Leu Arg Leu Gly Ala Leu Asp Ile  
 130 135 140  
 Thr Leu Met Gly Leu Pro Ile Glu Asp Pro Glu Ile Glu Thr Arg Leu  
 145 150 155 160  
 Ile Ser Leu Glu Glu Phe Cys Val Val Leu Pro Lys Asp His Arg Leu  
 165 170 175  
 Ala Gly Glu Gly Val Val Asp Leu Val Asp Leu Ala Lys Asp Gly Phe  
 180 185 190  
 Val Thr Thr Pro Glu Phe Ala Gly Ser Val Phe Arg Asn Ser Thr Phe  
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 Met Ala Val Lys Arg  
 1 5  
 aat gag ttg gaa ccc gag ctg acg tcc aac ccc aac cca tta agc gca 163  
 Asn Glu Leu Glu Pro Glu Leu Thr Ser Asn Pro Asn Pro Leu Ser Ala  
 10 15 20  
 gaa gtg cat cat ttg tat cct gag gaa act cgt ctt gca acg gag atc 211  
 Glu Val His His Leu Tyr Pro Glu Glu Thr Arg Leu Ala Thr Glu Ile  
 25 30 35  
 ctg gaa cgc acc aac aat tgg ctt gct gaa aaa ggg atc cct ccg ctg 259

Leu Glu Arg Thr Asn Asn Trp Leu Ala Glu Lys Gly Ile Pro Pro Leu  
                     40                                    45                                    50

cca cca gcg gaa gtt gta gcc atc tca tta cac ctg gtt aat gct ggt 307  
 Pro Pro Ala Glu Val Val Ala Ile Ser Leu His Leu Val Asn Ala Gly  
           55                                    60                                    65

ttc cgc acg gaa gac ctc gca gaa acc tac gtg atg act ggc gtt ttc 355  
 Phe Arg Thr Glu Asp Leu Ala Glu Thr Tyr Val Met Thr Gly Val Phe  
           70                                    75                                    80                                    85

gag cag ctc ttt gag gta atc gat tcc tcg ttt ggc atc acc ctt gac 403  
 Glu Gln Leu Phe Glu Val Ile Asp Ser Ser Phe Gly Ile Thr Leu Asp  
                                     90                                    95                                    100

cga caa tcc gtc aac gcc gca cgg ttt atc acc cac atg cgc tac ttc 451  
 Arg Gln Ser Val Asn Ala Ala Arg Phe Ile Thr His Met Arg Tyr Phe  
                                     105                                    110                                    115

ttt gtt cgc gtt cac cac gac gga caa ctc aac gac ggc atg tcc gtg 499  
 Phe Val Arg Val His His Asp Gly Gln Leu Asn Asp Gly Met Ser Val  
                     120                                    125                                    130

ctg cgc aac agc cta gaa att tcc cac ccg gat tcg gtg gca tgt gcg 547  
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gaa aga ctc agc caa atc ctc agc ctt cga ttg ggt gcc gaa ctt tcc 595  
 Glu Arg Leu Ser Gln Ile Leu Ser Leu Arg Leu Gly Ala Glu Leu Ser  
           150                                    155                                    160                                    165

tcc gac gag caa acc tac ctc gcg ctc cat gtc gcg agg ttg gct gaa 643  
 Ser Asp Glu Gln Thr Tyr Leu Ala Leu His Val Ala Arg Leu Ala Glu  
                                     170                                    175                                    180

gat cga ggt act acc gct gat taacaagttc taggcgcgaa tct 687  
 Asp Arg Gly Thr Thr Ala Asp  
                                     185

&lt;210&gt; 14

&lt;211&gt; 188

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 14

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Asn Pro Leu Ser Ala Glu Val His His Leu Tyr Pro Glu Glu Thr Arg  
                     20                                    25                                    30

Leu Ala Thr Glu Ile Leu Glu Arg Thr Asn Asn Trp Leu Ala Glu Lys  
                     35                                    40                                    45

Gly Ile Pro Pro Leu Pro Pro Ala Glu Val Val Ala Ile Ser Leu His  
           50                                    55                                    60

Leu Val Asn Ala Gly Phe Arg Thr Glu Asp Leu Ala Glu Thr Tyr Val  
           65                                    70                                    75                                    80



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Met Ala Gly Gly Asn																5
1																
cgc gaa cct gga cgt aca gtc acc tcc aag gtg atc gcc gta ctg gga																163
Arg Glu Pro Gly Arg Thr Val Thr Ser Lys Val Ile Ala Val Leu Gly																20
10 15																
gct ttt gaa cac acc atg cgt cca ctt ggt gtc act gaa atc gct gag																211
Ala Phe Glu His Thr Met Arg Pro Leu Gly Val Thr Glu Ile Ala Glu																35
25 30																
ctg gca gac ctc cca cca agt acc acc cac cgt ctc gtt tct gaa tta																259
Leu Ala Asp Leu Pro Pro Ser Thr Thr His Arg Leu Val Ser Glu Leu																50
40 45 50																
acc gaa ggc gga cta ctc agc aag aaa tct gat ggg cgc tac caa ttg																307
Thr Glu Gly Gly Leu Leu Ser Lys Lys Ser Asp Gly Arg Tyr Gln Leu																65
55 60 65																
ggc tta cgt atc tgg gaa ctc gcc caa aat aca gga cgg cag tta cgc																355
Gly Leu Arg Ile Trp Glu Leu Ala Gln Asn Thr Gly Arg Gln Leu Arg																85
70 75 80 85																
gac act gca cgc ccg ttc atc caa gag ctc tac tca ctt act tcc gag																403
Asp Thr Ala Arg Pro Phe Ile Gln Glu Leu Tyr Ser Leu Thr Ser Glu																

	90	95	100	
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Thr Ala Gln Leu Val Val Arg Asp Lys Asp Glu Ala Leu Leu Ile Asp				
	105	110	115	
cga gcc tac ggc acg aag aaa att cca cgc tcg gct cga gtc ggt ggt				499
Arg Ala Tyr Gly Thr Lys Lys Ile Pro Arg Ser Ala Arg Val Gly Gly				
	120	125	130	
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Arg Leu Pro Leu Asn Ser Thr Ala Val Gly Lys Ile Leu Leu Ala Phe				
	135	140	145	
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Asp Glu Pro Trp Val Lys Gln Ser Tyr Leu Lys Leu Pro Leu Asn Ala				
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tcc acc cca aag aca att gtg aat ccc gac gtc ttg gct gcg cag ctg				643
Ser Thr Pro Lys Thr Ile Val Asn Pro Asp Val Leu Ala Ala Gln Leu				
	170	175	180	
aaa caa att cac tcg caa ggc ttt gcc atc aca cat gac gag caa cga				691
Lys Gln Ile His Ser Gln Gly Phe Ala Ile Thr His Asp Glu Gln Arg				
	185	190	195	
atc ggc ggc gca tcg atc gcc gta ccg gtc tgg cat aca gga aaa ctg				739
Ile Gly Gly Ala Ser Ile Ala Val Pro Val Trp His Thr Gly Lys Leu				
	200	205	210	
gga gca gca ctg ggg ttg gtg gtt ccc acc gca cag gct gca aat ctt				787
Gly Ala Ala Leu Gly Leu Val Val Pro Thr Ala Gln Ala Ala Asn Leu				
	215	220	225	
gag cgc tat ctc ccg atc ctt cag gcg aca agt cag aga att aca aaa				835
Glu Arg Tyr Leu Pro Ile Leu Gln Ala Thr Ser Gln Arg Ile Thr Lys				
	230	235	240	245
gca acc gcg ctc att cct ttg gac aca ctt ttg gct tca cac aaa aat				883
Ala Thr Ala Leu Ile Pro Leu Asp Thr Leu Leu Ala Ser His Lys Asn				
	250	255	260	
gca gaa cga aaa ggc gat acc taaaccgcgcc ctccatctgc ata				927
Ala Glu Arg Lys Gly Asp Thr				
	265			

&lt;210&gt; 16

&lt;211&gt; 268

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 16

Met	Ala	Gly	Gly	Asn	Arg	Glu	Pro	Gly	Arg	Thr	Val	Thr	Ser	Lys	Val
1				5				10						15	

Ile	Ala	Val	Leu	Gly	Ala	Phe	Glu	His	Thr	Met	Arg	Pro	Leu	Gly	Val
	20						25						30		

Thr	Glu	Ile	Ala	Glu	Leu	Ala	Asp	Leu	Pro	Pro	Ser	Thr	Thr	His	Arg
	35						40					45			

Leu Val Ser Glu Leu Thr Glu Gly Gly Leu Leu Ser Lys Lys Ser Asp  
 50 55 60  
 Gly Arg Tyr Gln Leu Gly Leu Arg Ile Trp Glu Leu Ala Gln Asn Thr  
 65 70 75 80  
 Gly Arg Gln Leu Arg Asp Thr Ala Arg Pro Phe Ile Gln Glu Leu Tyr  
 85 90 95  
 Ser Leu Thr Ser Glu Thr Ala Gln Leu Val Val Arg Asp Lys Asp Glu  
 100 105 110  
 Ala Leu Leu Ile Asp Arg Ala Tyr Gly Thr Lys Lys Ile Pro Arg Ser  
 115 120 125  
 Ala Arg Val Gly Gly Arg Leu Pro Leu Asn Ser Thr Ala Val Gly Lys  
 130 135 140  
 Ile Leu Leu Ala Phe Asp Glu Pro Trp Val Lys Gln Ser Tyr Leu Lys  
 145 150 155 160  
 Leu Pro Leu Asn Ala Ser Thr Pro Lys Thr Ile Val Asn Pro Asp Val  
 165 170 175  
 Leu Ala Ala Gln Leu Lys Gln Ile His Ser Gln Gly Phe Ala Ile Thr  
 180 185 190  
 His Asp Glu Gln Arg Ile Gly Gly Ala Ser Ile Ala Val Pro Val Trp  
 195 200 205  
 His Thr Gly Lys Leu Gly Ala Ala Leu Gly Leu Val Val Pro Thr Ala  
 210 215 220  
 Gln Ala Ala Asn Leu Glu Arg Tyr Leu Pro Ile Leu Gln Ala Thr Ser  
 225 230 235 240  
 Gln Arg Ile Thr Lys Ala Thr Ala Leu Ile Pro Leu Asp Thr Leu Leu  
 245 250 255  
 Ala Ser His Lys Asn Ala Glu Arg Lys Gly Asp Thr  
 260 265

<210> 17  
 <211> 777  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(754)  
 <223> RXS00774

<400> 17  
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 acacaatcta atcattttgt gtgatctaac taaggagtgc atg gat aag gcg act 115  
 Met Asp Lys Ala Thr  
 1 5

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gat gcc ctc ctg cgc act tct ttg gca tcg gca gaa agc gct tta ggc 163
Asp Ala Leu Leu Arg Thr Ser Leu Ala Ser Ala Glu Ser Ala Leu Gly
      10                      15                      20

aat gca gaa aag ctt gaa gag ctt cgt act gga tgc gag tct caa gcc 211
Asn Ala Glu Lys Leu Glu Glu Leu Arg Thr Gly Cys Glu Ser Gln Ala
      25                      30                      35

gtc gaa ctt ttg gcg ctt gaa act cct gta gcc cgt gat ctt cgc cag 259
Val Glu Leu Leu Ala Leu Glu Thr Pro Val Ala Arg Asp Leu Arg Gln
      40                      45                      50

gtt gtc tcc tcc atc tac atc gtc gag gaa att acc cgt atg ggt gct 307
Val Val Ser Ser Ile Tyr Ile Val Glu Glu Ile Thr Arg Met Gly Ala
      55                      60                      65

ctg gca atg cac gtg gct aat tcc gtg cgc cgc cgt tac ccc gat ccg 355
Leu Ala Met His Val Ala Asn Ser Val Arg Arg Arg Tyr Pro Asp Pro
      70                      75                      80                      85

gtg atc ccg gag gac atg cgt ggc tat ttc aag gag atg gcc cgc ctc 403
Val Ile Pro Glu Asp Met Arg Gly Tyr Phe Lys Glu Met Ala Arg Leu
      90                      95                      100

gca gct gac atg aca gat cat att cgt cag atc ctc att gat cct gaa 451
Ala Ala Asp Met Thr Asp His Ile Arg Gln Ile Leu Ile Asp Pro Glu
      105                      110                      115

cca gat ctt gcc cta gag atg gct aaa agc gat gac gcg gtg gat gat 499
Pro Asp Leu Ala Leu Glu Met Ala Lys Ser Asp Asp Ala Val Asp Asp
      120                      125                      130

ctg cat cag cac atc atg cgt att ctc acg ctg cgt cct tgg cct cac 547
Leu His Gln His Ile Met Arg Ile Leu Thr Leu Arg Pro Trp Pro His
      135                      140                      145

gac acc aag agc gcg gtt gat ttg acg ctg ctt tcc cgc ttc tac gag 595
Asp Thr Lys Ser Ala Val Asp Leu Thr Leu Leu Ser Arg Phe Tyr Glu
      150                      155                      160                      165

cgt tac gcc gat cac acg gta aac gtg gcc gcc cgt atc att tac ctg 643
Arg Tyr Ala Asp His Thr Val Asn Val Ala Ala Arg Ile Ile Tyr Leu
      170                      175                      180

tcc acc ggg ctg cac ccg gag gag tac atg gaa aag cgc gag caa caa 691
Ser Thr Gly Leu His Pro Glu Glu Tyr Met Glu Lys Arg Glu Gln Gln
      185                      190                      195

agg gcc gat gcc gac atg gag aag cgc tgg gcc gag ctg gag cgg cag 739
Arg Ala Asp Ala Asp Met Glu Lys Arg Trp Ala Glu Leu Glu Arg Gln
      200                      205                      210

ttc cgc acc agc gag taaaaagctg cttctcgacg cta 777
Phe Arg Thr Ser Glu
      215

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&lt;210&gt; 18

&lt;211&gt; 218

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 18

Met Asp Lys Ala Thr Asp Ala Leu Leu Arg Thr Ser Leu Ala Ser Ala  
 1 5 10 15

Glu Ser Ala Leu Gly Asn Ala Glu Lys Leu Glu Glu Leu Arg Thr Gly  
 20 25 30

Cys Glu Ser Gln Ala Val Glu Leu Leu Ala Leu Glu Thr Pro Val Ala  
 35 40 45

Arg Asp Leu Arg Gln Val Val Ser Ser Ile Tyr Ile Val Glu Glu Ile  
 50 55 60

Thr Arg Met Gly Ala Leu Ala Met His Val Ala Asn Ser Val Arg Arg  
 65 70 75 80

Arg Tyr Pro Asp Pro Val Ile Pro Glu Asp Met Arg Gly Tyr Phe Lys  
 85 90 95

Glu Met Ala Arg Leu Ala Ala Asp Met Thr Asp His Ile Arg Gln Ile  
 100 105 110

Leu Ile Asp Pro Glu Pro Asp Leu Ala Leu Glu Met Ala Lys Ser Asp  
 115 120 125

Asp Ala Val Asp Asp Leu His Gln His Ile Met Arg Ile Leu Thr Leu  
 130 135 140

Arg Pro Trp Pro His Asp Thr Lys Ser Ala Val Asp Leu Thr Leu Leu  
 145 150 155 160

Ser Arg Phe Tyr Glu Arg Tyr Ala Asp His Thr Val Asn Val Ala Ala  
 165 170 175

Arg Ile Ile Tyr Leu Ser Thr Gly Leu His Pro Glu Glu Tyr Met Glu  
 180 185 190

Lys Arg Glu Gln Gln Arg Ala Asp Ala Asp Met Glu Lys Arg Trp Ala  
 195 200 205

Glu Leu Glu Arg Gln Phe Arg Thr Ser Glu  
 210 215

&lt;210&gt; 19

&lt;211&gt; 1362

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1339)

&lt;223&gt; RXN02493

&lt;400&gt; 19

ggttccgtag taaacccagg cggcacctac ctcgatcctg aggcagcagc agccggcgca 60

gcagcagtag caaacccagg taataagtag ctatttgtag gtg agc act ctt ctt 115  
 Val Ser Thr Leu Leu  
 1 5

gct ttc gta ttg ggc gtg gtc ctc atg ggc ctc gcc cta cct gcg tat	163
Ala Phe Val Leu Gly Val Val Leu Met Gly Leu Ala Leu Pro Ala Tyr	
10 15 20	
acg aaa att aaa gat cgg atg cgt cgc cac aag tcc gcg gtc acc ctg	211
Thr Lys Ile Lys Asp Arg Met Arg Arg His Lys Ser Ala Val Thr Leu	
25 30 35	
tcc gaa aac cag gtc acc acg gtg ggg cag gtc ctc cac ctg gcg att	259
Ser Glu Asn Gln Val Thr Thr Val Gly Gln Val Leu His Leu Ala Ile	
40 45 50	
caa ggc tcc cca acg gga atc acg gtt gtc gat cgc acc ggc gac gtc	307
Gln Gly Ser Pro Thr Gly Ile Thr Val Val Asp Arg Thr Gly Asp Val	
55 60 65	
atc tta tcc aac ggc cgc gcc cac gaa ttg ggc atc gtc cac gaa aga	355
Ile Leu Ser Asn Gly Arg Ala His Glu Leu Gly Ile Val His Glu Arg	
70 75 80 85	
tcc gtc gac ggc aac gtt tgg cgc gtc gcc cag gaa gcc ttc caa gac	403
Ser Val Asp Gly Asn Val Trp Arg Val Ala Gln Glu Ala Phe Gln Asp	
90 95 100	
caa gaa acc cac tca ctc gac gtc cac cca gac cgc aat ccg cgg cgc	451
Gln Glu Thr His Ser Leu Asp Val His Pro Asp Arg Asn Pro Arg Arg	
105 110 115	
ccg ggt agt cgc atc acc gca gtg cag gca gtg gtc aag cct tta acg	499
Pro Gly Ser Arg Ile Thr Ala Val Gln Ala Val Val Lys Pro Leu Thr	
120 125 130	
ctt atc gac gat cgt ttc gtg atc atc tat gcc tcc gac gaa tcc gaa	547
Leu Ile Asp Asp Arg Phe Val Ile Ile Tyr Ala Ser Asp Glu Ser Glu	
135 140 145	
aac gtg cgc atg gaa tcg gca cgc cga gac ttc gtc gca aac gtc tcc	595
Asn Val Arg Met Glu Ser Ala Arg Arg Asp Phe Val Ala Asn Val Ser	
150 155 160 165	
cac gaa ctg aaa acc ccc gtc ggc ggc atg gca ctc ctc gcg gaa gcc	643
His Glu Leu Lys Thr Pro Val Gly Gly Met Ala Leu Leu Ala Glu Ala	
170 175 180	
ctc atg gaa tcc tcc gac gac cca gaa caa gtc gaa tac ttc gga tcc	691
Leu Met Glu Ser Ser Asp Asp Pro Glu Gln Val Glu Tyr Phe Gly Ser	
185 190 195	
agg ctc cac cgc gaa gcc cac cgc atg gcc gac atg atc aac gaa ctg	739
Arg Leu His Arg Glu Ala His Arg Met Ala Asp Met Ile Asn Glu Leu	
200 205 210	
atc tcc ctt tcc aaa ctt cag ggc gcc gaa cga ctc cct gat atg gaa	787
Ile Ser Leu Ser Lys Leu Gln Gly Ala Glu Arg Leu Pro Asp Met Glu	
215 220 225	
ccc gtc cag gct gac gac atc atc agc gaa gcc atc gaa cgc acc caa	835
Pro Val Gln Ala Asp Asp Ile Ile Ser Glu Ala Ile Glu Arg Thr Gln	
230 235 240 245	

ctc gcc gcc gac aac gcc aac atc gaa atc att cgc ggc gac cgc acc 883  
 Leu Ala Ala Asp Asn Ala Asn Ile Glu Ile Ile Arg Gly Asp Arg Thr  
 250 255 260

ggc gtt tgg gta gaa gcc gat cga tcc ctg ctg gtc aca gcc ctg gcg 931  
 Gly Val Trp Val Glu Ala Asp Arg Ser Leu Leu Val Thr Ala Leu Ala  
 265 270 275

aac ctg atc agc aat gca atc aac tac tca cca aaa tca gtc ccc gtc 979  
 Asn Leu Ile Ser Asn Ala Ile Asn Tyr Ser Pro Lys Ser Val Pro Val  
 280 285 290

tcc gtt tca caa agc atc cga aac gac gtg gtc atg atc cga gta acc 1027  
 Ser Val Ser Gln Ser Ile Arg Asn Asp Val Val Met Ile Arg Val Thr  
 295 300 305

gac cgt ggc att ggc atc gca ccc gaa gac caa ggc cga gtt ttc gaa 1075  
 Asp Arg Gly Ile Gly Ile Ala Pro Glu Asp Gln Gly Arg Val Phe Glu  
 310 315 320 325

aga ttc ttc cgc gtc gac aaa gcc cgc tcc cgc caa acc ggc gga act 1123  
 Arg Phe Phe Arg Val Asp Lys Ala Arg Ser Arg Gln Thr Gly Gly Thr  
 330 335 340

ggc ctt ggc ctc gcg ata gtc aaa cat gtc atg gct aac cat ggc ggt 1171  
 Gly Leu Gly Leu Ala Ile Val Lys His Val Met Ala Asn His Gly Gly  
 345 350 355

agt att agt ttg tgg tca cgt cct gga aca ggc tcc aca ttt aca ctt 1219  
 Ser Ile Ser Leu Trp Ser Arg Pro Gly Thr Gly Ser Thr Phe Thr Leu  
 360 365 370

gaa ctc cct gta tac cac cca gag tcc aag gaa ccg gca gga tct aag 1267  
 Glu Leu Pro Val Tyr His Pro Glu Ser Lys Glu Pro Ala Gly Ser Lys  
 375 380 385

cag gga cct agt ttg gat tca cct att cgt acg act gcg tcc aaa gca 1315  
 Gln Gly Pro Ser Leu Asp Ser Pro Ile Arg Thr Thr Ala Ser Lys Ala  
 390 395 400 405

tct ggg cgc cga aag gaa aaa tca tgacgagaat cctgatcggt gaa 1362  
 Ser Gly Arg Arg Lys Glu Lys Ser  
 410

&lt;210&gt; 20

&lt;211&gt; 413

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 20

Val Ser Thr Leu Leu Ala Phe Val Leu Gly Val Val Leu Met Gly Leu  
 1 5 10 15

Ala Leu Pro Ala Tyr Thr Lys Ile Lys Asp Arg Met Arg Arg His Lys  
 20 25 30

Ser Ala Val Thr Leu Ser Glu Asn Gln Val Thr Thr Val Gly Gln Val  
 35 40 45

Leu His Leu Ala Ile Gln Gly Ser Pro Thr Gly Ile Thr Val Val Asp

50					55					60					
Arg	Thr	Gly	Asp	Val	Ile	Leu	Ser	Asn	Gly	Arg	Ala	His	Glu	Leu	Gly
65					70					75					80
Ile	Val	His	Glu	Arg	Ser	Val	Asp	Gly	Asn	Val	Trp	Arg	Val	Ala	Gln
				85					90					95	
Glu	Ala	Phe	Gln	Asp	Gln	Glu	Thr	His	Ser	Leu	Asp	Val	His	Pro	Asp
			100					105					110		
Arg	Asn	Pro	Arg	Arg	Pro	Gly	Ser	Arg	Ile	Thr	Ala	Val	Gln	Ala	Val
		115					120					125			
Val	Lys	Pro	Leu	Thr	Leu	Ile	Asp	Asp	Arg	Phe	Val	Ile	Ile	Tyr	Ala
	130					135					140				
Ser	Asp	Glu	Ser	Glu	Asn	Val	Arg	Met	Glu	Ser	Ala	Arg	Arg	Asp	Phe
145					150					155					160
Val	Ala	Asn	Val	Ser	His	Glu	Leu	Lys	Thr	Pro	Val	Gly	Gly	Met	Ala
				165					170					175	
Leu	Leu	Ala	Glu	Ala	Leu	Met	Glu	Ser	Ser	Asp	Asp	Pro	Glu	Gln	Val
			180					185					190		
Glu	Tyr	Phe	Gly	Ser	Arg	Leu	His	Arg	Glu	Ala	His	Arg	Met	Ala	Asp
		195					200					205			
Met	Ile	Asn	Glu	Leu	Ile	Ser	Leu	Ser	Lys	Leu	Gln	Gly	Ala	Glu	Arg
	210					215					220				
Leu	Pro	Asp	Met	Glu	Pro	Val	Gln	Ala	Asp	Asp	Ile	Ile	Ser	Glu	Ala
225					230					235					240
Ile	Glu	Arg	Thr	Gln	Leu	Ala	Ala	Asp	Asn	Ala	Asn	Ile	Glu	Ile	Ile
				245					250					255	
Arg	Gly	Asp	Arg	Thr	Gly	Val	Trp	Val	Glu	Ala	Asp	Arg	Ser	Leu	Leu
			260					265					270		
Val	Thr	Ala	Leu	Ala	Asn	Leu	Ile	Ser	Asn	Ala	Ile	Asn	Tyr	Ser	Pro
		275					280					285			
Lys	Ser	Val	Pro	Val	Ser	Val	Ser	Gln	Ser	Ile	Arg	Asn	Asp	Val	Val
	290					295					300				
Met	Ile	Arg	Val	Thr	Asp	Arg	Gly	Ile	Gly	Ile	Ala	Pro	Glu	Asp	Gln
305					310					315					320
Gly	Arg	Val	Phe	Glu	Arg	Phe	Phe	Arg	Val	Asp	Lys	Ala	Arg	Ser	Arg
				325					330					335	
Gln	Thr	Gly	Gly	Thr	Gly	Leu	Gly	Leu	Ala	Ile	Val	Lys	His	Val	Met
			340					345					350		
Ala	Asn	His	Gly	Gly	Ser	Ile	Ser	Leu	Trp	Ser	Arg	Pro	Gly	Thr	Gly
		355					360					365			
Ser	Thr	Phe	Thr	Leu	Glu	Leu	Pro	Val	Tyr	His	Pro	Glu	Ser	Lys	Glu
				370		375					380				



Pro Ala Gly Ser Lys Gln Gly Pro Ser Leu Asp Ser Pro Ile Arg Thr  
 385 390 395 400

Thr Ala Ser Lys Ala Ser Gly Arg Arg Lys Glu Lys Ser  
 405 410

<210> 21

<211> 1362

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1339)

<223> FRXA02493

<400> 21

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gcagcagtag caaaccaggg taataagtag ctattttagtag gtg agc act ctt ctt 115  
 Val Ser Thr Leu Leu  
 1 5

gct ttc gta ttg ggc gtg gtc ctc atg ggc ctc gcc cta cct gcg tat 163  
 Ala Phe Val Leu Gly Val Val Leu Met Gly Leu Ala Leu Pro Ala Tyr  
 10 15 20

acg aaa att aaa gat cgg atg cgt cgc cac aag tcc gcg gtc acc ctg 211  
 Thr Lys Ile Lys Asp Arg Met Arg Arg His Lys Ser Ala Val Thr Leu  
 25 30 35

tcc gaa aac cag gtc acc acg gtg ggg cag gtc ctc cac ctg gcg att 259  
 Ser Glu Asn Gln Val Thr Thr Val Gly Gln Val Leu His Leu Ala Ile  
 40 45 50

caa ggc tcc cca acg gga atc acg gtt gtc gat cgc acc ggc gac gtc 307  
 Gln Gly Ser Pro Thr Gly Ile Thr Val Val Asp Arg Thr Gly Asp Val  
 55 60 65

atc tta tcc aac ggc cgc gcc cac gaa ttg ggc atc gtc cac gaa aga 355  
 Ile Leu Ser Asn Gly Arg Ala His Glu Leu Gly Ile Val His Glu Arg  
 70 75 80 85

tcc gtc gac ggc aac gtt tgg cgc gtc gcc cag gaa gcc ttc caa gac 403  
 Ser Val Asp Gly Asn Val Trp Arg Val Ala Gln Glu Ala Phe Gln Asp  
 90 95 100

caa gaa acc cac tca ctc gac gtc cac cca gac cgc aat ccg cgg cgc 451  
 Gln Glu Thr His Ser Leu Asp Val His Pro Asp Arg Asn Pro Arg Arg  
 105 110 115

ccg ggt agt cgc atc acc gca gtg cag gca gtg gtc aag cct tta acg 499  
 Pro Gly Ser Arg Ile Thr Ala Val Gln Ala Val Val Lys Pro Leu Thr  
 120 125 130

ctt atc gac gat cgt ttc gtg atc atc tat gcc tcc gac gaa tcc gaa 547  
 Leu Ile Asp Asp Arg Phe Val Ile Ile Tyr Ala Ser Asp Glu Ser Glu  
 135 140 145

aac gtg cgc atg gaa tcg gca cgc cga gac ttc gtc gca aac gtc tcc	595
Asn Val Arg Met Glu Ser Ala Arg Arg Asp Phe Val Ala Asn Val Ser	
150 155 160 165	
cac gaa ctg aaa acc ccc gtc ggc ggc atg gca ctc ctc gcg gaa gcc	643
His Glu Leu Lys Thr Pro Val Gly Gly Met Ala Leu Leu Ala Glu Ala	
170 175 180	
ctc atg gaa tcc tcc gac gac cca gaa caa gtc gaa tac ttc gga tcc	691
Leu Met Glu Ser Ser Asp Asp Pro Glu Gln Val Glu Tyr Phe Gly Ser	
185 190 195	
agg ctc cac cgc gaa gcc cac cgc atg gcc gac atg atc aac gaa ctg	739
Arg Leu His Arg Glu Ala His Arg Met Ala Asp Met Ile Asn Glu Leu	
200 205 210	
atc tcc ctt tcc aaa ctt cag ggc gcc gaa cga ctc cct gat atg gaa	787
Ile Ser Leu Ser Lys Leu Gln Gly Ala Glu Arg Leu Pro Asp Met Glu	
215 220 225	
ccc gtc cag gct gac gac atc atc agc gaa gcc atc gaa cgc acc caa	835
Pro Val Gln Ala Asp Asp Ile Ile Ser Glu Ala Ile Glu Arg Thr Gln	
230 235 240 245	
ctc gcc gcc gac aac gcc aac atc gaa atc att cgc ggc gac cgc acc	883
Leu Ala Ala Asp Asn Ala Asn Ile Glu Ile Ile Arg Gly Asp Arg Thr	
250 255 260	
ggc gtt tgg gta gaa gcc gat cga tcc ctg ctg gtc aca gcc ctg gcg	931
Gly Val Trp Val Glu Ala Asp Arg Ser Leu Leu Val Thr Ala Leu Ala	
265 270 275	
aac ctg atc agc aat gca atc aac tac tca cca aaa tca gtc ccc gtc	979
Asn Leu Ile Ser Asn Ala Ile Asn Tyr Ser Pro Lys Ser Val Pro Val	
280 285 290	
tcc gtt tca caa agc atc cga aac gac gtg gtc atg atc cga gta acc	1027
Ser Val Ser Gln Ser Ile Arg Asn Asp Val Val Met Ile Arg Val Thr	
295 300 305	
gac cgt ggc att ggc atc gca ccc gaa gac caa ggc cga gtt ttc gaa	1075
Asp Arg Gly Ile Gly Ile Ala Pro Glu Asp Gln Gly Arg Val Phe Glu	
310 315 320 325	
aga ttc ttc cgc gtc gac aaa gcc cgc tcc cgc caa acc ggc gga act	1123
Arg Phe Phe Arg Val Asp Lys Ala Arg Ser Arg Gln Thr Gly Gly Thr	
330 335 340	
ggc ctt ggc ctc gcg ata gtc aaa cat gtc atg gct aac cat ggc ggt	1171
Gly Leu Gly Leu Ala Ile Val Lys His Val Met Ala Asn His Gly Gly	
345 350 355	
agt att agt ttg tgg tca cgt cct gga aca ggc tcc aca ttt aca ctt	1219
Ser Ile Ser Leu Trp Ser Arg Pro Gly Thr Gly Ser Thr Phe Thr Leu	
360 365 370	
gaa ctc cct gta tac cac cca gag tcc aag gaa ccg gca gga tct aag	1267
Glu Leu Pro Val Tyr His Pro Glu Ser Lys Glu Pro Ala Gly Ser Lys	
375 380 385	
cag gga cct agt ttg gat tca cct att cgt acg act gcg tcc aaa gca	1315

Gln Gly Pro Ser Leu Asp Ser Pro Ile Arg Thr Thr Ala Ser Lys Ala  
 390 395 400 405

tct ggg cgc cga aag gaa aaa tca tgacgagaat cctgacggtt gaa 1362  
 Ser Gly Arg Arg Lys Glu Lys Ser  
 410

<210> 22

<211> 413

<212> PRT

<213> Corynebacterium glutamicum

<400> 22

Val Ser Thr Leu Leu Ala Phe Val Leu Gly Val Val Leu Met Gly Leu  
 1 5 10 15

Ala Leu Pro Ala Tyr Thr Lys Ile Lys Asp Arg Met Arg Arg His Lys  
 20 25 30

Ser Ala Val Thr Leu Ser Glu Asn Gln Val Thr Thr Val Gly Gln Val  
 35 40 45

Leu His Leu Ala Ile Gln Gly Ser Pro Thr Gly Ile Thr Val Val Asp  
 50 55 60

Arg Thr Gly Asp Val Ile Leu Ser Asn Gly Arg Ala His Glu Leu Gly  
 65 70 75 80

Ile Val His Glu Arg Ser Val Asp Gly Asn Val Trp Arg Val Ala Gln  
 85 90 95

Glu Ala Phe Gln Asp Gln Glu Thr His Ser Leu Asp Val His Pro Asp  
 100 105 110

Arg Asn Pro Arg Arg Pro Gly Ser Arg Ile Thr Ala Val Gln Ala Val  
 115 120 125

Val Lys Pro Leu Thr Leu Ile Asp Asp Arg Phe Val Ile Ile Tyr Ala  
 130 135 140

Ser Asp Glu Ser Glu Asn Val Arg Met Glu Ser Ala Arg Arg Asp Phe  
 145 150 155 160

Val Ala Asn Val Ser His Glu Leu Lys Thr Pro Val Gly Gly Met Ala  
 165 170 175

Leu Leu Ala Glu Ala Leu Met Glu Ser Ser Asp Asp Pro Glu Gln Val  
 180 185 190

Glu Tyr Phe Gly Ser Arg Leu His Arg Glu Ala His Arg Met Ala Asp  
 195 200 205

Met Ile Asn Glu Leu Ile Ser Leu Ser Lys Leu Gln Gly Ala Glu Arg  
 210 215 220

Leu Pro Asp Met Glu Pro Val Gln Ala Asp Asp Ile Ile Ser Glu Ala  
 225 230 235 240

Ile Glu Arg Thr Gln Leu Ala Ala Asp Asn Ala Asn Ile Glu Ile Ile  
 245 250 255

Arg Gly Asp Arg Thr Gly Val Trp Val Glu Ala Asp Arg Ser Leu Leu  
 260 265 270  
 Val Thr Ala Leu Ala Asn Leu Ile Ser Asn Ala Ile Asn Tyr Ser Pro  
 275 280 285  
 Lys Ser Val Pro Val Ser Val Ser Gln Ser Ile Arg Asn Asp Val Val  
 290 295 300  
 Met Ile Arg Val Thr Asp Arg Gly Ile Gly Ile Ala Pro Glu Asp Gln  
 305 310 315 320  
 Gly Arg Val Phe Glu Arg Phe Phe Arg Val Asp Lys Ala Arg Ser Arg  
 325 330 335  
 Gln Thr Gly Gly Thr Gly Leu Gly Leu Ala Ile Val Lys His Val Met  
 340 345 350  
 Ala Asn His Gly Gly Ser Ile Ser Leu Trp Ser Arg Pro Gly Thr Gly  
 355 360 365  
 Ser Thr Phe Thr Leu Glu Leu Pro Val Tyr His Pro Glu Ser Lys Glu  
 370 375 380  
 Pro Ala Gly Ser Lys Gln Gly Pro Ser Leu Asp Ser Pro Ile Arg Thr  
 385 390 395 400  
 Thr Ala Ser Lys Ala Ser Gly Arg Arg Lys Glu Lys Ser  
 405 410

&lt;210&gt; 23

&lt;211&gt; 1578

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1555)

&lt;223&gt; RXN00631

&lt;400&gt; 23

cctacctgcg ccgcaagggtg gacacccagg atccgcagct aattcagact gttcgtggcg 60

ttggatatgt tctgcgcacc ccacgtagct aaattctcct atg gaa aat cct tat 115  
 Met Glu Asn Pro Tyr  
 1 5

gtt gct gcg ctc gat gac gaa aac caa gaa gtc ggc gta aaa aaa gaa 163  
 Val Ala Ala Leu Asp Asp Glu Asn Gln Glu Val Gly Val Lys Lys Glu  
 10 15 20

gca gaa aaa gaa cct gaa ata ggt ccc atc aga gct gcc gga cga gcc 211  
 Ala Glu Lys Glu Pro Glu Ile Gly Pro Ile Arg Ala Ala Gly Arg Ala  
 25 30 35

ata ccg ctg cgc acc cgc atc att ttg atc gtg gtg ggt atc gcc ggg 259  
 Ile Pro Leu Arg Thr Arg Ile Ile Leu Ile Val Val Gly Ile Ala Gly  
 40 45 50

ctt ggt ttg ctg gtc aac gcg att gct gtc tcc agc ctc atg cgt gaa	307
Leu Gly Leu Leu Val Asn Ala Ile Ala Val Ser Ser Leu Met Arg Glu	
55 60 65	
ggt tcc tat acc cgc atg gat caa gag cta gag acc tcg atg ggg acg	355
Val Ser Tyr Thr Arg Met Asp Gln Glu Leu Glu Thr Ser Met Gly Thr	
70 75 80 85	
tgg gcg cat aac gtt gag ctg ttt aat ttc gat ggc gtc cgc caa ggg	403
Trp Ala His Asn Val Glu Leu Phe Asn Phe Asp Gly Val Arg Gln Gly	
90 95 100	
cca ccc agc gat tat tat gtg gcc aag gtt ttt cct gat gga tcc agc	451
Pro Pro Ser Asp Tyr Tyr Val Ala Lys Val Phe Pro Asp Gly Ser Ser	
105 110 115	
atc atc ttc aac gat gca caa tcg gca ccc gat cta gct gaa acc acc	499
Ile Ile Phe Asn Asp Ala Gln Ser Ala Pro Asp Leu Ala Glu Thr Thr	
120 125 130	
atc ggt act ggt cca cac act gtg gat gct gct agc ggt tct gcc tcc	547
Ile Gly Thr Gly Pro His Thr Val Asp Ala Ala Ser Gly Ser Ala Ser	
135 140 145	
aac act ccg tgg cgt gtg atg gcg gaa aag aac ggt gac att atc acc	595
Asn Thr Pro Trp Arg Val Met Ala Glu Lys Asn Gly Asp Ile Ile Thr	
150 155 160 165	
gtg gtg ggt aaa agc atg ggg cgt gaa aca aac ctg ctg tac cga ttg	643
Val Val Gly Lys Ser Met Gly Arg Glu Thr Asn Leu Leu Tyr Arg Leu	
170 175 180	
gtg atg gtg cag atg atc atc ggc gcg ctg att ctg gtt gct att ttg	691
Val Met Val Gln Met Ile Ile Gly Ala Leu Ile Leu Val Ala Ile Leu	
185 190 195	
att act tca ctc ttc cta gtc aga cgc tcg ttg cgg ccg ttg aga gaa	739
Ile Thr Ser Leu Phe Leu Val Arg Arg Ser Leu Arg Pro Leu Arg Glu	
200 205 210	
ggt gaa gag acc gcc acc agg att gcg ggc ggt gat ttg gat cga cgt	787
Val Glu Glu Thr Ala Thr Arg Ile Ala Gly Gly Asp Leu Asp Arg Arg	
215 220 225	
gtc ccg cag tgg cca atg acc aca gaa gtc gga cag ctg tcg aat gcc	835
Val Pro Gln Trp Pro Met Thr Thr Glu Val Gly Gln Leu Ser Asn Ala	
230 235 240 245	
ctc aat atc atg ttg gag cag ctc caa gcc tca att ctg acc gcc cag	883
Leu Asn Ile Met Leu Glu Gln Leu Gln Ala Ser Ile Leu Thr Ala Gln	
250 255 260	
caa aaa gaa gct cag atg cgc cga ttc gtt ggc gat gcc tcc cac gag	931
Gln Lys Glu Ala Gln Met Arg Arg Phe Val Gly Asp Ala Ser His Glu	
265 270 275	
ctc cgc aca cca ctg acc tct gtg aag ggc ttc acc gag ctg tat tca	979
Leu Arg Thr Pro Leu Thr Ser Val Lys Gly Phe Thr Glu Leu Tyr Ser	
280 285 290	
tca ggt gca aca gat gat gcc aac tgg gtc atg tcc aag atc ggt ggc	1027

Ser Gly Ala Thr Asp Asp Ala Asn Trp Val Met Ser Lys Ile Gly Gly  
 295 300 305  
 gaa gcc caa cgc atg agt gtg ctt gtg gaa gac ctc ctg tca ctg acg 1075  
 Glu Ala Gln Arg Met Ser Val Leu Val Glu Asp Leu Leu Ser Leu Thr  
 310 315 320 325  
 cgt gcc gaa ggc cag caa atg gag aag cac cgc gtt gac gtg ctg gaa 1123  
 Arg Ala Glu Gly Gln Gln Met Glu Lys His Arg Val Asp Val Leu Glu  
 330 335 340  
 ctc gcc ttg gca gta cgc gga tcc atg cga gca gcc tgg cca gat cgc 1171  
 Leu Ala Leu Ala Val Arg Gly Ser Met Arg Ala Ala Trp Pro Asp Arg  
 345 350 355  
 aca gtc aat gta tcc aac aaa gct gag tcc att ccg gtt gtc aaa ggc 1219  
 Thr Val Asn Val Ser Asn Lys Ala Glu Ser Ile Pro Val Val Lys Gly  
 360 365 370  
 gac cca act cgc ctc cac caa gtg ctt acc aac ctg gtt gcc aac gga 1267  
 Asp Pro Thr Arg Leu His Gln Val Leu Thr Asn Leu Val Ala Asn Gly  
 375 380 385  
 cta aac cac ggc gga ccg gac gcg gaa gtc agc att gag atc aac acc 1315  
 Leu Asn His Gly Gly Pro Asp Ala Glu Val Ser Ile Glu Ile Asn Thr  
 390 395 400 405  
 gat gga caa aac gtg agg att ctc gtg gca gac aac ggt gtc gga atg 1363  
 Asp Gly Gln Asn Val Arg Ile Leu Val Ala Asp Asn Gly Val Gly Met  
 410 415 420  
 tct gaa gaa gat gct cag cat atc ttc gag cgt ttc tac cgc gcc gat 1411  
 Ser Glu Glu Asp Ala Gln His Ile Phe Glu Arg Phe Tyr Arg Ala Asp  
 425 430 435  
 tcc tcc cgc tca cgc gca tcc ggc gga tcg ggc ctc ggc ctt gcg atc 1459  
 Ser Ser Arg Ser Arg Ala Ser Gly Gly Ser Gly Leu Gly Leu Ala Ile  
 440 445 450  
 acg aaa tcc ctg gtc gaa ggc cac ggc ggc aca gtc acc gtc gac agc 1507  
 Thr Lys Ser Leu Val Glu His Gly Gly Thr Val Thr Val Asp Ser  
 455 460 465  
 gtg caa ggc gaa ggc acg gtg ttc acg atc acc ttg ccg gcg gtt tct 1555  
 Val Gln Gly Glu Gly Thr Val Phe Thr Ile Thr Leu Pro Ala Val Ser  
 470 475 480 485  
 taaaggcatc aagggccgga aaa 1578

&lt;210&gt; 24

&lt;211&gt; 485

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 24

Met Glu Asn Pro Tyr Val Ala Ala Leu Asp Asp Glu Asn Gln Glu Val  
 1 5 10 15

Gly Val Lys Lys Glu Ala Glu Lys Glu Pro Glu Ile Gly Pro Ile Arg  
 20 25 30

Ala Ala Gly Arg Ala Ile Pro Leu Arg Thr Arg Ile Ile Leu Ile Val  
 35 40 45  
 Val Gly Ile Ala Gly Leu Gly Leu Leu Val Asn Ala Ile Ala Val Ser  
 50 55 60  
 Ser Leu Met Arg Glu Val Ser Tyr Thr Arg Met Asp Gln Glu Leu Glu  
 65 70 75 80  
 Thr Ser Met Gly Thr Trp Ala His Asn Val Glu Leu Phe Asn Phe Asp  
 85 90 95  
 Gly Val Arg Gln Gly Pro Pro Ser Asp Tyr Tyr Val Ala Lys Val Phe  
 100 105 110  
 Pro Asp Gly Ser Ser Ile Ile Phe Asn Asp Ala Gln Ser Ala Pro Asp  
 115 120 125  
 Leu Ala Glu Thr Thr Ile Gly Thr Gly Pro His Thr Val Asp Ala Ala  
 130 135 140  
 Ser Gly Ser Ala Ser Asn Thr Pro Trp Arg Val Met Ala Glu Lys Asn  
 145 150 155 160  
 Gly Asp Ile Ile Thr Val Val Gly Lys Ser Met Gly Arg Glu Thr Asn  
 165 170 175  
 Leu Leu Tyr Arg Leu Val Met Val Gln Met Ile Ile Gly Ala Leu Ile  
 180 185 190  
 Leu Val Ala Ile Leu Ile Thr Ser Leu Phe Leu Val Arg Arg Ser Leu  
 195 200 205  
 Arg Pro Leu Arg Glu Val Glu Glu Thr Ala Thr Arg Ile Ala Gly Gly  
 210 215 220  
 Asp Leu Asp Arg Arg Val Pro Gln Trp Pro Met Thr Thr Glu Val Gly  
 225 230 235 240  
 Gln Leu Ser Asn Ala Leu Asn Ile Met Leu Glu Gln Leu Gln Ala Ser  
 245 250 255  
 Ile Leu Thr Ala Gln Gln Lys Glu Ala Gln Met Arg Arg Phe Val Gly  
 260 265 270  
 Asp Ala Ser His Glu Leu Arg Thr Pro Leu Thr Ser Val Lys Gly Phe  
 275 280 285  
 Thr Glu Leu Tyr Ser Ser Gly Ala Thr Asp Asp Ala Asn Trp Val Met  
 290 295 300  
 Ser Lys Ile Gly Gly Glu Ala Gln Arg Met Ser Val Leu Val Glu Asp  
 305 310 315 320  
 Leu Leu Ser Leu Thr Arg Ala Glu Gly Gln Gln Met Glu Lys His Arg  
 325 330 335  
 Val Asp Val Leu Glu Leu Ala Leu Ala Val Arg Gly Ser Met Arg Ala  
 340 345 350

Ala Trp Pro Asp Arg Thr Val Asn Val Ser Asn Lys Ala Glu Ser Ile  
 355 360 365

Pro Val Val Lys Gly Asp Pro Thr Arg Leu His Gln Val Leu Thr Asn  
 370 375 380

Leu Val Ala Asn Gly Leu Asn His Gly Gly Pro Asp Ala Glu Val Ser  
 385 390 395 400

Ile Glu Ile Asn Thr Asp Gly Gln Asn Val Arg Ile Leu Val Ala Asp  
 405 410 415

Asn Gly Val Gly Met Ser Glu Glu Asp Ala Gln His Ile Phe Glu Arg  
 420 425 430

Phe Tyr Arg Ala Asp Ser Ser Arg Ser Arg Ala Ser Gly Gly Ser Gly  
 435 440 445

Leu Gly Leu Ala Ile Thr Lys Ser Leu Val Glu Gly His Gly Gly Thr  
 450 455 460

Val Thr Val Asp Ser Val Gln Gly Glu Gly Thr Val Phe Thr Ile Thr  
 465 470 475 480

Leu Pro Ala Val Ser  
 485

<210> 25  
 <211> 1606  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (12)..(1583)  
 <223> RXN00291

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 Val Ala Thr Val Ala Leu Val Val Ala Ile Cys Thr Gly  
 1 5 10

att ttc gca gtt ttg atg atg gat cag atg aaa act gag gcc gag cac 98  
 Ile Phe Ala Val Leu Met Met Asp Gln Met Lys Thr Glu Ala Glu His  
 15 20 25

aca gcg ctg tcc atc gga cgt tgg gtg gca tcc aac ccg cag atc cgc 146  
 Thr Ala Leu Ser Ile Gly Arg Trp Val Ala Ser Asn Pro Gln Ile Arg  
 30 35 40 45

gag gaa gta gcg ctt gat act caa aca gga gca aac cca tcg gcc gaa 194  
 Glu Glu Val Ala Leu Asp Thr Gln Thr Gly Ala Asn Pro Ser Ala Glu  
 50 55 60

gaa tta gcc gat gga gat atc caa gcg gtt gca cag gcg gcc aat gaa 242  
 Glu Leu Ala Asp Gly Asp Ile Gln Ala Val Ala Gln Ala Ala Asn Glu  
 65 70 75

cgc act gga gct ttg ttt gtc gtt atc act gac ggt tta ggt atc cgc 290  
 Arg Thr Gly Ala Leu Phe Val Val Ile Thr Asp Gly Leu Gly Ile Arg



80	85	90	
ctg tcc cac cca gat gag gaa cgt ctg ggg gag cag gtg agc act agc Leu Ser His Pro Asp Glu Glu Arg Leu Gly Glu Gln Val Ser Thr Ser 95 100 105			338
ttt gag gct gcc atg cgg ggt gaa gaa acc atg gcg tgg gag act ggg Phe Glu Ala Ala Met Arg Gly Glu Glu Thr Met Ala Trp Glu Thr Gly 110 115 120 125			386
acc ctc ggt gcg tcc gcg cga gca aaa gtg cct atc ttt gcg ccg gat Thr Leu Gly Ala Ser Ala Arg Ala Lys Val Pro Ile Phe Ala Pro Asp 130 135 140			434
tct agt gtt cca gtc ggt gag gtc agt gtt ggg ttt gag cga gac agt Ser Ser Val Pro Val Gly Glu Val Ser Val Gly Phe Glu Arg Asp Ser 145 150 155			482
gtg tat tcc cgc ctg ccc atg ttc ctc gcc gcc ctt gct ctt att tct Val Tyr Ser Arg Leu Pro Met Phe Leu Ala Ala Leu Ala Leu Ile Ser 160 165 170			530
gtg ttg gga atc ctt atc ggc gtg ggt gta gcc atg ggc atg cga cgc Val Leu Gly Ile Leu Ile Gly Val Gly Val Ala Met Gly Met Arg Arg 175 180 185			578
cgt tgg gaa cgc gtg acc ttg ggt ttg cag ccg gag gag cta gtg acc Arg Trp Glu Arg Val Thr Leu Gly Leu Gln Pro Glu Glu Leu Val Thr 190 195 200 205			626
ctt gtg caa aat cag act gca gtc atc gat ggc att gat gag ggc gtg Leu Val Gln Asn Gln Thr Ala Val Ile Asp Gly Ile Asp Glu Gly Val 210 215 220			674
ctg gcg ctg agc cca aac gga aca att ggg gtg cat aat gag cag gcg Leu Ala Leu Ser Pro Asn Gly Thr Ile Gly Val His Asn Glu Gln Ala 225 230 235			722
caa tcc atg att ggt gca ggt cct atg agt ggc agg acg ttg aaa gaa Gln Ser Met Ile Gly Ala Gly Pro Met Ser Gly Arg Thr Leu Lys Glu 240 245 250			770
cta ggg ctt gac ctg ggt ctt gat ggc gtt gta ttg cat ggt cag cat Leu Gly Leu Asp Leu Gly Leu Asp Gly Val Val Leu His Gly Gln His 255 260 265			818
ccg gaa acc gtt gcc cat aac ggc agg atc ctc tat ctg gat ttc cac Pro Glu Thr Val Ala His Asn Gly Arg Ile Leu Tyr Leu Asp Phe His 270 275 280 285			866
ccc gtg cgc cgt ggg gat caa gat tta ggc tac gtg gta acc atc cgc Pro Val Arg Arg Gly Asp Gln Asp Leu Gly Tyr Val Val Thr Ile Arg 290 295 300			914
gat cgt acc gac atc att gaa ctc agt gaa cgc ctc gac tct gtg cgc Asp Arg Thr Asp Ile Ile Glu Leu Ser Glu Arg Leu Asp Ser Val Arg 305 310 315			962
acc atg acc cac gca ctc cgc gcc cag cgc cac gag ttt gcc aac cgc Thr Met Thr His Ala Leu Arg Ala Gln Arg His Glu Phe Ala Asn Arg 320 325 330			1010

atc cac acc gca aca ggg ctt atc gac gcc ggc cgc gtc cac gac gcg 1058  
 Ile His Thr Ala Thr Gly Leu Ile Asp Ala Gly Arg Val His Asp Ala  
 335 340 345  
 gca gag ttt cta ggc gat ata tcc cgc aac ggg gga cag tca cat cca 1106  
 Ala Glu Phe Leu Gly Asp Ile Ser Arg Asn Gly Gly Gln Ser His Pro  
 350 355 360 365  
 ttg atc gga tca gcg cac ctc aat gaa gca ttt ttg agc tca ttt tta 1154  
 Leu Ile Gly Ser Ala His Leu Asn Glu Ala Phe Leu Ser Ser Phe Leu  
 370 375 380  
 agt act gct tct att tcg gca tct gaa aag ggc gtt agt ctg cgc atc 1202  
 Ser Thr Ala Ser Ile Ser Ala Ser Glu Lys Gly Val Ser Leu Arg Ile  
 385 390 395  
 aac tct gac acg ctc atc ctt ggc act gtt aaa gat cca gaa gat gta 1250  
 Asn Ser Asp Thr Leu Ile Leu Gly Thr Val Lys Asp Pro Glu Asp Val  
 400 405 410  
 gca acc att ttg ggt aat tta atc aac aat gcc atc gac gcc gcg gtg 1298  
 Ala Thr Ile Leu Gly Asn Leu Ile Asn Asn Ala Ile Asp Ala Ala Val  
 415 420 425  
 gca ggt gaa gcc cca cgg tgg att gag ctt acg ttg atg gat gat gcc 1346  
 Ala Gly Glu Ala Pro Arg Trp Ile Glu Leu Thr Leu Met Asp Asp Ala  
 430 435 440 445  
 gat acg ctg gtc att tct gtt gca gat tct ggt cct gga atc cca gag 1394  
 Asp Thr Leu Val Ile Ser Val Ala Asp Ser Gly Pro Gly Ile Pro Glu  
 450 455 460  
 ggc gtg gat gta ttt gcc aca gcc acc cag ata gga gac tct gaa gat 1442  
 Gly Val Asp Val Phe Ala Thr Ala Thr Gln Ile Gly Asp Ser Glu Asp  
 465 470 475  
 aat gaa cgc acc cac ggg cat ggc att ggt cta aaa ctg tgc cgg gct 1490  
 Asn Glu Arg Thr His Gly His Gly Ile Gly Leu Lys Leu Cys Arg Ala  
 480 485 490  
 ttg gct aga tca cat ggt ggc gat gtc tgg gtg att gat aga gga acc 1538  
 Leu Ala Arg Ser His Gly Gly Asp Val Trp Val Ile Asp Arg Gly Thr  
 495 500 505  
 gaa gat ggc gct gta ttt gga gtg aaa cta ccg gga gta atg gag 1583  
 Glu Asp Gly Ala Val Phe Gly Val Lys Leu Pro Gly Val Met Glu  
 510 515 520  
 taatggatca aacacttaaa gtt 1606

&lt;210&gt; 26

&lt;211&gt; 524

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 26

Val Ala Thr Val Ala Leu Val Val Ala Ile Cys Thr Gly Ile Phe Ala  
 1 5 10 15

Val Leu Met Met Asp Gln Met Lys Thr Glu Ala Glu His Thr Ala Leu  
                     20                                    25                                    30  
 Ser Ile Gly Arg Trp Val Ala Ser Asn Pro Gln Ile Arg Glu Glu Val  
                     35                                    40                                    45  
 Ala Leu Asp Thr Gln Thr Gly Ala Asn Pro Ser Ala Glu Glu Leu Ala  
                     50                                    55                                    60  
 Asp Gly Asp Ile Gln Ala Val Ala Gln Ala Ala Asn Glu Arg Thr Gly  
                     65                                    70                                    75                                    80  
 Ala Leu Phe Val Val Ile Thr Asp Gly Leu Gly Ile Arg Leu Ser His  
                                     85                                    90                                    95  
 Pro Asp Glu Glu Arg Leu Gly Glu Gln Val Ser Thr Ser Phe Glu Ala  
                     100                                    105                                    110  
 Ala Met Arg Gly Glu Glu Thr Met Ala Trp Glu Thr Gly Thr Leu Gly  
                     115                                    120                                    125  
 Ala Ser Ala Arg Ala Lys Val Pro Ile Phe Ala Pro Asp Ser Ser Val  
                     130                                    135                                    140  
 Pro Val Gly Glu Val Ser Val Gly Phe Glu Arg Asp Ser Val Tyr Ser  
 145                                    150                                    155                                    160  
 Arg Leu Pro Met Phe Leu Ala Ala Leu Ala Leu Ile Ser Val Leu Gly  
                                     165                                    170                                    175  
 Ile Leu Ile Gly Val Gly Val Ala Met Gly Met Arg Arg Arg Trp Glu  
                     180                                    185                                    190  
 Arg Val Thr Leu Gly Leu Gln Pro Glu Glu Leu Val Thr Leu Val Gln  
                     195                                    200                                    205  
 Asn Gln Thr Ala Val Ile Asp Gly Ile Asp Glu Gly Val Leu Ala Leu  
                     210                                    215                                    220  
 Ser Pro Asn Gly Thr Ile Gly Val His Asn Glu Gln Ala Gln Ser Met  
 225                                    230                                    235                                    240  
 Ile Gly Ala Gly Pro Met Ser Gly Arg Thr Leu Lys Glu Leu Gly Leu  
                     245                                    250                                    255  
 Asp Leu Gly Leu Asp Gly Val Val Leu His Gly Gln His Pro Glu Thr  
                     260                                    265                                    270  
 Val Ala His Asn Gly Arg Ile Leu Tyr Leu Asp Phe His Pro Val Arg  
                     275                                    280                                    285  
 Arg Gly Asp Gln Asp Leu Gly Tyr Val Val Thr Ile Arg Asp Arg Thr  
                     290                                    295                                    300  
 Asp Ile Ile Glu Leu Ser Glu Arg Leu Asp Ser Val Arg Thr Met Thr  
 305                                    310                                    315                                    320  
 His Ala Leu Arg Ala Gln Arg His Glu Phe Ala Asn Arg Ile His Thr  
                     325                                    330                                    335  
 Ala Thr Gly Leu Ile Asp Ala Gly Arg Val His Asp Ala Ala Glu Phe

340										345					350				
Leu	Gly	Asp	Ile	Ser	Arg	Asn	Gly	Gly	Gln	Ser	His	Pro	Leu	Ile	Gly				
		355					360					365							
Ser	Ala	His	Leu	Asn	Glu	Ala	Phe	Leu	Ser	Ser	Phe	Leu	Ser	Thr	Ala				
		370				375					380								
Ser	Ile	Ser	Ala	Ser	Glu	Lys	Gly	Val	Ser	Leu	Arg	Ile	Asn	Ser	Asp				
		385			390					395					400				
Thr	Leu	Ile	Leu	Gly	Thr	Val	Lys	Asp	Pro	Glu	Asp	Val	Ala	Thr	Ile				
			405						410					415					
Leu	Gly	Asn	Leu	Ile	Asn	Asn	Ala	Ile	Asp	Ala	Ala	Val	Ala	Gly	Glu				
		420						425					430						
Ala	Pro	Arg	Trp	Ile	Glu	Leu	Thr	Leu	Met	Asp	Asp	Ala	Asp	Thr	Leu				
		435					440					445							
Val	Ile	Ser	Val	Ala	Asp	Ser	Gly	Pro	Gly	Ile	Pro	Glu	Gly	Val	Asp				
		450				455					460								
Val	Phe	Ala	Thr	Ala	Thr	Gln	Ile	Gly	Asp	Ser	Glu	Asp	Asn	Glu	Arg				
		465			470					475					480				
Thr	His	Gly	His	Gly	Ile	Gly	Leu	Lys	Leu	Cys	Arg	Ala	Leu	Ala	Arg				
			485					490						495					
Ser	His	Gly	Gly	Asp	Val	Trp	Val	Ile	Asp	Arg	Gly	Thr	Glu	Asp	Gly				
		500						505					510						
Ala	Val	Phe	Gly	Val	Lys	Leu	Pro	Gly	Val	Met	Glu								
		515					520												

<210> 27  
 <211> 1097  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(1074)  
 <223> FRXA00291

<400> 27																
gcc	gcc	ctt	gct	ctt	att	tct	gtg	ttg	gga	atc	ctt	atc	ggc	gtg	ggt	48
Ala	Ala	Leu	Ala	Leu	Ile	Ser	Val	Leu	Gly	Ile	Leu	Ile	Gly	Val	Gly	
1				5					10					15		
gta gcc atg ggc atg cga cgc cgt tgg gaa cgc gtg acc ttg ggt ttg																96
Val	Ala	Met	Gly	Met	Arg	Arg	Arg	Trp	Glu	Arg	Val	Thr	Leu	Gly	Leu	
			20					25					30			
cag ccg gag gag cta gtg acc ctt gtg caa aat cag act gca gtc atc																144
Gln	Pro	Glu	Glu	Leu	Val	Thr	Leu	Val	Gln	Asn	Gln	Thr	Ala	Val	Ile	
		35					40					45				
gat ggc att gat gag ggc gtg ctg gcg ctg agc cca aac gga aca att																192
Asp	Gly	Ile	Asp	Glu	Gly	Val	Leu	Ala	Leu	Ser	Pro	Asn	Gly	Thr	Ile	

50	55	60	
ggg gtg cat aat gag cag gcg caa tcc atg att ggt gca ggt cct atg Gly Val His Asn Glu Gln Ala Gln Ser Met Ile Gly Ala Gly Pro Met 65 70 75 80			240
agt ggc agg acg ttg aaa gaa cta ggg ctt gac ctg ggt ctt gat ggc Ser Gly Arg Thr Leu Lys Glu Leu Gly Leu Asp Leu Gly Leu Asp Gly 85 90 95			288
gtt gta ttg cat ggt cag cat ccg gaa acc gtt gcc cat aac ggc agg Val Val Leu His Gly Gln His Pro Glu Thr Val Ala His Asn Gly Arg 100 105 110			336
atc ctc tat ctg gat ttc cac ccc gtg cgc cgt ggg gat caa gat tta Ile Leu Tyr Leu Asp Phe His Pro Val Arg Arg Gly Asp Gln Asp Leu 115 120 125			384
ggc tac gtg gta acc atc cgc gat cgt acc gac atc att gaa ctc agt Gly Tyr Val Val Thr Ile Arg Asp Arg Thr Asp Ile Ile Glu Leu Ser 130 135 140			432
gaa cgc ctc gac tct gtg cgc acc atg acc cac gca ctc cgc gcc cag Glu Arg Leu Asp Ser Val Arg Thr Met Thr His Ala Leu Arg Ala Gln 145 150 155 160			480
cgc cac gag ttt gcc aac cgc atc cac acc gca aca ggg ctt atc gac Arg His Glu Phe Ala Asn Arg Ile His Thr Ala Thr Gly Leu Ile Asp 165 170 175			528
gcc ggc cgc gtc cac gac gcg gca gag ttt cta ggc gat ata tcc cgc Ala Gly Arg Val His Asp Ala Ala Glu Phe Leu Gly Asp Ile Ser Arg 180 185 190			576
aac ggg gga cag tca cat cca ttg atc gga tca gcg cac ctc aat gaa Asn Gly Gly Gln Ser His Pro Leu Ile Gly Ser Ala His Leu Asn Glu 195 200 205			624
gca ttt ttg agc tca ttt tta agt act gct tct att tcg gca tct gaa Ala Phe Leu Ser Ser Phe Leu Ser Thr Ala Ser Ile Ser Ala Ser Glu 210 215 220			672
aag ggc gtt agt ctg cgc atc aac tct gac acg ctc atc ctt ggc act Lys Gly Val Ser Leu Arg Ile Asn Ser Asp Thr Leu Ile Leu Gly Thr 225 230 235 240			720
gtt aaa gat cca gaa gat gta gca acc att ttg ggt aat tta atc aac Val Lys Asp Pro Glu Asp Val Ala Thr Ile Leu Gly Asn Leu Ile Asn 245 250 255			768
aat gcc atc gac gcc gcg gtg gca ggt gaa gcc cca cgg tgg att gag Asn Ala Ile Asp Ala Ala Val Ala Gly Glu Ala Pro Arg Trp Ile Glu 260 265 270			816
ctt acg ttg atg gat gat gcc gat acg ctg gtc att tct gtt gca gat Leu Thr Leu Met Asp Asp Ala Asp Thr Leu Val Ile Ser Val Ala Asp 275 280 285			864
tct ggt cct gga atc cca gag ggc gtg gat gta ttt gcc aca gcc acc Ser Gly Pro Gly Ile Pro Glu Gly Val Asp Val Phe Ala Thr Ala Thr 290 295 300			912

cag ata gga gac tct gaa gat aat gaa cgc acc cac ggg cat ggc att 960  
 Gln Ile Gly Asp Ser Glu Asp Asn Glu Arg Thr His Gly His Gly Ile  
 305 310 315 320  
 ggt cta aaa ctg tgc cgg gct ttg gct aga tca cat ggt ggc gat gtc 1008  
 Gly Leu Lys Leu Cys Arg Ala Leu Ala Arg Ser His Gly Gly Asp Val  
 325 330 335  
 tgg gtg att gat aga gga acc gaa gat ggc gct gta ttt gga gtg aaa 1056  
 Trp Val Ile Asp Arg Gly Thr Glu Asp Gly Ala Val Phe Gly Val Lys  
 340 345 350  
 cta ccg gga gta atg gag taatggatca aacacttaaa gtt 1097  
 Leu Pro Gly Val Met Glu  
 355

<210> 28  
 <211> 358  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 28  
 Ala Ala Leu Ala Leu Ile Ser Val Leu Gly Ile Leu Ile Gly Val Gly  
 1 5 10 15  
 Val Ala Met Gly Met Arg Arg Arg Trp Glu Arg Val Thr Leu Gly Leu  
 20 25 30  
 Gln Pro Glu Glu Leu Val Thr Leu Val Gln Asn Gln Thr Ala Val Ile  
 35 40 45  
 Asp Gly Ile Asp Glu Gly Val Leu Ala Leu Ser Pro Asn Gly Thr Ile  
 50 55 60  
 Gly Val His Asn Glu Gln Ala Gln Ser Met Ile Gly Ala Gly Pro Met  
 65 70 75 80  
 Ser Gly Arg Thr Leu Lys Glu Leu Gly Leu Asp Leu Gly Leu Asp Gly  
 85 90 95  
 Val Val Leu His Gly Gln His Pro Glu Thr Val Ala His Asn Gly Arg  
 100 105 110  
 Ile Leu Tyr Leu Asp Phe His Pro Val Arg Arg Gly Asp Gln Asp Leu  
 115 120 125  
 Gly Tyr Val Val Thr Ile Arg Asp Arg Thr Asp Ile Ile Glu Leu Ser  
 130 135 140  
 Glu Arg Leu Asp Ser Val Arg Thr Met Thr His Ala Leu Arg Ala Gln  
 145 150 155 160  
 Arg His Glu Phe Ala Asn Arg Ile His Thr Ala Thr Gly Leu Ile Asp  
 165 170 175  
 Ala Gly Arg Val His Asp Ala Ala Glu Phe Leu Gly Asp Ile Ser Arg  
 180 185 190  
 Asn Gly Gly Gln Ser His Pro Leu Ile Gly Ser Ala His Leu Asn Glu

195					200					205					
Ala	Phe	Leu	Ser	Ser	Phe	Leu	Ser	Thr	Ala	Ser	Ile	Ser	Ala	Ser	Glu
210						215					220				
Lys	Gly	Val	Ser	Leu	Arg	Ile	Asn	Ser	Asp	Thr	Leu	Ile	Leu	Gly	Thr
225					230					235					240
Val	Lys	Asp	Pro	Glu	Asp	Val	Ala	Thr	Ile	Leu	Gly	Asn	Leu	Ile	Asn
				245					250					255	
Asn	Ala	Ile	Asp	Ala	Ala	Val	Ala	Gly	Glu	Ala	Pro	Arg	Trp	Ile	Glu
			260					265					270		
Leu	Thr	Leu	Met	Asp	Asp	Ala	Asp	Thr	Leu	Val	Ile	Ser	Val	Ala	Asp
		275					280					285			
Ser	Gly	Pro	Gly	Ile	Pro	Glu	Gly	Val	Asp	Val	Phe	Ala	Thr	Ala	Thr
	290					295					300				
Gln	Ile	Gly	Asp	Ser	Glu	Asp	Asn	Glu	Arg	Thr	His	Gly	His	Gly	Ile
305					310					315					320
Gly	Leu	Lys	Leu	Cys	Arg	Ala	Leu	Ala	Arg	Ser	His	Gly	Gly	Asp	Val
				325					330					335	
Trp	Val	Ile	Asp	Arg	Gly	Thr	Glu	Asp	Gly	Ala	Val	Phe	Gly	Val	Lys
			340					345					350		
Leu	Pro	Gly	Val	Met	Glu										
		355													

<210> 29  
 <211> 1620  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1597)  
 <223> RXA00129

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 tcgcattgta gataaatggc gaacctcact gcaggttcgc gtg ctc ggc tcc atc 115  
 Val Leu Gly Ser Ile  
 1 5  
 ttc acc gca tca gct gtc gtg atg atc ctt ttg ggg ctg ggc atg ctg 163  
 Phe Thr Ala Ser Ala Val Val Met Ile Leu Leu Gly Leu Gly Met Leu  
 10 15 20  
 act gta ttc acc caa cgg ttg gtg gat cag aaa atc gat att gcg agc 211  
 Thr Val Phe Thr Gln Arg Leu Val Asp Gln Lys Ile Asp Ile Ala Ser  
 25 30 35  
 tcc gaa atc gac cgc gcc cgc gtc atc gtc gaa gag caa atc acc gca 259  
 Ser Glu Ile Asp Arg Ala Arg Val Ile Val Glu Glu Gln Ile Thr Ala  
 40 45 50

tcc ggc gcc tca aca tcg gtg cag gcg cga gtg aac tct gcc cgc gct	307
Ser Gly Ala Ser Thr Ser Val Gln Ala Arg Val Asn Ser Ala Arg Ala	
55 60 65	
gcg ctc tcc agc ttg ggt acc agc ggc ggt aca gaa acc aac gcc gcc	355
Ala Leu Ser Ser Leu Gly Thr Ser Gly Gly Thr Glu Thr Asn Ala Ala	
70 75 80 85	
tac gat cca gtc gtg ttg gtg aac aac gat gac ctg gtg gtc tct ccc	403
Tyr Asp Pro Val Val Leu Val Asn Asn Asp Asp Leu Val Val Ser Pro	
90 95 100	
gag ggt tac caa atc cca gaa cgt ctg cga tac ttc gtc tct gag aac	451
Glu Gly Tyr Gln Ile Pro Glu Arg Leu Arg Tyr Phe Val Ser Glu Asn	
105 110 115	
caa gtc tcg tat cag ttc tcc agc atc gac caa ggc gac gga tcg tcc	499
Gln Val Ser Tyr Gln Phe Ser Ser Ile Asp Gln Gly Asp Gly Ser Ser	
120 125 130	
tac caa gcg ctc atc atc gga acg ccc acg gaa agc gac atc ccg aac	547
Tyr Gln Ala Leu Ile Ile Gly Thr Pro Thr Glu Ser Asp Ile Pro Asn	
135 140 145	
ctc cag gtg tat ctg gtg ttc tcc atg gaa agc gac gaa tcc tct ctt	595
Leu Gln Val Tyr Leu Val Phe Ser Met Glu Ser Asp Glu Ser Ser Leu	
150 155 160 165	
gct ctc atg cga gga ctc ctc tca gct gca ctg ctg atc gtg gtg gtg	643
Ala Leu Met Arg Gly Leu Leu Ser Ala Ala Leu Leu Ile Val Val Val	
170 175 180	
ctg ctg gtc ggt atc gca tgg cta gcc acc caa cag gtc acc gcg ccg	691
Leu Leu Val Gly Ile Ala Trp Leu Ala Thr Gln Gln Val Thr Ala Pro	
185 190 195	
gtg cgt tcg gcg agc cgg att gcg gag cgt ttc gct caa ggc aaa ctg	739
Val Arg Ser Ala Ser Arg Ile Ala Glu Arg Phe Ala Gln Gly Lys Leu	
200 205 210	
cgt gaa cgc atg gtg gtg gaa ggc gaa gac gag atg gcc cgc ctg gcg	787
Arg Glu Arg Met Val Val Glu Gly Glu Asp Glu Met Ala Arg Leu Ala	
215 220 225	
gtg tcc ttc aac gcg atg gcc gaa tcg ctg tcc gcg cag atc acc aaa	835
Val Ser Phe Asn Ala Met Ala Glu Ser Leu Ser Ala Gln Ile Thr Lys	
230 235 240 245	
ttg gag gaa tac ggc aat ctg caa cga caa ttc aca tcg gat gtc tca	883
Leu Glu Glu Tyr Gly Asn Leu Gln Arg Gln Phe Thr Ser Asp Val Ser	
250 255 260	
cac gaa ttg cgc aca ccg ctg aca acg gtg cgc atg gct gct gat cta	931
His Glu Leu Arg Thr Pro Leu Thr Thr Val Arg Met Ala Ala Asp Leu	
265 270 275	
att gcc gat agt gaa gat gaa ctt tca ccc ggt gcg cgc cgc gcc agc	979
Ile Ala Asp Ser Glu Asp Glu Leu Ser Pro Gly Ala Arg Arg Ala Ser	
280 285 290	



caa ctg atg aac agg gag ttg gac cga ttc gag tcg ctg ctg agc gat 1027  
 Gln Leu Met Asn Arg Glu Leu Asp Arg Phe Glu Ser Leu Leu Ser Asp  
 295 300 305

ctg ttg gaa att tcc cga cac gac gcc ggc gtt gcc gaa ctg tcc acc 1075  
 Leu Leu Glu Ile Ser Arg His Asp Ala Gly Val Ala Glu Leu Ser Thr  
 310 315 320 325

gcg ctt cac gat gtc cgc atc cca gtg cga tcg gca ttg gaa caa gta 1123  
 Ala Leu His Asp Val Arg Ile Pro Val Arg Ser Ala Leu Glu Gln Val  
 330 335 340

caa cac ttg gcc acc gag ctc gat gtg gaa ttg ctt gtt aat ttg ccc 1171  
 Gln His Leu Ala Thr Glu Leu Asp Val Glu Leu Leu Val Asn Leu Pro  
 345 350 355

gaa gaa gcg atc aac att caa ggc gat tcc agg cgc atc gaa aga atc 1219  
 Glu Glu Ala Ile Asn Ile Gln Gly Asp Ser Arg Arg Ile Glu Arg Ile  
 360 365 370

att cgc aac ctt cta gcc aat gcg atc gac cac tcc aag ggc ttg cct 1267  
 Ile Arg Asn Leu Leu Ala Asn Ala Ile Asp His Ser Lys Gly Leu Pro  
 375 380 385

gtt gag ttg aaa gtt gcc gac aac gtg gac gca gta gcg atc gtt gtt 1315  
 Val Glu Leu Lys Val Ala Asp Asn Val Asp Ala Val Ala Ile Val Val  
 390 395 400 405

att gat cac ggc gtc ggc ctg aaa cct gga caa gac gaa ttg gtg ttc 1363  
 Ile Asp His Gly Val Gly Leu Lys Pro Gly Gln Asp Glu Leu Val Phe  
 410 415 420

aac aga ttc tgg cga gcc gac cct tcg cgc gtc cgc cat tct ggt ggc 1411  
 Asn Arg Phe Trp Arg Ala Asp Pro Ser Arg Val Arg His Ser Gly Gly  
 425 430 435

acc ggc ctg ggt ctt gcg att tct cgc gaa gat gcg atg ctt cat gga 1459  
 Thr Gly Leu Gly Leu Ala Ile Ser Arg Glu Asp Ala Met Leu His Gly  
 440 445 450

gga aac ctt gat gcg gcg gga acg atc ggt gtt ggt tcc att ttc cgt 1507  
 Gly Asn Leu Asp Ala Ala Gly Thr Ile Gly Val Gly Ser Ile Phe Arg  
 455 460 465

ttg gtc ttg cct aaa gaa ccg cat gga aat tat cgt gaa gca ccg atc 1555  
 Leu Val Leu Pro Lys Glu Pro His Gly Asn Tyr Arg Glu Ala Pro Ile  
 470 475 480 485

ccg ttg atc gct cca gag aca ccg tgg gaa ggg gag cag cag 1597  
 Pro Leu Ile Ala Pro Glu Thr Pro Trp Glu Gly Glu Gln Gln  
 490 495

tgagtaaaat ttcgacgaaa ctg 1620

&lt;210&gt; 30

&lt;211&gt; 499

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 30

Val Leu Gly Ser Ile Phe Thr Ala Ser Ala Val Val Met Ile Leu Leu  
 1 5 10 15  
 Gly Leu Gly Met Leu Thr Val Phe Thr Gln Arg Leu Val Asp Gln Lys  
 20 25 30  
 Ile Asp Ile Ala Ser Ser Glu Ile Asp Arg Ala Arg Val Ile Val Glu  
 35 40 45  
 Glu Gln Ile Thr Ala Ser Gly Ala Ser Thr Ser Val Gln Ala Arg Val  
 50 55 60  
 Asn Ser Ala Arg Ala Ala Leu Ser Ser Leu Gly Thr Ser Gly Gly Thr  
 65 70 75 80  
 Glu Thr Asn Ala Ala Tyr Asp Pro Val Val Leu Val Asn Asn Asp Asp  
 85 90 95  
 Leu Val Val Ser Pro Glu Gly Tyr Gln Ile Pro Glu Arg Leu Arg Tyr  
 100 105 110  
 Phe Val Ser Glu Asn Gln Val Ser Tyr Gln Phe Ser Ser Ile Asp Gln  
 115 120 125  
 Gly Asp Gly Ser Ser Tyr Gln Ala Leu Ile Ile Gly Thr Pro Thr Glu  
 130 135 140  
 Ser Asp Ile Pro Asn Leu Gln Val Tyr Leu Val Phe Ser Met Glu Ser  
 145 150 155 160  
 Asp Glu Ser Ser Leu Ala Leu Met Arg Gly Leu Leu Ser Ala Ala Leu  
 165 170 175  
 Leu Ile Val Val Val Leu Leu Val Gly Ile Ala Trp Leu Ala Thr Gln  
 180 185 190  
 Gln Val Thr Ala Pro Val Arg Ser Ala Ser Arg Ile Ala Glu Arg Phe  
 195 200 205  
 Ala Gln Gly Lys Leu Arg Glu Arg Met Val Val Glu Gly Glu Asp Glu  
 210 215 220  
 Met Ala Arg Leu Ala Val Ser Phe Asn Ala Met Ala Glu Ser Leu Ser  
 225 230 235 240  
 Ala Gln Ile Thr Lys Leu Glu Glu Tyr Gly Asn Leu Gln Arg Gln Phe  
 245 250 255  
 Thr Ser Asp Val Ser His Glu Leu Arg Thr Pro Leu Thr Thr Val Arg  
 260 265 270  
 Met Ala Ala Asp Leu Ile Ala Asp Ser Glu Asp Glu Leu Ser Pro Gly  
 275 280 285  
 Ala Arg Arg Ala Ser Gln Leu Met Asn Arg Glu Leu Asp Arg Phe Glu  
 290 295 300  
 Ser Leu Leu Ser Asp Leu Leu Glu Ile Ser Arg His Asp Ala Gly Val  
 305 310 315 320  
 Ala Glu Leu Ser Thr Ala Leu His Asp Val Arg Ile Pro Val Arg Ser

325								330				335			
Ala	Leu	Glu	Gln	Val	Gln	His	Leu	Ala	Thr	Glu	Leu	Asp	Val	Glu	Leu
			340						345				350		
Leu	Val	Asn	Leu	Pro	Glu	Glu	Ala	Ile	Asn	Ile	Gln	Gly	Asp	Ser	Arg
		355					360					365			
Arg	Ile	Glu	Arg	Ile	Ile	Arg	Asn	Leu	Leu	Ala	Asn	Ala	Ile	Asp	His
	370					375					380				
Ser	Lys	Gly	Leu	Pro	Val	Glu	Leu	Lys	Val	Ala	Asp	Asn	Val	Asp	Ala
385					390				395						400
Val	Ala	Ile	Val	Val	Ile	Asp	His	Gly	Val	Gly	Leu	Lys	Pro	Gly	Gln
			405						410					415	
Asp	Glu	Leu	Val	Phe	Asn	Arg	Phe	Trp	Arg	Ala	Asp	Pro	Ser	Arg	Val
		420							425				430		
Arg	His	Ser	Gly	Gly	Thr	Gly	Leu	Gly	Leu	Ala	Ile	Ser	Arg	Glu	Asp
		435					440					445			
Ala	Met	Leu	His	Gly	Gly	Asn	Leu	Asp	Ala	Ala	Gly	Thr	Ile	Gly	Val
	450					455					460				
Gly	Ser	Ile	Phe	Arg	Leu	Val	Leu	Pro	Lys	Glu	Pro	His	Gly	Asn	Tyr
465					470					475					480
Arg	Glu	Ala	Pro	Ile	Pro	Leu	Ile	Ala	Pro	Glu	Thr	Pro	Trp	Glu	Gly
			485						490					495	

Glu Gln Gln

<210> 31  
 <211> 1455  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1432)  
 <223> RXN00651

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 catgatggaa gcagcgagga tagtaggtaa tgtacgacgc atg cag tca agc cta 115  
 Met Gln Ser Ser Leu  
 1 5  
 gat cgt gtg tcg gaa acc gga cgc aat gag ctc gat gtt gaa acc ctt 163  
 Asp Arg Val Ser Glu Thr Gly Arg Asn Glu Leu Asp Val Glu Thr Leu  
 10 15 20  
 gtg aag aag ggg aat caa ccg ggc gcg atg agc tat cgc aac agt atc 211  
 Val Lys Lys Gly Asn Gln Pro Gly Ala Met Ser Tyr Arg Asn Ser Ile  
 25 30 35

cac att ttg aca gcc tcg ctg ctg gtc gtg ggg ttg gga gct tcc gcc	259
His Ile Leu Thr Ala Ser Leu Leu Val Val Gly Leu Gly Ala Ser Ala	
40 45 50	
cgc ctg acg ctg ccg atg ttt gcg ctg tcg tgc gtg ctg ttg ttt gtg	307
Arg Leu Thr Leu Pro Met Phe Ala Leu Ser Cys Val Leu Leu Phe Val	
55 60 65	
tgg ggt ttt ctg tac ttc tat gga tca acc aaa cgc gta gat ttg agc	355
Trp Gly Phe Leu Tyr Phe Tyr Gly Ser Thr Lys Arg Val Asp Leu Ser	
70 75 80 85	
cac ggc atg cag ctg ggc tgg ctg ttt gtg ctg acg ctg gtg tgg att	403
His Gly Met Gln Leu Gly Trp Leu Phe Val Leu Thr Leu Val Trp Ile	
90 95 100	
ttt atg gtg ccg atc gtg ccc gtg tcc att tat ctg ctg ttc ccg ctg	451
Phe Met Val Pro Ile Val Pro Val Ser Ile Tyr Leu Leu Phe Pro Leu	
105 110 115	
ttt ttc ctc tat cta cag gtg atg cct gac gtg aga ggc att att gcg	499
Phe Phe Leu Tyr Leu Gln Val Met Pro Asp Val Arg Gly Ile Ile Ala	
120 125 130	
att ttg ggt gcg aca gcg att gcg att gcc agc cag tat tcc gtg ggg	547
Ile Leu Gly Ala Thr Ala Ile Ala Ile Ala Ser Gln Tyr Ser Val Gly	
135 140 145	
ttg acc ttt ggt ggt gtg atg ggt ccg gtg gtc tct gcg atc gtg acc	595
Leu Thr Phe Gly Gly Val Met Gly Pro Val Val Ser Ala Ile Val Thr	
150 155 160 165	
gtg gct att gat tac gcg ttc cgc acg ttg tgg cgg gtg aat aat gaa	643
Val Ala Ile Asp Tyr Ala Phe Arg Thr Leu Trp Arg Val Asn Asn Glu	
170 175 180	
aag cag gaa ttg att gat cag ttg att gaa act cgc tcc cag ctg gcg	691
Lys Gln Glu Leu Ile Asp Gln Leu Ile Glu Thr Arg Ser Gln Leu Ala	
185 190 195	
gtg acg gaa cga aat gcg ggt att gct gcg gaa cgt caa cgt att gcg	739
Val Thr Glu Arg Asn Ala Gly Ile Ala Ala Glu Arg Gln Arg Ile Ala	
200 205 210	
cat gaa att cat gac acg gtc gcc cag gga ctc tcc tcc att caa atg	787
His Glu Ile His Asp Thr Val Ala Gln Gly Leu Ser Ser Ile Gln Met	
215 220 225	
ctg ctg cat gtc tct gaa cag gag att ctc gtt gct gag atg gaa gag	835
Leu Leu His Val Ser Glu Gln Glu Ile Leu Val Ala Glu Met Glu Glu	
230 235 240 245	
aag cca aag gag gcg atc gtg aag aag atg cgc ctt gcc cga caa aca	883
Lys Pro Lys Glu Ala Ile Val Lys Lys Met Arg Leu Ala Arg Gln Thr	
250 255 260	
gcc tcc gac aat ctc agt gag gct cgc gcg atg att gcg gcg ttg caa	931
Ala Ser Asp Asn Leu Ser Glu Ala Arg Ala Met Ile Ala Ala Leu Gln	
265 270 275	
ccg gca gcg ctg tct aaa acc tcc ttg gaa gca gca ctt cac cgc gtc	979

Pro Ala Ala Leu Ser Lys Thr Ser Leu Glu Ala Ala Leu His Arg Val  
 280 285 290

aca gaa ccg ttg ttg ggt att aat ttt gtg att tct gtc gac ggt gat 1027  
 Thr Glu Pro Leu Leu Gly Ile Asn Phe Val Ile Ser Val Asp Gly Asp  
 295 300 305

gtt cgc caa ctg ccc atg aaa act gaa gcc acc ctt ctg cga att gct 1075  
 Val Arg Gln Leu Pro Met Lys Thr Glu Ala Thr Leu Leu Arg Ile Ala  
 310 315 320 325

caa ggt gcg atc gga aat gtg gcg aaa cat tca gag gcg aaa aac tgc 1123  
 Gln Gly Ala Ile Gly Asn Val Ala Lys His Ser Glu Ala Lys Asn Cys  
 330 335 340

cac gtg aca cta acc tac gaa gac aca gaa gta cgc ctt gat gtg gtt 1171  
 His Val Thr Leu Thr Tyr Glu Asp Thr Glu Val Arg Leu Asp Val Val  
 345 350 355

gat gac ggt gtg ggt ttt gag cct tcg gaa gtg tcc agt acc ccc gct 1219  
 Asp Asp Gly Val Gly Phe Glu Pro Ser Glu Val Ser Ser Thr Pro Ala  
 360 365 370

ggc ctt ggc cat atc ggc tta acc gca ttg cag cag cgt gcg atg gaa 1267  
 Gly Leu Gly His Ile Gly Leu Thr Ala Leu Gln Gln Arg Ala Met Glu  
 375 380 385

ttg cac ggc gaa gtt ata gtg gaa tct gca tat ggg cag ggt act gcg 1315  
 Leu His Gly Glu Val Ile Val Glu Ser Ala Tyr Gly Gln Gly Thr Ala  
 390 395 400 405

gta tct gca gca ttg ccg gtg gag cca cca gag ggg ttt gtc ggg gcg 1363  
 Val Ser Ala Ala Leu Pro Val Glu Pro Glu Gly Phe Val Gly Ala  
 410 415 420

ccg gtt ttg gca gat tcg gac tca agt gct aca ggc gag gtt gaa cta 1411  
 Pro Val Leu Ala Asp Ser Asp Ser Ser Ala Thr Gly Glu Val Glu Leu  
 425 430 435

agt tct cca act gac gat gag taaggctaga ctaaagtacg att 1455  
 Ser Ser Pro Thr Asp Asp Glu  
 440

&lt;210&gt; 32

&lt;211&gt; 444

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 32

Met Gln Ser Ser Leu Asp Arg Val Ser Glu Thr Gly Arg Asn Glu Leu  
 1 5 10 15

Asp Val Glu Thr Leu Val Lys Lys Gly Asn Gln Pro Gly Ala Met Ser  
 20 25 30

Tyr Arg Asn Ser Ile His Ile Leu Thr Ala Ser Leu Leu Val Val Gly  
 35 40 45

Leu Gly Ala Ser Ala Arg Leu Thr Leu Pro Met Phe Ala Leu Ser Cys  
 50 55 60

Val Leu Leu Phe Val Trp Gly Phe Leu Tyr Phe Tyr Gly Ser Thr Lys  
 65 70 75 80  
 Arg Val Asp Leu Ser His Gly Met Gln Leu Gly Trp Leu Phe Val Leu  
 85 90 95  
 Thr Leu Val Trp Ile Phe Met Val Pro Ile Val Pro Val Ser Ile Tyr  
 100 105 110  
 Leu Leu Phe Pro Leu Phe Phe Leu Tyr Leu Gln Val Met Pro Asp Val  
 115 120 125  
 Arg Gly Ile Ile Ala Ile Leu Gly Ala Thr Ala Ile Ala Ile Ala Ser  
 130 135 140  
 Gln Tyr Ser Val Gly Leu Thr Phe Gly Gly Val Met Gly Pro Val Val  
 145 150 155 160  
 Ser Ala Ile Val Thr Val Ala Ile Asp Tyr Ala Phe Arg Thr Leu Trp  
 165 170 175  
 Arg Val Asn Asn Glu Lys Gln Glu Leu Ile Asp Gln Leu Ile Glu Thr  
 180 185 190  
 Arg Ser Gln Leu Ala Val Thr Glu Arg Asn Ala Gly Ile Ala Ala Glu  
 195 200 205  
 Arg Gln Arg Ile Ala His Glu Ile His Asp Thr Val Ala Gln Gly Leu  
 210 215 220  
 Ser Ser Ile Gln Met Leu Leu His Val Ser Glu Gln Glu Ile Leu Val  
 225 230 235 240  
 Ala Glu Met Glu Glu Lys Pro Lys Glu Ala Ile Val Lys Lys Met Arg  
 245 250 255  
 Leu Ala Arg Gln Thr Ala Ser Asp Asn Leu Ser Glu Ala Arg Ala Met  
 260 265 270  
 Ile Ala Ala Leu Gln Pro Ala Ala Leu Ser Lys Thr Ser Leu Glu Ala  
 275 280 285  
 Ala Leu His Arg Val Thr Glu Pro Leu Leu Gly Ile Asn Phe Val Ile  
 290 295 300  
 Ser Val Asp Gly Asp Val Arg Gln Leu Pro Met Lys Thr Glu Ala Thr  
 305 310 315 320  
 Leu Leu Arg Ile Ala Gln Gly Ala Ile Gly Asn Val Ala Lys His Ser  
 325 330 335  
 Glu Ala Lys Asn Cys His Val Thr Leu Thr Tyr Glu Asp Thr Glu Val  
 340 345 350  
 Arg Leu Asp Val Val Asp Asp Gly Val Gly Phe Glu Pro Ser Glu Val  
 355 360 365  
 Ser Ser Thr Pro Ala Gly Leu Gly His Ile Gly Leu Thr Ala Leu Gln  
 370 375 380

Gln Arg Ala Met Glu Leu His Gly Glu Val Ile Val Glu Ser Ala Tyr  
385 390 395 400

Gly Gln Gly Thr Ala Val Ser Ala Ala Leu Pro Val Glu Pro Pro Glu  
405 410 415

Gly Phe Val Gly Ala Pro Val Leu Ala Asp Ser Asp Ser Ser Ala Thr  
420 425 430

Gly Glu Val Glu Leu Ser Ser Pro Thr Asp Asp Glu  
435 440

<210> 33

<211> 1455

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1432)

<223> FRXA00651

<400> 33

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catgatggaa gcagcgagga tagtaggtaa tgtacgacgc atg cag tca agc cta 115  
Met Gln Ser Ser Leu  
1 5

gat cgt gtg tcg gaa acc gga cgc aat gag ctc gat gtt gaa acc ctt 163  
Asp Arg Val Ser Glu Thr Gly Arg Asn Glu Leu Asp Val Glu Thr Leu  
10 15 20

gtg aag aag ggg aat caa ccg ggc gcg atg agc tat cgc aac agt atc 211  
Val Lys Lys Gly Asn Gln Pro Gly Ala Met Ser Tyr Arg Asn Ser Ile  
25 30 35

cac att ttg aca gcc tcg ctg ctg gtc gtg ggg ttg gga gct tcc gcc 259  
His Ile Leu Thr Ala Ser Leu Leu Val Val Gly Leu Gly Ala Ser Ala  
40 45 50

cgc ctg acg ctg ccg atg ttt gcg ctg tcg tgc gtg ctg ttg ttt gtg 307  
Arg Leu Thr Leu Pro Met Phe Ala Leu Ser Cys Val Leu Leu Phe Val  
55 60 65

tgg ggt ttt ctg tac ttc tat gga tca acc aaa cgc gta gat ttg agc 355  
Trp Gly Phe Leu Tyr Phe Tyr Gly Ser Thr Lys Arg Val Asp Leu Ser  
70 75 80 85

cac ggc atg cag ctg ggc tgg ctg ttt gtg ctg acg ctg gtg tgg att 403  
His Gly Met Gln Leu Gly Trp Leu Phe Val Leu Thr Leu Val Trp Ile  
90 95 100

ttt atg gtg ccg atc gtg ccc gtg tcc att tat ctg ctg ttc ccg ctg 451  
Phe Met Val Pro Ile Val Pro Val Ser Ile Tyr Leu Leu Phe Pro Leu  
105 110 115

ttt ttc ctc tat cta cag gtg atg cct gac gtg aga ggc att att gcg 499  
Phe Phe Leu Tyr Leu Gln Val Met Pro Asp Val Arg Gly Ile Ile Ala  
120 125 130

att ttg ggt gcg aca gcg att gcg att gcc agc cag tat tcc gtg ggg Ile Leu Gly Ala Thr Ala Ile Ala Ile Ala Ser Gln Tyr Ser Val Gly 135 140 145	547
ttg acc ttt ggt ggt gtg atg ggt ccg gtg gtc tct gcg atc gtg acc Leu Thr Phe Gly Gly Val Met Gly Pro Val Val Ser Ala Ile Val Thr 150 155 160 165	595
gtg gct att gat tac gcg ttc cgc acg ttg tgg cgg gtg aat aat gaa Val Ala Ile Asp Tyr Ala Phe Arg Thr Leu Trp Arg Val Asn Asn Glu 170 175 180	643
aag cag gaa ttg att gat cag ttg att gaa act cgc tcc cag ctg gcg Lys Gln Glu Leu Ile Asp Gln Leu Ile Glu Thr Arg Ser Gln Leu Ala 185 190 195	691
gtg acg gaa cga aat gcg ggt att gct gcg gaa cgt caa cgt att gcg Val Thr Glu Arg Asn Ala Gly Ile Ala Ala Glu Arg Gln Arg Ile Ala 200 205 210	739
cat gaa att cat gac acg gtc gcc cag gga ctc tcc tcc att caa atg His Glu Ile His Asp Thr Val Ala Gln Gly Leu Ser Ser Ile Gln Met 215 220 225	787
ctg ctg cat gtc tct gaa cag gag att ctc gtt gct gag atg gaa gag Leu Leu His Val Ser Glu Gln Glu Ile Leu Val Ala Glu Met Glu Glu 230 235 240 245	835
aag cca aag gag gcg atc gtg aag aag atg cgc ctt gcc cga caa aca Lys Pro Lys Glu Ala Ile Val Lys Lys Met Arg Leu Ala Arg Gln Thr 250 255 260	883
gcc tcc gac aat ctc agt gag gct cgc gcg atg att gcg gcg ttg caa Ala Ser Asp Asn Leu Ser Glu Ala Arg Ala Met Ile Ala Ala Leu Gln 265 270 275	931
ccg gca gcg ctg tct aaa acc tcc ttg gaa gca gca ctt cac cgc gtc Pro Ala Ala Leu Ser Lys Thr Ser Leu Glu Ala Ala Leu His Arg Val 280 285 290	979
aca gaa ccg ttg ttg ggt att aat ttt gtg att tct gtc gac ggt gat Thr Glu Pro Leu Leu Gly Ile Asn Phe Val Ile Ser Val Asp Gly Asp 295 300 305	1027
gtt cgc caa ctg ccc atg aaa act gaa gcc acc ctt ctg cga att gct Val Arg Gln Leu Pro Met Lys Thr Glu Ala Thr Leu Leu Arg Ile Ala 310 315 320 325	1075
caa ggt gcg atc gga aat gtg gcg aaa cat tca gag gcg aaa aac tgc Gln Gly Ala Ile Gly Asn Val Ala Lys His Ser Glu Ala Lys Asn Cys 330 335 340	1123
cac gtg aca cta acc tac gaa gac aca gaa gta cgc ctt gat gtg gtt His Val Thr Leu Thr Tyr Glu Asp Thr Glu Val Arg Leu Asp Val Val 345 350 355	1171
gat gac ggt gtg ggt ttt gag cct tcg gaa gtg tcc agt acc ccc gct Asp Asp Gly Val Gly Phe Glu Pro Ser Glu Val Ser Ser Thr Pro Ala 360 365 370	1219



ggc ctt ggc cat atc ggc tta acc gca ttg cag cag cgt gcg atg gaa 1267  
 Gly Leu Gly His Ile Gly Leu Thr Ala Leu Gln Gln Arg Ala Met Glu  
 375 380 385

ttg cac ggc gaa gtt ata gtg gaa tct gca tat ggg cag ggt act gcg 1315  
 Leu His Gly Glu Val Ile Val Glu Ser Ala Tyr Gly Gln Gly Thr Ala  
 390 395 400 405

gta tct gca gca ttg ccg gtg gag cca cca gag ggg ttt gtc ggg gcg 1363  
 Val Ser Ala Ala Leu Pro Val Glu Pro Pro Glu Gly Phe Val Gly Ala  
 410 415 420

ccg gtt ttg gca gat tcg gac tca agt gct aca ggc gag gtt gaa cta 1411  
 Pro Val Leu Ala Asp Ser Asp Ser Ser Ala Thr Gly Glu Val Glu Leu  
 425 430 435

agt tct cca act gac gat gag taaggctaga ctaaagtacg att 1455  
 Ser Ser Pro Thr Asp Asp Glu  
 440

<210> 34

<211> 444

<212> PRT

<213> Corynebacterium glutamicum

<400> 34

Met Gln Ser Ser Leu Asp Arg Val Ser Glu Thr Gly Arg Asn Glu Leu  
 1 5 10 15

Asp Val Glu Thr Leu Val Lys Lys Gly Asn Gln Pro Gly Ala Met Ser  
 20 25 30

Tyr Arg Asn Ser Ile His Ile Leu Thr Ala Ser Leu Leu Val Val Gly  
 35 40 45

Leu Gly Ala Ser Ala Arg Leu Thr Leu Pro Met Phe Ala Leu Ser Cys  
 50 55 60

Val Leu Leu Phe Val Trp Gly Phe Leu Tyr Phe Tyr Gly Ser Thr Lys  
 65 70 75 80

Arg Val Asp Leu Ser His Gly Met Gln Leu Gly Trp Leu Phe Val Leu  
 85 90 95

Thr Leu Val Trp Ile Phe Met Val Pro Ile Val Pro Val Ser Ile Tyr  
 100 105 110

Leu Leu Phe Pro Leu Phe Phe Leu Tyr Leu Gln Val Met Pro Asp Val  
 115 120 125

Arg Gly Ile Ile Ala Ile Leu Gly Ala Thr Ala Ile Ala Ile Ala Ser  
 130 135 140

Gln Tyr Ser Val Gly Leu Thr Phe Gly Gly Val Met Gly Pro Val Val  
 145 150 155 160

Ser Ala Ile Val Thr Val Ala Ile Asp Tyr Ala Phe Arg Thr Leu Trp  
 165 170 175

Arg Val Asn Asn Glu Lys Gln Glu Leu Ile Asp Gln Leu Ile Glu Thr

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<210> 35
<211> 558
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101) .. (535)
<223> RXA00006
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&lt;400&gt; 35

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agaagatggt cgcctatcca ccccgtagaa gaagataaaa atg gtc gat ttt gac 115  
 Met Val Asp Phe Asp  
 1 5

acc atc gca gcc cga ctt gtc acc gaa aca gaa gaa gca atc atc tac 163  
 Thr Ile Ala Ala Arg Leu Val Thr Glu Thr Glu Glu Ala Ile Ile Tyr  
 10 15 20

gcc acc cgc gat gga ata atc aga ctc tgg aac ggc ggc tcc gag aaa 211  
 Ala Thr Arg Asp Gly Ile Ile Arg Leu Trp Asn Gly Gly Ser Glu Lys  
 25 30 35

ctc ttt gga tac acg gcc ggc gaa gcc ctt gga aaa tca ctc gac atc 259  
 Leu Phe Gly Tyr Thr Ala Gly Glu Ala Leu Gly Lys Ser Leu Asp Ile  
 40 45 50

atc att ccc gaa aaa cac cgc aag gcc cac tgg gac gga tgg gat cgc 307  
 Ile Ile Pro Glu Lys His Arg Lys Ala His Trp Asp Gly Trp Asp Arg  
 55 60 65

gtc atg gaa tcc ggc gaa act cgc tat ggc tcc gaa ccg ctt aac gtt 355  
 Val Met Glu Ser Gly Glu Thr Arg Tyr Gly Ser Glu Pro Leu Asn Val  
 70 75 80 85

cca ggc att cgt gcc gat gga tcc aaa atg tct ttg gaa ttc tcc atc 403  
 Pro Gly Ile Arg Ala Asp Gly Ser Lys Met Ser Leu Glu Phe Ser Ile  
 90 95 100

acc atc ctg aag gac gat tcc gga aaa atc gaa ggc gtt gca gct ttt 451  
 Thr Ile Leu Lys Asp Asp Ser Gly Lys Ile Glu Gly Val Ala Ala Phe  
 105 110 115

ctc cgc gat gtc acc gcc aat tgg gat gag aaa aag gcc ctg cgg atc 499  
 Leu Arg Asp Val Thr Ala Asn Trp Asp Glu Lys Lys Ala Leu Arg Ile  
 120 125 130

cga atc aaa gag ttg gaa cgc caa atc gag ggc cat taaggagatt 545  
 Arg Ile Lys Glu Leu Glu Arg Gln Ile Glu Gly His  
 135 140 145

cttgggtgcg cgg 558

&lt;210&gt; 36

&lt;211&gt; 145

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 36

Met Val Asp Phe Asp Thr Ile Ala Ala Arg Leu Val Thr Glu Thr Glu  
 1 5 10 15

Glu Ala Ile Ile Tyr Ala Thr Arg Asp Gly Ile Ile Arg Leu Trp Asn  
 20 25 30

Gly Gly Ser Glu Lys Leu Phe Gly Tyr Thr Ala Gly Glu Ala Leu Gly  
 35 40 45

Lys Ser Leu Asp Ile Ile Ile Pro Glu Lys His Arg Lys Ala His Trp  
 50 55 60  
 Asp Gly Trp Asp Arg Val Met Glu Ser Gly Glu Thr Arg Tyr Gly Ser  
 65 70 75 80  
 Glu Pro Leu Asn Val Pro Gly Ile Arg Ala Asp Gly Ser Lys Met Ser  
 85 90 95  
 Leu Glu Phe Ser Ile Thr Ile Leu Lys Asp Asp Ser Gly Lys Ile Glu  
 100 105 110  
 Gly Val Ala Ala Phe Leu Arg Asp Val Thr Ala Asn Trp Asp Glu Lys  
 115 120 125  
 Lys Ala Leu Arg Ile Arg Ile Lys Glu Leu Glu Arg Gln Ile Glu Gly  
 130 135 140  
 His  
 145

<210> 37  
 <211> 1008  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(985)  
 <223> RXA01860

<400> 37  
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 tatcggcggg acgctctttt ctgatgctcg tgcccaagggt gtg aat cca ttc att 115  
 Val Asn Pro Phe Ile  
 1 5  
 ctt gct gat cag ctg ctt tac gat gct aag cac gca ggt aga aat cgg 163  
 Leu Ala Asp Gln Leu Leu Tyr Asp Ala Lys His Ala Gly Arg Asn Arg  
 10 15 20  
 gtt gcg gtg cgc aga gct gaa aac acc att gtc cgc tca gct aag ccc 211  
 Val Ala Val Arg Arg Ala Glu Asn Thr Ile Val Arg Ser Ala Lys Pro  
 25 30 35  
 gca ttc tca gtt gag gaa ctt tcg gag atc ctg gag tca cat tct att 259  
 Ala Phe Ser Val Glu Glu Leu Ser Glu Ile Leu Glu Ser His Ser Ile  
 40 45 50  
 cgc ctc gag ctg cag ccg atc cta gaa ctt gaa aca ggt cgg gtg ggt 307  
 Arg Leu Glu Leu Gln Pro Ile Leu Glu Leu Glu Thr Gly Arg Val Gly  
 55 60 65  
 gca gcc gaa ggt ctg ctc cga atc aac ttg gat ggc acc gat gtt cct 355  
 Ala Ala Glu Gly Leu Leu Arg Ile Asn Leu Asp Gly Thr Asp Val Pro  
 70 75 80 85  
 acg ggg cag ttt gtt cag tcg gtt gaa cag gcc ggg cta gcc ccg aag 403  
 Thr Gly Gln Phe Val Gln Ser Val Glu Gln Ala Gly Leu Ala Pro Lys

	90	95	100	
ctt gat atc gca gtc atg aga gaa gga att aat cat att gag agg ctg				451
Leu Asp Ile Ala Val Met Arg Glu Gly Ile Asn His Ile Glu Arg Leu	105	110	115	
aga gct gtg tgt ccg act ttc agc ctc gct ttg aat ctg tcg ggc tat				499
Arg Ala Val Cys Pro Thr Phe Ser Leu Ala Leu Asn Leu Ser Gly Tyr	120	125	130	
tct ctg agc tcg gcg aaa ata ccg gag gaa cta aga gcc gaa ttt aga				547
Ser Leu Ser Ser Ala Lys Ile Arg Glu Glu Leu Arg Ala Glu Phe Arg	135	140	145	
gct cgc gat ctg cca agg gga tca att agg ttt gag att act gag acc				595
Ala Arg Asp Leu Pro Arg Gly Ser Ile Arg Phe Glu Ile Thr Glu Thr	150	155	160	165
gct ccg att gaa gac att gac gcg gca aaa gag ttt gtg cag atg ttg				643
Ala Pro Ile Glu Asp Ile Asp Ala Ala Lys Glu Phe Val Gln Met Leu	170	175	180	
aaa gat ttt ggc ttc cac atc gta atc gat gac ttt ggc gca gga cat				691
Lys Asp Phe Gly Phe His Ile Val Ile Asp Asp Phe Gly Ala Gly His	185	190	195	
gag cct tat caa tat cta aag aag ttc gac ttt agc gtg ctg aag att				739
Glu Pro Tyr Gln Tyr Leu Lys Lys Phe Asp Phe Ser Val Leu Lys Ile	200	205	210	
gca ggt gaa ttc ata gaa ggt atg gtc acc aac cgc gtg gac cga agc				787
Ala Gly Glu Phe Ile Glu Gly Met Val Thr Asn Arg Val Asp Arg Ser	215	220	225	
atc gtc gaa tct att gct caa ctt gct aag gat gag gag atg gaa act				835
Ile Val Glu Ser Ile Ala Gln Leu Ala Lys Asp Glu Glu Met Glu Thr	230	235	240	245
gtc gcc gag ttt gtt tca agc aag gag att ttg gag gcg gta cga gag				883
Val Ala Glu Phe Val Ser Ser Lys Glu Ile Leu Glu Ala Val Arg Glu	250	255	260	
ata ggc gta acg tac gcc cag ggt ttc cat att ggt aaa tct aag ccg				931
Ile Gly Val Thr Tyr Ala Gln Gly Phe His Ile Gly Lys Ser Lys Pro	265	270	275	
att gat gaa ttt ata gct act tat ctc gag acg aac caa acc gct acc				979
Ile Asp Glu Phe Ile Ala Thr Tyr Leu Glu Thr Asn Gln Thr Ala Thr	280	285	290	
tgg ggg taggaagaat atgaaaaaga aga				1008
Trp Gly	295			

&lt;210&gt; 38

&lt;211&gt; 295

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 38

Val Asn Pro Phe Ile Leu Ala Asp Gln Leu Leu Tyr Asp Ala Lys His  
 1 5 10 15  
 Ala Gly Arg Asn Arg Val Ala Val Arg Arg Ala Glu Asn Thr Ile Val  
 20 25 30  
 Arg Ser Ala Lys Pro Ala Phe Ser Val Glu Glu Leu Ser Glu Ile Leu  
 35 40 45  
 Glu Ser His Ser Ile Arg Leu Glu Leu Gln Pro Ile Leu Glu Leu Glu  
 50 55 60  
 Thr Gly Arg Val Gly Ala Ala Glu Gly Leu Leu Arg Ile Asn Leu Asp  
 65 70 75 80  
 Gly Thr Asp Val Pro Thr Gly Gln Phe Val Gln Ser Val Glu Gln Ala  
 85 90 95  
 Gly Leu Ala Pro Lys Leu Asp Ile Ala Val Met Arg Glu Gly Ile Asn  
 100 105 110  
 His Ile Glu Arg Leu Arg Ala Val Cys Pro Thr Phe Ser Leu Ala Leu  
 115 120 125  
 Asn Leu Ser Gly Tyr Ser Leu Ser Ser Ala Lys Ile Arg Glu Glu Leu  
 130 135 140  
 Arg Ala Glu Phe Arg Ala Arg Asp Leu Pro Arg Gly Ser Ile Arg Phe  
 145 150 155 160  
 Glu Ile Thr Glu Thr Ala Pro Ile Glu Asp Ile Asp Ala Ala Lys Glu  
 165 170 175  
 Phe Val Gln Met Leu Lys Asp Phe Gly Phe His Ile Val Ile Asp Asp  
 180 185 190  
 Phe Gly Ala Gly His Glu Pro Tyr Gln Tyr Leu Lys Lys Phe Asp Phe  
 195 200 205  
 Ser Val Leu Lys Ile Ala Gly Glu Phe Ile Glu Gly Met Val Thr Asn  
 210 215 220  
 Arg Val Asp Arg Ser Ile Val Glu Ser Ile Ala Gln Leu Ala Lys Asp  
 225 230 235 240  
 Glu Glu Met Glu Thr Val Ala Glu Phe Val Ser Ser Lys Glu Ile Leu  
 245 250 255  
 Glu Ala Val Arg Glu Ile Gly Val Thr Tyr Ala Gln Gly Phe His Ile  
 260 265 270  
 Gly Lys Ser Lys Pro Ile Asp Glu Phe Ile Ala Thr Tyr Leu Glu Thr  
 275 280 285  
 Asn Gln Thr Ala Thr Trp Gly  
 290 295

&lt;210&gt; 39

&lt;211&gt; 2088

&lt;212&gt; DNA

$\langle 220 \rangle$ 

<221> CDS

<222> (101) .. (2065)

<223> RXA01861

<400> 39

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cgttagtcgc aattgtgtgg ccatcagtgg gaatcgctgt gtg gtg gcc cgt gac 115  
Val Val Ala Arg Asp  
1 5

ctg cag aag ctg gaa aaa ctt cgc ctg att tgt gga tac gtg ttt cta 163  
Leu Gln Lys Leu Glu Lys Leu Arg Leu Ile Cys Gly Tyr Val Phe Leu  
10 15 20

gtc cca gcc ata tac ctg cac ttt ttt gcg gaa acc tcc ctc agg gga 211  
Val Pro Ala Ile Tyr Leu His Phe Phe Ala Glu Thr Ser Leu Arg Gly  
25 30 35

gtg att ctg gca gga att gcg cac gct atc gca ggt cct ggc gtt gca 259  
Val Ile Leu Ala Gly Ile Ala His Ala Ile Ala Gly Pro Gly Val Ala  
40 45 50

ctg gtt atg gca ttc atg gaa aat gcg caa ttg cca gaa ctg ttg cgt 307  
Leu Val Met Ala Phe Met Glu Asn Ala Gln Leu Pro Glu Leu Leu Arg  
55 60 65

aaa cgg cat gca ttc gca ccc ttc tcc cat att cgc ctt cca ggc gat 355  
Lys Arg His Ala Phe Ala Pro Phe Ser His Ile Arg Leu Pro Gly Asp  
70 75 80 85

gta ttc cgg ctc ctc gtc gcg ggc att gtc atg gtc gca ata tcc aaa 403  
Val Phe Arg Leu Leu Val Ala Gly Ile Val Met Val Ala Ile Ser Lys  
90 95 100

ttg	att	gtg	att	ctt	gct	tat	gca	ctg	gca	gat	ttg	cgc	tat	tca	ttc	451
Leu	Ile	Val	Ile	Leu	Ala	Tyr	Ala	Leu	Ala	Asp	Leu	Pro	Tyr	Ser	Phe	
			105					110					115			

acc ctt tat ctg acg atg gcc ctt cgt gac ttg act ggc att att gtg 499  
Thr Leu Tyr Leu Thr Met Ala Leu Arg Asp Leu Thr Gly Ile Ile Val  
120 125 130

ggt gcc ggg ccc gga att gca ctt tcg acg ccg ctg gta cta aat att 547  
Val Ala Gly Pro Gly Ile Ala Leu Ser Thr Pro Leu Val Leu Asn Ile  
135 140 145

cac cga tca gca tgg cgc gag ttc gca gtt gtt atc ata gct acg gtc 595  
 His Arg Ser Ala Trp Arg Glu Phe Ala Val Val Ile Ile Ala Thr Val  
 150 155 160 165

gga gtg ctg gcg ctc att ttc gga ttt gct gtg gat ctt ccg acg gtc 643  
Gly Val Leu Ala Leu Ile Phe Gly Phe Ala Val Asp Leu Pro Thr Val  
170 175 180

tac ttg gca atg ttg cca ttg tat tgg agt gca acc cgt ctt cca gtg 691  
 Tyr Leu Ala Met Leu Pro Leu Tyr Trp Ser Ala Thr Arg Leu Pro Val  
 185 190 195

ctt tta gcc gtt ctt cat gcg gtg ttt act tca gca ata gtc gta att	739
Leu Leu Ala Val Leu His Ala Val Phe Thr Ser Ala Ile Val Val Ile	
200 205 210	
ctg tat ttc cta tta ggt acc gga tct ttt gcg att acg gat gaa tcc	787
Leu Tyr Phe Leu Leu Gly Thr Gly Ser Phe Ala Ile Thr Asp Glu Ser	
215 220 225	
ata ctg gtg cag gca acg aca att cag ctt ttt gtt ctg atg tgt atc	835
Ile Leu Val Gln Ala Thr Thr Ile Gln Leu Phe Val Leu Met Cys Ile	
230 235 240 245	
ttg ttg tcg cta gtt gtg tca acg aca gtc cag cag aca tca gca ctg	883
Leu Leu Ser Leu Val Val Ser Thr Thr Val Gln Gln Thr Ser Ala Leu	
250 255 260	
gtt gaa gag cta gag gtg gta gcg aag acc ctt cct gat gcg ctt ttt	931
Val Glu Glu Leu Glu Val Val Ala Lys Thr Leu Pro Asp Ala Leu Phe	
265 270 275	
atc gta aac aaa aat gga aca gca ttt cct gtt aac gca ggc gcg aaa	979
Ile Val Asn Lys Asn Gly Thr Ala Phe Pro Val Asn Ala Gly Ala Lys	
280 285 290	
aat ttc gtc aag caa tca ccg gat ggg cat tat tcc atg ccg aaa cta	1027
Asn Phe Val Lys Gln Ser Pro Asp Gly His Tyr Ser Met Pro Lys Leu	
295 300 305	
cag aat ata gac ggt gaa ccc atg gat gag aaa gaa agt ccg agc agt	1075
Gln Asn Ile Asp Gly Glu Pro Met Asp Glu Lys Glu Ser Pro Ser Ser	
310 315 320 325	
atg gcc ttg cgt gga caa ggt gtc gaa gga gta tta gcc aag tta ggt	1123
Met Ala Leu Arg Gly Gln Gly Val Glu Gly Val Leu Ala Lys Leu Gly	
330 335 340	
gaa gta ctg gga gaa gat ccg gac ttg gcg cgt cga atc ttc gaa att	1171
Glu Val Leu Gly Glu Asp Pro Asp Leu Ala Arg Arg Ile Phe Glu Ile	
345 350 355	
agt gcc tca ccg atg tat ctg cgt gga gaa act gaa ccg ggt cat gcg	1219
Ser Ala Ser Pro Met Tyr Leu Arg Gly Glu Thr Glu Pro Gly His Ala	
360 365 370	
ctc gtg att tgg cat gac agt act aat gag tat tac acg atg caa caa	1267
Leu Val Ile Trp His Asp Ser Thr Asn Glu Tyr Tyr Thr Met Gln Gln	
375 380 385	
ttg acg ctt gca tat gaa gaa tcg cgg ctg cta ttt gaa aaa gcc cct	1315
Leu Thr Leu Ala Tyr Glu Glu Ser Arg Leu Leu Phe Glu Lys Ala Pro	
390 395 400 405	
caa ggg att gcc atg ctg gac cct tcg gga gaa atc gta atg gcg aat	1363
Gln Gly Ile Ala Met Leu Asp Pro Ser Gly Glu Ile Val Met Ala Asn	
410 415 420	
cga tcc ttt ggt gac ttg gtg gga acg act cct gtt cga ctc cta gga	1411
Arg Ser Phe Gly Asp Leu Val Gly Thr Thr Pro Val Arg Leu Leu Gly	
425 430 435	



cga aat cta gag gat ttc gga gta gag gag gga acc atg gaa tac gtg	1459
Arg Asn Leu Glu Asp Phe Gly Val Glu Glu Gly Thr Met Glu Tyr Val	
440 445 450	
acc cct gtt ctg tcg gac cca gaa gcc gtt gtg cac tta gat cgt tcg	1507
Thr Pro Val Leu Ser Asp Pro Glu Ala Val Val His Leu Asp Arg Ser	
455 460 465	
ctc gaa aca ttg aga ggt aaa cag aaa aac gtt gct atg tca ttt agc	1555
Leu Glu Thr Leu Arg Gly Lys Gln Lys Asn Val Ala Met Ser Phe Ser	
470 475 480 485	
tcg atg ggc aat gtt gga ggc aga atc gga act tta ctc gtt aat gtt	1603
Ser Met Gly Asn Val Gly Gly Arg Ile Gly Thr Leu Leu Val Asn Val	
490 495 500	
gtc gat gta acc gag cgc caa gaa ctc atc gag ctt gtg gag cat ttg	1651
Val Asp Val Thr Glu Arg Gln Glu Leu Ile Glu Leu Val Glu His Leu	
505 510 515	
gcg gat cat gac tcc ctg aca gga ttg gtc aat cgc agg cgg ctg gaa	1699
Ala Asp His Asp Ser Leu Thr Gly Leu Val Asn Arg Arg Arg Leu Glu	
520 525 530	
tct gat atc gaa gag ctt atc ctc aag aat gaa cgc gat tcg acc gat	1747
Ser Asp Ile Glu Glu Leu Ile Leu Lys Asn Glu Arg Asp Ser Thr Asp	
535 540 545	
agt gca ttg ttg ctt ttg gat ctg gat tac ttc aag gaa gtt aat gat	1795
Ser Ala Leu Leu Leu Leu Asp Leu Asp Tyr Phe Lys Glu Val Asn Asp	
550 555 560 565	
tcc ctc ggc cat gag gct ggt gac cag ttg ctt att gag ttt gct gag	1843
Ser Leu Gly His Glu Ala Gly Asp Gln Leu Leu Ile Glu Phe Ala Glu	
570 575 580	
atc ctc aaa gac agc gtg agg gat tcc gac att gtc gga cgc atc ggc	1891
Ile Leu Lys Asp Ser Val Arg Asp Ser Asp Ile Val Gly Arg Ile Gly	
585 590 595	
ggc gat gaa ttc gtt att gtt ttg cct gac aca gac agg gat ggc gct	1939
Gly Asp Glu Phe Val Ile Val Leu Pro Asp Thr Asp Arg Asp Gly Ala	
600 605 610	
gaa gca atc ggt ata aga att att gag ttg gtc aat cag cac ttc aaa	1987
Glu Ala Ile Gly Ile Arg Ile Ile Glu Leu Val Asn Gln His Phe Lys	
615 620 625	
ggc cga gga aaa gtg tta tcg cgg gtg tca agt aaa gta tcg gcg gga	2035
Gly Arg Gly Lys Val Leu Ser Arg Val Ser Ser Lys Val Ser Ala Gly	
630 635 640 645	
cgc tct ttt ctg atg ctc gtg ccc aag gtg tgaatccatt cattcttgct	2085
Arg Ser Phe Leu Met Leu Val Pro Lys Val	
650 655	
gat	2088

&lt;210&gt; 40

&lt;211&gt; 655

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 40

Val	Val	Ala	Arg	Asp	Leu	Gln	Lys	Leu	Glu	Lys	Leu	Arg	Leu	Ile	Cys
1				5					10					15	
Gly	Tyr	Val	Phe	Leu	Val	Pro	Ala	Ile	Tyr	Leu	His	Phe	Phe	Ala	Glu
			20					25						30	
Thr	Ser	Leu	Arg	Gly	Val	Ile	Leu	Ala	Gly	Ile	Ala	His	Ala	Ile	Ala
		35					40					45			
Gly	Pro	Gly	Val	Ala	Leu	Val	Met	Ala	Phe	Met	Glu	Asn	Ala	Gln	Leu
	50					55					60				
Pro	Glu	Leu	Leu	Arg	Lys	Arg	His	Ala	Phe	Ala	Pro	Phe	Ser	His	Ile
	65				70					75					80
Arg	Leu	Pro	Gly	Asp	Val	Phe	Arg	Leu	Leu	Val	Ala	Gly	Ile	Val	Met
				85					90					95	
Val	Ala	Ile	Ser	Lys	Leu	Ile	Val	Ile	Leu	Ala	Tyr	Ala	Leu	Ala	Asp
			100					105					110		
Leu	Pro	Tyr	Ser	Phe	Thr	Leu	Tyr	Leu	Thr	Met	Ala	Leu	Arg	Asp	Leu
		115					120					125			
Thr	Gly	Ile	Ile	Val	Val	Ala	Gly	Pro	Gly	Ile	Ala	Leu	Ser	Thr	Pro
	130					135					140				
Leu	Val	Leu	Asn	Ile	His	Arg	Ser	Ala	Trp	Arg	Glu	Phe	Ala	Val	Val
145					150					155					160
Ile	Ile	Ala	Thr	Val	Gly	Val	Leu	Ala	Leu	Ile	Phe	Gly	Phe	Ala	Val
				165					170					175	
Asp	Leu	Pro	Thr	Val	Tyr	Leu	Ala	Met	Leu	Pro	Leu	Tyr	Trp	Ser	Ala
			180					185					190		
Thr	Arg	Leu	Pro	Val	Leu	Leu	Ala	Val	Leu	His	Ala	Val	Phe	Thr	Ser
		195					200					205			
Ala	Ile	Val	Val	Ile	Leu	Tyr	Phe	Leu	Leu	Gly	Thr	Gly	Ser	Phe	Ala
	210					215					220				
Ile	Thr	Asp	Glu	Ser	Ile	Leu	Val	Gln	Ala	Thr	Thr	Ile	Gln	Leu	Phe
225					230					235					240
Val	Leu	Met	Cys	Ile	Leu	Leu	Ser	Leu	Val	Val	Ser	Thr	Thr	Val	Gln
				245					250					255	
Gln	Thr	Ser	Ala	Leu	Val	Glu	Glu	Leu	Glu	Val	Val	Ala	Lys	Thr	Leu
			260					265					270		
Pro	Asp	Ala	Leu	Phe	Ile	Val	Asn	Lys	Asn	Gly	Thr	Ala	Phe	Pro	Val
		275					280					285			
Asn	Ala	Gly	Ala	Lys	Asn	Phe	Val	Lys	Gln	Ser	Pro	Asp	Gly	His	Tyr
	290					295					300				

Ser Met Pro Lys Leu Gln Asn Ile Asp Gly Glu Pro Met Asp Glu Lys  
 305 310 315 320  
 Glu Ser Pro Ser Ser Met Ala Leu Arg Gly Gln Gly Val Glu Gly Val  
 325 330 335  
 Leu Ala Lys Leu Gly Glu Val Leu Gly Glu Asp Pro Asp Leu Ala Arg  
 340 345 350  
 Arg Ile Phe Glu Ile Ser Ala Ser Pro Met Tyr Leu Arg Gly Glu Thr  
 355 360 365  
 Glu Pro Gly His Ala Leu Val Ile Trp His Asp Ser Thr Asn Glu Tyr  
 370 375 380  
 Tyr Thr Met Gln Gln Leu Thr Leu Ala Tyr Glu Glu Ser Arg Leu Leu  
 385 390 395 400  
 Phe Glu Lys Ala Pro Gln Gly Ile Ala Met Leu Asp Pro Ser Gly Glu  
 405 410 415  
 Ile Val Met Ala Asn Arg Ser Phe Gly Asp Leu Val Gly Thr Thr Pro  
 420 425 430  
 Val Arg Leu Leu Gly Arg Asn Leu Glu Asp Phe Gly Val Glu Glu Gly  
 435 440 445  
 Thr Met Glu Tyr Val Thr Pro Val Leu Ser Asp Pro Glu Ala Val Val  
 450 455 460  
 His Leu Asp Arg Ser Leu Glu Thr Leu Arg Gly Lys Gln Lys Asn Val  
 465 470 475 480  
 Ala Met Ser Phe Ser Ser Met Gly Asn Val Gly Gly Arg Ile Gly Thr  
 485 490 495  
 Leu Leu Val Asn Val Val Asp Val Thr Glu Arg Gln Glu Leu Ile Glu  
 500 505 510  
 Leu Val Glu His Leu Ala Asp His Asp Ser Leu Thr Gly Leu Val Asn  
 515 520 525  
 Arg Arg Arg Leu Glu Ser Asp Ile Glu Glu Leu Ile Leu Lys Asn Glu  
 530 535 540  
 Arg Asp Ser Thr Asp Ser Ala Leu Leu Leu Leu Asp Leu Asp Tyr Phe  
 545 550 555 560  
 Lys Glu Val Asn Asp Ser Leu Gly His Glu Ala Gly Asp Gln Leu Leu  
 565 570 575  
 Ile Glu Phe Ala Glu Ile Leu Lys Asp Ser Val Arg Asp Ser Asp Ile  
 580 585 590  
 Val Gly Arg Ile Gly Gly Asp Glu Phe Val Ile Val Leu Pro Asp Thr  
 595 600 605  
 Asp Arg Asp Gly Ala Glu Ala Ile Gly Ile Arg Ile Ile Glu Leu Val  
 610 615 620  
 Asn Gln His Phe Lys Gly Arg Gly Lys Val Leu Ser Arg Val Ser Ser

<400> 41															
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tcgacaccat ccgaggtggt ggctaccgga tggccttcaa atg Met 1 aca Thr 1 gcc Ala 1 ctc Leu 1 atc Ile 5 115															
cca gct cgc cac agc ctg act ttt cgt ctg ctc acc gcg cag ctt gct 163 Pro Ala Arg His Ser Leu Thr Phe Arg Leu Leu Thr Ala Gln Leu Ala 20															
gtg gtg ttg atc agt ctg ctg gcc gcc ctg att gtg gct gcc ttg gta 211 Val Val Leu Ile Ser Leu Leu Ala Ala Leu Ile Val Ala Ala Leu Val 35															
ggg cct gca att ttc aat tct cac ctg gat ctt tcc ggc ccg att gat 259 Gly Pro Ala Ile Phe Asn Ser His Leu Asp Leu Ser Gly Pro Ile Asp 50															
ccc cgc cag acg gat ttc cac att cag gag gcc tac cgg gac gcc aat 307 Pro Arg Gln Thr Asp Phe His Ile Gln Glu Ala Tyr Arg Asp Ala Asn 65															
tac att gcc ctc gca gcg gca ctt ccc acc gca gtg ttg agc tcc att 355 Tyr Ile Ala Leu Ala Ala Ala Leu Pro Thr Ala Val Leu Ser Ser Ile 85															
ggt gtg agt ttt tgg ctt tcc cac cgc ctg ggc cag ccg ttg tgg cga 403 Gly Val Ser Phe Trp Leu Ser His Arg Leu Gly Gln Pro Leu Trp Arg 100															
ctg tcc cgg gct gca act gcc atg agc tcc ggc gac tac cag gtg cgc 451 Leu Ser Arg Ala Ala Thr Ala Met Ser Ser Gly Asp Tyr Gln Val Arg 115															
gta ccc att tcc gat gtg gat aaa gag gtc gct gct cta tct ctc gcc 499 Val Pro Ile Ser Asp Val Asp Lys Glu Val Ala Ala Leu Ser Leu Ala 130															
ttc aat tcc atg gcg gat cag ctc gaa cac aca gaa gaa ctc cgc cga 547 Phe Asn Ser Met Ala Asp Gln Leu Glu His Thr Glu Glu Leu Arg Arg 145															
aac atg ctc tcc gat cta tcc cat gaa atg aac act ccc ctt tcc gtc 595 Asn Met Leu Ser Asp Leu Ser His Glu Met Asn Thr Pro Leu Ser Val															

150	155	160	165	
ctc ctt gtt tat gtc gac ggt ttg cag gac ggc atg gtg gag tgg gac				643
Leu Leu Val Tyr Val Asp Gly Leu Gln Asp Gly Met Val Glu Trp Asp	170	175	180	
gcc gac acc cac gca gtt ttc gcc gag caa ctt ggc cgg ctt tcc cgc				691
Ala Asp Thr His Ala Val Phe Ala Glu Gln Leu Gly Arg Leu Ser Arg	185	190	195	
ctc aca tca gat ctt gat gat gtc tct aga gcc caa gaa cac cgc ttc				739
Leu Thr Ser Asp Leu Asp Asp Val Ser Arg Ala Gln Glu His Arg Phe	200	205	210	
gac ctg gtc tac agc acc gtc gcc atc ggt ggt ctc att cac aat gcc				787
Asp Leu Val Tyr Ser Thr Val Ala Ile Gly Gly Leu Ile His Asn Ala	215	220	225	
gcc gga gcc gcc gca ggt tcc tac caa gaa aaa ggc gtg gcc ctg gaa				835
Ala Gly Ala Ala Ala Gly Ser Tyr Gln Glu Lys Gly Val Ala Leu Glu	230	235	240	245
gta aca ggc agc gat tcc acc gaa ctc atc cgc gtt gat agc caa cgc				883
Val Thr Gly Ser Asp Ser Thr Glu Leu Ile Arg Val Asp Ser Gln Arg	250	255	260	
ttc gcc caa gtc atg gcc aac ctc ttc tcc aac gcc ttg cgg cac acc				931
Phe Ala Gln Val Met Ala Asn Leu Phe Ser Asn Ala Leu Arg His Thr	265	270	275	
ccc gcc ggt ggg aaa gtt cac gtc cgc gtc ctg cgt caa ggc gtg gga				979
Pro Ala Gly Gly Lys Val His Val Arg Val Leu Arg Gln Gly Val Gly	280	285	290	
acc atc gtc atc gaa gtc ata gac aac ggc gaa gga atc gcc cct gaa				1027
Thr Ile Val Ile Glu Val Ile Asp Asn Gly Glu Gly Ile Ala Pro Glu	295	300	305	
cac gta aaa tac gtt ttc gaa cgc tac ttc cgc gcc aaa cga tcc gac				1075
His Val Lys Tyr Val Phe Glu Arg Tyr Phe Arg Ala Lys Arg Ser Asp	310	315	320	325
tcc gac gac caa tcc ggc tcc gga atc ggc ctc acc atc tcc cgc gca				1123
Ser Asp Asp Gln Ser Gly Ser Gly Ile Gly Leu Thr Ile Ser Arg Ala	330	335	340	
ctc atc gaa gcg caa ggt ggc aca cta acc gca gaa tcc gct ggc ctg				1171
Leu Ile Glu Ala Gln Gly Gly Thr Leu Thr Ala Glu Ser Ala Gly Leu	345	350	355	
ggc aaa ggc gcg aaa ttt acc atc cga cta ccc ctt tta agc aaa				1216
Gly Lys Gly Ala Lys Phe Thr Ile Arg Leu Pro Leu Leu Ser Lys	360	365	370	
taaaaaaatt gcttttcgac gct				1239

&lt;210&gt; 42

&lt;211&gt; 372

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 42

Met	Thr	Ala	Leu	Ile	Pro	Ala	Arg	His	Ser	Leu	Thr	Phe	Arg	Leu	Leu	1	5	10	15
Thr	Ala	Gln	Leu	Ala	Val	Val	Leu	Ile	Ser	Leu	Leu	Ala	Ala	Leu	Ile	20	25	30	
Val	Ala	Ala	Leu	Val	Gly	Pro	Ala	Ile	Phe	Asn	Ser	His	Leu	Asp	Leu	35	40	45	
Ser	Gly	Pro	Ile	Asp	Pro	Arg	Gln	Thr	Asp	Phe	His	Ile	Gln	Glu	Ala	50	55	60	
Tyr	Arg	Asp	Ala	Asn	Tyr	Ile	Ala	Leu	Ala	Ala	Ala	Leu	Pro	Thr	Ala	65	70	75	80
Val	Leu	Ser	Ser	Ile	Gly	Val	Ser	Phe	Trp	Leu	Ser	His	Arg	Leu	Gly	85	90	95	
Gln	Pro	Leu	Trp	Arg	Leu	Ser	Arg	Ala	Ala	Thr	Ala	Met	Ser	Ser	Gly	100	105	110	
Asp	Tyr	Gln	Val	Arg	Val	Pro	Ile	Ser	Asp	Val	Asp	Lys	Glu	Val	Ala	115	120	125	
Ala	Leu	Ser	Leu	Ala	Phe	Asn	Ser	Met	Ala	Asp	Gln	Leu	Glu	His	Thr	130	135	140	
Glu	Glu	Leu	Arg	Arg	Asn	Met	Leu	Ser	Asp	Leu	Ser	His	Glu	Met	Asn	145	150	155	160
Thr	Pro	Leu	Ser	Val	Leu	Leu	Val	Tyr	Val	Asp	Gly	Leu	Gln	Asp	Gly	165	170	175	
Met	Val	Glu	Trp	Asp	Ala	Asp	Thr	His	Ala	Val	Phe	Ala	Glu	Gln	Leu	180	185	190	
Gly	Arg	Leu	Ser	Arg	Leu	Thr	Ser	Asp	Leu	Asp	Asp	Val	Ser	Arg	Ala	195	200	205	
Gln	Glu	His	Arg	Phe	Asp	Leu	Val	Tyr	Ser	Thr	Val	Ala	Ile	Gly	Gly	210	215	220	
Leu	Ile	His	Asn	Ala	Ala	Gly	Ala	Ala	Ala	Gly	Ser	Tyr	Gln	Glu	Lys	225	230	235	240
Gly	Val	Ala	Leu	Glu	Val	Thr	Gly	Ser	Asp	Ser	Thr	Glu	Leu	Ile	Arg	245	250	255	
Val	Asp	Ser	Gln	Arg	Phe	Ala	Gln	Val	Met	Ala	Asn	Leu	Phe	Ser	Asn	260	265	270	
Ala	Leu	Arg	His	Thr	Pro	Ala	Gly	Gly	Lys	Val	His	Val	Arg	Val	Leu	275	280	285	
Arg	Gln	Gly	Val	Gly	Thr	Ile	Val	Ile	Glu	Val	Ile	Asp	Asn	Gly	Glu	290	295	300	
Gly	Ile	Ala	Pro	Glu	His	Val	Lys	Tyr	Val	Phe	Glu	Arg	Tyr	Phe	Arg	305	310	315	320

<400> 43																
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ctgcagccga cgggattaag gcagctaaca ttgagacacg atg aat aaa gat ttc																115
Met Asn Lys Asp Phe																5
1																
tgg acc gca ggc tgg acc gcc cgc tgg ttt tcg cgc ggg gtt tcc ctt																163
Trp Thr Ala Gly Trp Thr Ala Arg Trp Phe Ser Arg Gly Val Ser Leu																20
10 15																
ttg gcc agc cca gtt acc gcc cca ctg aac tct tgg cgg aga ttg cct																211
Leu Ala Ser Pro Val Thr Ala Pro Leu Asn Ser Trp Arg Arg Leu Pro																35
25 30																
aac ttg gcc aag tac acc ctc tac acc agg gtg tcg ttg caa gcg atc																259
Asn Leu Ala Lys Tyr Thr Leu Tyr Thr Arg Val Ser Leu Gln Ala Ile																50
40 45																
ccc gtg gtg ttg ctg tcg gcg tat ttc ctg ggc atc gta gct aat gca																307
Pro Val Val Leu Leu Ser Ala Tyr Phe Leu Gly Ile Val Ala Asn Ala																65
55 60																
ggc acc ctg aat ccc tca ttt gtg tgg ctg ctg ggt ttc tcg gtc atc																355
Gly Thr Leu Asn Pro Ser Phe Val Trp Leu Leu Gly Phe Ser Val Ile																85
70 75 80																
ctt tta ata gtg acg gta ttg gtt tat gaa tat cag cca tcg ctg aat																403
Leu Leu Ile Val Thr Val Leu Val Tyr Glu Tyr Gln Pro Ser Leu Asn																100
90 95																
tct cat cct agg cgc agc gta cag ccg ttc ttc ttc acc ggg ttg gtg																451
Ser His Pro Arg Arg Ser Val Gln Pro Phe Phe Phe Thr Gly Leu Val																115
105 110																
ctc aac gtt tta ggc gtt gtg gtg tct gtg gtg ctt caa att ccg ggc																499
Leu Asn Val Leu Gly Val Val Val Ser Val Val Leu Gln Ile Pro Gly																

120	125	130	
tta aac atg tcg gac aac acc cga gca act gcc ctt att ttc act ctt Leu Asn Met Ser Asp Asn Thr Arg Ala Thr Ala Leu Ile Phe Thr Leu 135 140 145			547
acc tgc gta ttt ctg ctt tcg atc gcc tac att ccg tgg atg aat tac Thr Cys Val Phe Leu Leu Ser Ile Ala Tyr Ile Pro Trp Met Asn Tyr 150 155 160 165			595
cga tgg gtt tgg ctg atc gca atg tct gca gtg ttg tgg tgg acc agc Arg Trp Val Trp Leu Ile Ala Met Ser Ala Val Leu Trp Trp Thr Ser 170 175 180			643
aca acg act gat tat tta agt gca ttg tgg gtg gtt atc ccg cca ctc Thr Thr Thr Asp Tyr Leu Ser Ala Leu Trp Val Val Ile Pro Pro Leu 185 190 195			691
atg gca gga acc gtc cga ctt tcc gta tgg acc gtc gat gtc atg aaa Met Ala Gly Thr Val Arg Leu Ser Val Trp Thr Val Asp Val Met Lys 200 205 210			739
gag gtt gag cgt tcc cgc gaa ttg gaa gcc tcc ctc cgc gtc acc gaa Glu Val Glu Arg Ser Arg Glu Leu Glu Ala Ser Leu Arg Val Thr Glu 215 220 225			787
gaa cgc ctt cgt ttc gcc cag gaa ctc cac gac act tta gga caa cac Glu Arg Leu Arg Phe Ala Gln Glu Leu His Asp Thr Leu Gly Gln His 230 235 240 245			835
ctg gcg gca atg tcc gtg aaa tca gaa ctg gcg ctt gcc ctg gcg aaa Leu Ala Ala Met Ser Val Lys Ser Glu Leu Ala Leu Ala Leu Ala Lys 250 255 260			883
cgc ggc gac gac cgc ctc gaa aac gag ctg cgt gag ctc caa aaa ctc Arg Gly Asp Asp Arg Leu Glu Asn Glu Leu Arg Glu Leu Gln Lys Leu 265 270 275			931
acc cgc acc tcc atg tcg gaa atg cgc gac gtc gtc tcc ggc tac cgc Thr Arg Thr Ser Met Ser Glu Met Arg Asp Val Val Ser Gly Tyr Arg 280 285 290			979
acc gtc aac ctc gcc acg gaa atc gag ggc gct aaa agt ttg ctt gcc Thr Val Asn Leu Ala Thr Glu Ile Glu Gly Ala Lys Ser Leu Leu Ala 295 300 305			1027
gac gcc cac atc cac ctt tcc gtc atc ggc acc acg tcc cag gtg tca Asp Ala His Ile His Leu Ser Val Ile Gly Thr Thr Ser Gln Val Ser 310 315 320 325			1075
ccc gct cac cga gaa ctg tgc gcg tgg ctt gtc cgg gaa gcc acc aca Pro Ala His Arg Glu Leu Cys Ala Trp Leu Val Arg Glu Ala Thr Thr 330 335 340			1123
aac att ctg cgc cac tct gat gca acg gat gcc acc ctc acg ttg agc Asn Ile Leu Arg His Ser Asp Ala Thr Asp Ala Thr Leu Thr Leu Ser 345 350 355			1171
agc aca gag gtg cgc atg gac aac aat ggt gtg aac aag gac atc ggc Ser Thr Glu Val Arg Met Asp Asn Asn Gly Val Asn Lys Asp Ile Gly 360 365 370			1219



aga ctc tct ggt ctc agc gcc ctg cgc tca cga gcg gaa tca gcc gga 1267  
 Arg Leu Ser Gly Leu Ser Ala Leu Arg Ser Arg Ala Glu Ser Ala Gly  
 375 380 385

atg acg ctc att gtg tcc cgc gaa gac gac cag ttc agc gtc cgc atg 1315  
 Met Thr Leu Ile Val Ser Arg Glu Asp Asp Gln Phe Ser Val Arg Met  
 390 395 400 405

ctc att aat gca cct gca aat aca cct gca gaa aag gaa gct 1357  
 Leu Ile Asn Ala Pro Ala Asn Thr Pro Ala Glu Lys Glu Ala  
 410 415

taaatgattt ccatttccat cgc 1380

<210> 44

<211> 419

<212> PRT

<213> Corynebacterium glutamicum

<400> 44

Met Asn Lys Asp Phe Trp Thr Ala Gly Trp Thr Ala Arg Trp Phe Ser  
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Arg Gly Val Ser Leu Leu Ala Ser Pro Val Thr Ala Pro Leu Asn Ser  
 20 25 30

Trp Arg Arg Leu Pro Asn Leu Ala Lys Tyr Thr Leu Tyr Thr Arg Val  
 35 40 45

Ser Leu Gln Ala Ile Pro Val Val Leu Leu Ser Ala Tyr Phe Leu Gly  
 50 55 60

Ile Val Ala Asn Ala Gly Thr Leu Asn Pro Ser Phe Val Trp Leu Leu  
 65 70 75 80

Gly Phe Ser Val Ile Leu Leu Ile Val Thr Val Leu Val Tyr Glu Tyr  
 85 90 95

Gln Pro Ser Leu Asn Ser His Pro Arg Arg Ser Val Gln Pro Phe Phe  
 100 105 110

Phe Thr Gly Leu Val Leu Asn Val Leu Gly Val Val Val Ser Val Val  
 115 120 125

Leu Gln Ile Pro Gly Leu Asn Met Ser Asp Asn Thr Arg Ala Thr Ala  
 130 135 140

Leu Ile Phe Thr Leu Thr Cys Val Phe Leu Leu Ser Ile Ala Tyr Ile  
 145 150 155 160

Pro Trp Met Asn Tyr Arg Trp Val Trp Leu Ile Ala Met Ser Ala Val  
 165 170 175

Leu Trp Trp Thr Ser Thr Thr Thr Asp Tyr Leu Ser Ala Leu Trp Val  
 180 185 190

Val Ile Pro Pro Leu Met Ala Gly Thr Val Arg Leu Ser Val Trp Thr  
 195 200 205

Val Asp Val Met Lys Glu Val Glu Arg Ser Arg Glu Leu Glu Ala Ser  
 210 215 220  
 Leu Arg Val Thr Glu Glu Arg Leu Arg Phe Ala Gln Glu Leu His Asp  
 225 230 235 240  
 Thr Leu Gly Gln His Leu Ala Ala Met Ser Val Lys Ser Glu Leu Ala  
 245 250 255  
 Leu Ala Leu Ala Lys Arg Gly Asp Asp Arg Leu Glu Asn Glu Leu Arg  
 260 265 270  
 Glu Leu Gln Lys Leu Thr Arg Thr Ser Met Ser Glu Met Arg Asp Val  
 275 280 285  
 Val Ser Gly Tyr Arg Thr Val Asn Leu Ala Thr Glu Ile Glu Gly Ala  
 290 295 300  
 Lys Ser Leu Leu Ala Asp Ala His Ile His Leu Ser Val Ile Gly Thr  
 305 310 315 320  
 Thr Ser Gln Val Ser Pro Ala His Arg Glu Leu Cys Ala Trp Leu Val  
 325 330 335  
 Arg Glu Ala Thr Thr Asn Ile Leu Arg His Ser Asp Ala Thr Asp Ala  
 340 345 350  
 Thr Leu Thr Leu Ser Ser Thr Glu Val Arg Met Asp Asn Asn Gly Val  
 355 360 365  
 Asn Lys Asp Ile Gly Arg Leu Ser Gly Leu Ser Ala Leu Arg Ser Arg  
 370 375 380  
 Ala Glu Ser Ala Gly Met Thr Leu Ile Val Ser Arg Glu Asp Asp Gln  
 385 390 395 400  
 Phe Ser Val Arg Met Leu Ile Asn Ala Pro Ala Asn Thr Pro Ala Glu  
 405 410 415  
 Lys Glu Ala

<210> 45  
 <211> 895  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(895)  
 <223> FRXA01211

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 ctgcagccga cgggattaag gcagctaaca ttgagacacg atg aat aaa gat ttc 115  
 Met Asn Lys Asp Phe  
 1 5  
 tgg acc gca ggc tgg acc gcc cgc tgg ttt tcg cgc ggg gtt tcc ctt 163

Trp	Thr	Ala	Gly	Trp	Thr	Ala	Arg	Trp	Phe	Ser	Arg	Gly	Val	Ser	Leu	
				10					15					20		
ttg	gcc	agc	cca	gtt	acc	gcc	cca	ctg	aac	tct	tgg	cgg	aga	ttg	cct	211
Leu	Ala	Ser	Pro	Val	Thr	Ala	Pro	Leu	Asn	Ser	Trp	Arg	Arg	Leu	Pro	
			25					30					35			
aac	ttg	gcc	aag	tac	acc	ctc	tac	acc	agg	gtg	tcg	ttg	caa	gcg	atc	259
Asn	Leu	Ala	Lys	Tyr	Thr	Leu	Tyr	Thr	Arg	Val	Ser	Leu	Gln	Ala	Ile	
		40					45					50				
ccc	gtg	gtg	ttg	ctg	tcg	gcg	tat	ttc	ctg	ggc	atc	gta	gct	aat	gca	307
Pro	Val	Val	Leu	Leu	Ser	Ala	Tyr	Phe	Leu	Gly	Ile	Val	Ala	Asn	Ala	
	55					60					65					
ggc	acc	ctg	aat	ccc	tca	ttt	gtg	tgg	ctg	ctg	ggt	ttc	tcg	gtc	atc	355
Gly	Thr	Leu	Asn	Pro	Ser	Phe	Val	Trp	Leu	Leu	Gly	Phe	Ser	Val	Ile	
70					75				80						85	
ctt	tta	ata	gtg	acg	gta	ttg	gtt	tat	gaa	tat	cag	cca	tcg	ctg	aat	403
Leu	Leu	Ile	Val	Thr	Val	Leu	Val	Tyr	Glu	Tyr	Gln	Pro	Ser	Leu	Asn	
				90				95						100		
tct	cat	cct	agg	cgc	agc	gta	cag	ccg	ttc	ttc	ttc	acc	ggg	ttg	gtg	451
Ser	His	Pro	Arg	Arg	Ser	Val	Gln	Pro	Phe	Phe	Phe	Thr	Gly	Leu	Val	
			105					110					115			
ctc	aac	gtt	tta	ggc	gtt	gtg	gtg	tct	gtg	gtg	ctt	caa	att	ccg	ggc	499
Leu	Asn	Val	Leu	Gly	Val	Val	Val	Ser	Val	Val	Leu	Gln	Ile	Pro	Gly	
		120				125						130				
tta	aac	atg	tcg	gac	aac	acc	cga	gca	act	gcc	ctt	att	ttc	act	ctt	547
Leu	Asn	Met	Ser	Asp	Asn	Thr	Arg	Ala	Thr	Ala	Leu	Ile	Phe	Thr	Leu	
	135					140					145					
acc	tgc	gta	ttt	ctg	ctt	tcg	atc	gcc	tac	att	ccg	tgg	atg	aat	tac	595
Thr	Cys	Val	Phe	Leu	Leu	Ser	Ile	Ala	Tyr	Ile	Pro	Trp	Met	Asn	Tyr	
150					155				160						165	
cga	tgg	gtt	tgg	ctg	atc	gca	atg	tct	gca	gtg	ttg	tgg	tgg	acc	agc	643
Arg	Trp	Val	Trp	Leu	Ile	Ala	Met	Ser	Ala	Val	Leu	Trp	Trp	Thr	Ser	
				170				175						180		
aca	acg	act	gat	tat	tta	agt	gca	ttg	tgg	gtg	gtt	atc	ccg	cca	ctc	691
Thr	Thr	Thr	Asp	Tyr	Leu	Ser	Ala	Leu	Trp	Val	Val	Ile	Pro	Pro	Leu	
			185					190					195			
atg	gca	gga	acc	gtc	cga	ctt	tcc	gta	tgg	acc	gtc	gat	gtc	atg	aaa	739
Met	Ala	Gly	Thr	Val	Arg	Leu	Ser	Val	Trp	Thr	Val	Asp	Val	Met	Lys	
		200					205					210				
gag	gtt	gag	cgt	tcc	cgc	gaa	ttg	gaa	gcc	tcc	ctc	cgc	gtc	acc	gaa	787
Glu	Val	Glu	Arg	Ser	Arg	Glu	Leu	Glu	Ala	Ser	Leu	Arg	Val	Thr	Glu	
	215					220					225					
gaa	cgc	ctt	cgt	ttc	gcc	cag	gaa	ctc	cac	gac	act	tta	gga	caa	cac	835
Glu	Arg	Leu	Arg	Phe	Ala	Gln	Glu	Leu	His	Asp	Thr	Leu	Gly	Gln	His	
230					235					240					245	
ctg	gcg	gca	atg	tcc	gtg	aaa	tca	gaa	ctg	gcg	ctt	gcc	ctg	gcg	aaa	883
Leu	Ala	Ala	Met	Ser	Val	Lys	Ser	Glu	Leu	Ala	Leu	Ala	Leu	Ala	Lys	

250

255

260

cgc ggc gac gac  
 Arg Gly Asp Asp  
 265

895

<210> 46  
 <211> 265  
 <212> PRT  
 <213> Corynebacterium glutamicum

&lt;400&gt; 46

Met Asn Lys Asp Phe Trp Thr Ala Gly Trp Thr Ala Arg Trp Phe Ser  
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Arg Gly Val Ser Leu Leu Ala Ser Pro Val Thr Ala Pro Leu Asn Ser  
 20 25 30

Trp Arg Arg Leu Pro Asn Leu Ala Lys Tyr Thr Leu Tyr Thr Arg Val  
 35 40 45

Ser Leu Gln Ala Ile Pro Val Val Leu Leu Ser Ala Tyr Phe Leu Gly  
 50 55 60

Ile Val Ala Asn Ala Gly Thr Leu Asn Pro Ser Phe Val Trp Leu Leu  
 65 70 75 80

Gly Phe Ser Val Ile Leu Leu Ile Val Thr Val Leu Val Tyr Glu Tyr  
 85 90 95

Gln Pro Ser Leu Asn Ser His Pro Arg Arg Ser Val Gln Pro Phe Phe  
 100 105 110

Phe Thr Gly Leu Val Leu Asn Val Leu Gly Val Val Val Ser Val Val  
 115 120 125

Leu Gln Ile Pro Gly Leu Asn Met Ser Asp Asn Thr Arg Ala Thr Ala  
 130 135 140

Leu Ile Phe Thr Leu Thr Cys Val Phe Leu Leu Ser Ile Ala Tyr Ile  
 145 150 155 160

Pro Trp Met Asn Tyr Arg Trp Val Trp Leu Ile Ala Met Ser Ala Val  
 165 170 175

Leu Trp Trp Thr Ser Thr Thr Thr Asp Tyr Leu Ser Ala Leu Trp Val  
 180 185 190

Val Ile Pro Pro Leu Met Ala Gly Thr Val Arg Leu Ser Val Trp Thr  
 195 200 205

Val Asp Val Met Lys Glu Val Glu Arg Ser Arg Glu Leu Glu Ala Ser  
 210 215 220

Leu Arg Val Thr Glu Glu Arg Leu Arg Phe Ala Gln Glu Leu His Asp  
 225 230 235 240

Thr Leu Gly Gln His Leu Ala Ala Met Ser Val Lys Ser Glu Leu Ala  
 245 250 255

Leu Ala Leu Ala Lys Arg Gly Asp Asp  
           260                          265

<210> 47  
 <211> 529  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(529)  
 <223> RXA01248

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   Met Ala Asp Arg Thr  
   1                          5  
 ccg acc acc gcc acg ccc ccg ggg cgg gtg ctg gtc gtc gat gat gaa 163  
 Pro Thr Thr Ala Thr Pro Pro Gly Arg Val Leu Val Val Asp Asp Glu  
                           10                          15                          20  
 caa ccc ctg gct cag atg gtg gcc tcc tac ctc atc cgg gcc ggc attc 211  
 Gln Pro Leu Ala Gln Met Val Ala Ser Tyr Leu Ile Arg Ala Gly Phe  
                           25                          30                          35  
 gac acc cgc cag gcg cac acc ggc acc cag gcc gtg gac gag gcc cgt 259  
 Asp Thr Arg Gln Ala His Thr Gly Thr Gln Ala Val Asp Glu Ala Arg  
                           40                          45                          50  
 cgc ttt tcc ccc gat gtt gtg gtg ctg gat ctg ggg ctg ccc gaa ctc 307  
 Arg Phe Ser Pro Asp Val Val Val Leu Asp Leu Gly Leu Pro Glu Leu  
                           55                          60                          65  
 gac ggc ctg gag gtg tgc cga cgg atc cgc acc ttc tcg gac tgc tac 355  
 Asp Gly Leu Glu Val Cys Arg Arg Ile Arg Thr Phe Ser Asp Cys Tyr  
                           70                          75                          80                          85  
 atc ctc atg ctc acc gcg cgt ggc agc gag gac gac aag atc agc ggt 403  
 Ile Leu Met Leu Thr Ala Arg Gly Ser Glu Asp Asp Lys Ile Ser Gly  
                           90                          95                          100  
 ttg acc ctg ggg gcg gat gac tac atc acc aaa cct ttt agc atc cgg 451  
 Leu Thr Leu Gly Ala Asp Asp Tyr Ile Thr Lys Pro Phe Ser Ile Arg  
                           105                          110                          115  
 gaa ctg gtg acc cgg gtg cat gcg gtg ctg cgc cgc ccg cgc acc agc 499  
 Glu Leu Val Thr Arg Val His Ala Val Leu Arg Arg Pro Arg Thr Ser  
                           120                          125                          130  
 acc acc cca ccg cag gtg acc acc ccc ttg 529  
 Thr Thr Pro Pro Gln Val Thr Thr Pro Leu  
                           135                          140

<210> 48  
 <211> 143  
 <212> PRT

<213> Corynebacterium glutamicum

<400> 48

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Met Ala Asp Arg Thr Pro Thr Thr Ala Thr Pro Pro Gly Arg Val Leu
 1           5           10           15

Val Val Asp Asp Glu Gln Pro Leu Ala Gln Met Val Ala Ser Tyr Leu
          20           25           30

Ile Arg Ala Gly Phe Asp Thr Arg Gln Ala His Thr Gly Thr Gln Ala
          35           40           45

Val Asp Glu Ala Arg Arg Phe Ser Pro Asp Val Val Val Leu Asp Leu
          50           55           60

Gly Leu Pro Glu Leu Asp Gly Leu Glu Val Cys Arg Arg Ile Arg Thr
          65           70           75           80

Phe Ser Asp Cys Tyr Ile Leu Met Leu Thr Ala Arg Gly Ser Glu Asp
          85           90           95

Asp Lys Ile Ser Gly Leu Thr Leu Gly Ala Asp Asp Tyr Ile Thr Lys
          100          105          110

Pro Phe Ser Ile Arg Glu Leu Val Thr Arg Val His Ala Val Leu Arg
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Arg Pro Arg Thr Ser Thr Thr Pro Pro Gln Val Thr Thr Pro Leu
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<210> 49

<211> 846

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(823)

<223> RXA02668

<400> 49

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tgttgttaat caggaaacag aaaaggccat acttgaaacc atg acg aac ccc tcc 115
                               Met Thr Asn Pro Ser
                               1           5

ccc gcg cta aat gaa acc ctt tcc ggc agg gtg ctg atc gtt gaa gat 163
Pro Ala Leu Asn Glu Thr Leu Ser Gly Arg Val Leu Ile Val Glu Asp
          10           15           20

gag cgc cct ctt gct cgc atg att tcg ctt tat tta agc aaa gcg ggt 211
Glu Arg Pro Leu Ala Arg Met Ile Ser Leu Tyr Leu Ser Lys Ala Gly
          25           30           35

ttc gat acc acc acg atc cac gac ggc gcc gct gct cca gat aag gtc 259
Phe Asp Thr Thr Thr Ile His Asp Gly Ala Ala Ala Pro Asp Lys Val
          40           45           50

gct cac ctg cgc ccc gac gtg gtc att ttg gat ctt ggg ctg cct ggt 307

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Ala	His	Leu	Arg	Pro	Asp	Val	Val	Ile	Leu	Asp	Leu	Gly	Leu	Pro	Gly		
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ctt	gat	ggt	ttg	gaa	gtg	tgc	aaa	cgc	atc	cgc	gcg	ttc	acc	gat	tgc	355	
Leu	Asp	Gly	Leu	Glu	Val	Cys	Lys	Arg	Ile	Arg	Ala	Phe	Thr	Asp	Cys	85	
70					75					80							
tac	atc	cta	atg	ctc	acc	gcc	agg	ggt	tca	gag	cgg	gat	cgg	att	aca	403	
Tyr	Ile	Leu	Met	Leu	Thr	Ala	Arg	Gly	Ser	Glu	Arg	Asp	Arg	Ile	Thr	100	
				90					95								
ggt	ttg	gaa	att	ggg	gct	gat	gat	tac	atc	acc	aag	ccg	ttt	aat	atc	451	
Gly	Leu	Glu	Ile	Gly	Ala	Asp	Asp	Tyr	Ile	Thr	Lys	Pro	Phe	Asn	Ile	115	
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cgc	gaa	ctt	gtc	att	cgt	atc	cag	tca	gta	atg	cgt	cgc	cct	cga	aaa	499	
Arg	Glu	Leu	Val	Ile	Arg	Ile	Gln	Ser	Val	Met	Arg	Arg	Pro	Arg	Lys	130	
		120					125										
atc	gat	gaa	acc	atc	caa	aat	ggt	ttg	acc	ttg	act	tat	ggc	cac	att	547	
Ile	Asp	Glu	Thr	Ile	Gln	Asn	Gly	Leu	Thr	Leu	Thr	Tyr	Gly	His	Ile	145	
						140											
gag	ctg	gac	acc	ttg	gcg	cat	gaa	gtc	act	gtc	aaa	ggc	gtt	ggg	gtg	595	
Glu	Leu	Asp	Thr	Leu	Ala	His	Glu	Val	Thr	Val	Lys	Gly	Val	Gly	Val	165	
150					155					160							
aca	ctg	acc	cgc	aca	gaa	ttt	gag	ctg	ctt	caa	gcc	ctc	atg	cac	aaa	643	
Thr	Leu	Thr	Arg	Thr	Glu	Phe	Glu	Leu	Leu	Gln	Ala	Leu	Met	His	Lys	180	
				170					175								
ccg	gga	gag	gca	gtg	tct	agg	cgt	gat	ttg	gtc	agc	caa	gtg	tgg	gat	691	
Pro	Gly	Glu	Ala	Val	Ser	Arg	Arg	Asp	Leu	Val	Ser	Gln	Val	Trp	Asp	195	
			185					190									
acc	acc	tgg	gtt	ggc	gat	gaa	cgc	atc	gtt	gac	gtg	cac	att	gga	aat	739	
Thr	Thr	Trp	Val	Gly	Asp	Glu	Arg	Ile	Val	Asp	Val	His	Ile	Gly	Asn	210	
		200					205										
ctg	cgc	cgc	aag	ctg	gaa	gca	cct	gcg	ccg	ggt	tca	cac	ttc	atc	gac	787	
Leu	Arg	Arg	Lys	Leu	Glu	Ala	Pro	Ala	Pro	Gly	Ser	His	Phe	Ile	Asp	225	
			215			220											
acc	atc	cga	ggt	gtt	ggc	tac	cgg	atg	gcc	ttc	aaa	tgacagccct				833	
Thr	Ile	Arg	Gly	Val	Gly	Tyr	Arg	Met	Ala	Phe	Lys					240	
230					235												
catcccagct	cgc																846

&lt;210&gt; 50

&lt;211&gt; 241

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 50

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Leu	Ile	Val	Glu	Asp	Glu	Arg	Pro	Leu	Ala	Arg	Met	Ile	Ser	Leu	Tyr	
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<212> DNA
<213> Corynebacterium glutamicum
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<223> RXA02632
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gaggaagtct gtcacggact ggaagacgaa aagggtatcg atg aaa att tta gtt 115
               Met Lys Ile Leu Val
               1       5

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gtt gat gac gag caa gct gta cgt gac tcc ttg cga cgt tcc ctt tcg	163
Val Asp Asp Glu Gln Ala Val Arg Asp Ser Leu Arg Arg Ser Leu Ser	
10 15 20	
ttc aac gga tac aac gtt gtt ctc gca gaa gac ggc atc caa gca cta	211
Phe Asn Gly Tyr Asn Val Val Leu Ala Glu Asp Gly Ile Gln Ala Leu	
25 30 35	
gag atg att gac aag gaa cag cct gct ttg gtg atc ctc gat gtc atg	259
Glu Met Ile Asp Lys Glu Gln Pro Ala Leu Val Ile Leu Asp Val Met	
40 45 50	
atg cct ggt atg gac gga ctt gag gtc tgt cgc cac ctt cgc agc gaa	307
Met Pro Gly Met Asp Gly Leu Glu Val Cys Arg His Leu Arg Ser Glu	
55 60 65	
ggc gat gat cgg cca att ctt att ctt act gcc cgc gat aat gtt tct	355
Gly Asp Asp Arg Pro Ile Leu Ile Leu Thr Ala Arg Asp Asn Val Ser	
70 75 80 85	
gat cgt gtt ggt ggc ctc gat gca ggc gca gat gac tat ttg gct aaa	403
Asp Arg Val Gly Gly Leu Asp Ala Gly Ala Asp Asp Tyr Leu Ala Lys	
90 95 100	
cca ttt gct ctt gaa gag ctg ttg gcg cgc gtc cgt tca ctg gtg cgt	451
Pro Phe Ala Leu Glu Glu Leu Leu Ala Arg Val Arg Ser Leu Val Arg	
105 110 115	
cgc tct gca gtg gaa tca aat cag agt tcc agc att gaa cag gct cta	499
Arg Ser Ala Val Glu Ser Asn Gln Ser Ser Ser Ile Glu Gln Ala Leu	
120 125 130	
tta tct tgt ggc gat ttg acg ctt gac cca gaa agt cga gat gtc tac	547
Leu Ser Cys Gly Asp Leu Thr Leu Asp Pro Glu Ser Arg Asp Val Tyr	
135 140 145	
cgc aac gga cgc gcc atc agc ctt act cga aca gag ttc gcg ctc ctg	595
Arg Asn Gly Arg Ala Ile Ser Leu Thr Arg Thr Glu Phe Ala Leu Leu	
150 155 160 165	
caa ttg ctc ctc aaa aac caa agg aaa gtg ctc act cgc gcc cag att	643
Gln Leu Leu Leu Lys Asn Gln Arg Lys Val Leu Thr Arg Ala Gln Ile	
170 175 180	
ttg gaa gag gta tgg ggc tgc gat ttc ccc act tca ggc aat gcc ctc	691
Leu Glu Glu Val Trp Gly Cys Asp Phe Pro Thr Ser Gly Asn Ala Leu	
185 190 195	
gag gtc tac att gga tac ctt cga cgc aag act gaa ttg gaa gga gaa	739
Glu Val Tyr Ile Gly Tyr Leu Arg Arg Lys Thr Glu Leu Glu Gly Glu	
200 205 210	
gac cgc ctg atc cat aca gta cga gga gtc gga tac gtc ctg cga gag	787
Asp Arg Leu Ile His Thr Val Arg Gly Val Gly Tyr Val Leu Arg Glu	
215 220 225	
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Thr Ala Pro	
230	

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 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 52  
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           20                  25                  30  
 Gly Ile Gln Ala Leu Glu Met Ile Asp Lys Glu Gln Pro Ala Leu Val  
           35                  40                  45  
 Ile Leu Asp Val Met Met Pro Gly Met Asp Gly Leu Glu Val Cys Arg  
       50                  55                  60  
 His Leu Arg Ser Glu Gly Asp Asp Arg Pro Ile Leu Ile Leu Thr Ala  
       65                  70                  75                  80  
 Arg Asp Asn Val Ser Asp Arg Val Gly Gly Leu Asp Ala Gly Ala Asp  
                   85                  90                  95  
 Asp Tyr Leu Ala Lys Pro Phe Ala Leu Glu Glu Leu Leu Ala Arg Val  
           100                  105                  110  
 Arg Ser Leu Val Arg Arg Ser Ala Val Glu Ser Asn Gln Ser Ser Ser  
       115                  120                  125  
 Ile Glu Gln Ala Leu Leu Ser Cys Gly Asp Leu Thr Leu Asp Pro Glu  
       130                  135                  140  
 Ser Arg Asp Val Tyr Arg Asn Gly Arg Ala Ile Ser Leu Thr Arg Thr  
       145                  150                  155                  160  
 Glu Phe Ala Leu Leu Gln Leu Leu Leu Lys Asn Gln Arg Lys Val Leu  
           165                  170                  175  
 Thr Arg Ala Gln Ile Leu Glu Glu Val Trp Gly Cys Asp Phe Pro Thr  
           180                  185                  190  
 Ser Gly Asn Ala Leu Glu Val Tyr Ile Gly Tyr Leu Arg Arg Lys Thr  
       195                  200                  205  
 Glu Leu Glu Gly Glu Asp Arg Leu Ile His Thr Val Arg Gly Val Gly  
       210                  215                  220  
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<220>  
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                                     Met Ser Leu Arg Trp
                                     1 5

cgc ttg gct ttg ctg agc gcc act ttg gta gct ttc gcc gtt ggt gtt 163
Arg Leu Ala Leu Leu Ser Ala Thr Leu Val Ala Phe Ala Val Gly Val
                        10 15 20

att act gtt gct gca tat tgg tct gtc tcc agc tat gtc acc aac tca 211
Ile Thr Val Ala Ala Tyr Trp Ser Val Ser Ser Tyr Val Thr Asn Ser
                        25 30 35

atc gat cgt gat ctg gaa aaa caa gcg gat gca atg ctt gga cga gcc 259
Ile Asp Arg Asp Leu Glu Lys Gln Ala Asp Ala Met Leu Gly Arg Ala
                        40 45 50

agt gaa gcg gga ttc tat gca acc gca gaa acc gaa att gct ctg tta 307
Ser Glu Ala Gly Phe Tyr Ala Thr Ala Glu Thr Glu Ile Ala Leu Leu
                        55 60 65

ggg gaa tat gcc agt gac act cga atc gcc tta atc cca cct ggg tgg 355
Gly Glu Tyr Ala Ser Asp Thr Arg Ile Ala Leu Ile Pro Pro Gly Trp
70 75 80 85

gaa tac gtc atc ggt gaa tcc ata tca ctg cct gat tca gat ttc ctt 403
Glu Tyr Val Ile Gly Glu Ser Ile Ser Leu Pro Asp Ser Asp Phe Leu
                        90 95 100

aag agt aaa gaa gcg ggg aaa cag atc ctc gta aca agt gct gag cgc 451
Lys Ser Lys Glu Ala Gly Lys Gln Ile Leu Val Thr Ser Ala Glu Arg
105 110 115

att ctc atg aaa cga gat agc tcg ggc aca gtg gtg gtt ttt gct aaa 499
Ile Leu Met Lys Arg Asp Ser Ser Gly Thr Val Val Val Phe Ala Lys
120 125 130

gat atg gtg gat acc gat cgg cag ctc acg gtg ctt ggc gtc att ctc 547
Asp Met Val Asp Thr Asp Arg Gln Leu Thr Val Leu Gly Val Ile Leu
135 140 145

ttg atc att ggc ggc agt ggt gtt ttg gcg tcg att ctg ctt ggt ttc 595
Leu Ile Ile Gly Gly Ser Gly Val Leu Ala Ser Ile Leu Leu Gly Phe
150 155 160 165

atc att gcg aag gag ggg ctg aaa cca ctg tca aag ctg cag cgt gcc 643
Ile Ile Ala Lys Glu Gly Leu Lys Pro Leu Ser Lys Leu Gln Arg Ala
170 175 180

gtc gaa gag atc gaa cga act gat gag ctt cgt gcg att ccc gtg gtg 691
Val Glu Glu Ile Glu Arg Thr Asp Glu Leu Arg Ala Ile Pro Val Val
185 190 195

gga aat gat gag ttc gct aag ttg act cgt agt ttc aat gac atg ctc 739
Gly Asn Asp Glu Phe Ala Lys Leu Thr Arg Ser Phe Asn Asp Met Leu
200 205 210

aag gca ctg cgg gag tct cgt acc cgg caa tct cag ttg gtg gca gat 787

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Lys Ala 215	Leu	Arg	Glu	Ser	Arg 220	Thr	Arg	Gln	Ser	Gln 225	Leu	Val	Ala	Asp		
gca Ala 230	gga Gly	cac His	gag Glu	ctg Leu	aaa Lys 235	act Thr	cca Pro	ctg Leu	acc Thr	tca Ser 240	atg Met	cgg Arg	aca Thr	aat Asn	att Ile 245	835
gaa Glu	ttg Leu	ctg Leu	ttg Leu	atg Met 250	gca Ala	acc Thr	aac Asn	agt Ser	gga Gly 255	gga Gly	tcg Ser	gga Gly	atc Ile	ccc Pro 260	aag Lys	883
gaa Glu	gaa Glu	ttg Leu	gat Asp 265	ggc Gly	ctt Leu	cag Gln	cgt Arg	gat Asp 270	gta Val	ttg Leu	gcg Ala	cag Gln	atg Met 275	acc Thr	gaa Glu	931
atg Met	tct Ser	gat Asp 280	ttg Leu	att Ile	ggg Gly	gat Asp	ctt Leu 285	gtt Val	gat Asp	ctt Leu	gcg Ala	cgt Arg 290	gaa Glu	gaa Glu	acc Thr	979
gcc Ala 295	gaa Glu	acg Thr	tca Ser	agc Ser	att Ile	gta Val 300	gat Asp	ctc Leu	aac Asn	caa Gln	gtg Val 305	ttg Leu	gaa Glu	att Ile	gcg Ala	1027
ctt Leu 310	gac Asp	cga Arg	atg Met	gaa Glu	agc Ser 315	cgt Arg	cgc Arg	atg Met	acg Thr	gtg Val 320	cgg Arg	ata Ile	gat Asp	gtt Val	tcc Ser 325	1075
gag Glu	act Thr	gtg Val	gat Asp	tgg Trp 330	aaa Lys	ctg Leu	ctg Leu	ggc Gly	gat Asp 335	gat Asp	ttt Phe	tcc Ser	tta Leu	acc Thr 340	agg Arg	1123
gca Ala	tta Leu	gta Val	aat Asn 345	gtt Val	ttg Leu	gat Asp	aat Asn	gcc Ala 350	att Ile	aaa Lys	tgg Trp	tcg Ser	cct Pro 355	gag Glu	aat Asn	1171
ggc Gly	att Ile	gtt Val 360	cga Arg	gtg Val	tcg Ser	atg Met	tca Ser 365	cag Gln	atc Ile	gac Asp	aaa Lys	gca Ala 370	acg Thr	gtc Val	cgc Arg	1219
att Ile	gtt Val 375	att Ile	gat Asp	gat Asp	tca Ser 380	ggg Gly	cct Pro	gga Gly	att Ile	gct Ala 385	gaa Glu	aaa Lys	gaa Glu	cga Arg	gga Gly	1267
tta Leu 390	gtt Val	ttg Leu	gaa Glu	cgg Arg	ttc Phe 395	tat Tyr	cgc Arg	gcc Ala	gtc Val	agc Ser 400	tcc Ser	cgt Arg	tcc Ser	atg Met	ccg Pro 405	1315
gga Gly	tcg Ser	gga Gly	tta Leu	ggg Gly 410	ctt Leu	gcc Ala	atc Ile	gtg Val	aat Asn 415	cag Gln	gtt Val	gtg Val	aat Asn	cgg Arg 420	cat His	1363
ggg Gly	ggc Gly	caa Gln	ctc Leu	gtt Val 425	gtg Val	ggg Gly	gaa Glu	tca Ser 430	gat Asp	gat Asp	ggc Gly	gga Gly	acg Thr 435	aga Arg	atc Ile	1411
act Thr	att Ile	gat Asp 440	ttg Leu	cca Pro	ggg Gly	gaa Glu	ccc Pro 445	att Ile	cgc Arg	agc Ser	ggg Gly	ttc Phe 450	gaa Glu	aat Asn	gtc Val	1459
gat Asp	gat Asp	taaaccacta				aagagctcac				agg						1488

455

&lt;210&gt; 54

&lt;211&gt; 455

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 54

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Phe Ala Val Gly Val Ile Thr Val Ala Ala Tyr Trp Ser Val Ser Ser  
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Tyr Val Thr Asn Ser Ile Asp Arg Asp Leu Glu Lys Gln Ala Asp Ala  
 35 40 45

Met Leu Gly Arg Ala Ser Glu Ala Gly Phe Tyr Ala Thr Ala Glu Thr  
 50 55 60

Glu Ile Ala Leu Leu Gly Glu Tyr Ala Ser Asp Thr Arg Ile Ala Leu  
 65 70 75 80

Ile Pro Pro Gly Trp Glu Tyr Val Ile Gly Glu Ser Ile Ser Leu Pro  
 85 90 95

Asp Ser Asp Phe Leu Lys Ser Lys Glu Ala Gly Lys Gln Ile Leu Val  
 100 105 110

Thr Ser Ala Glu Arg Ile Leu Met Lys Arg Asp Ser Ser Gly Thr Val  
 115 120 125

Val Val Phe Ala Lys Asp Met Val Asp Thr Asp Arg Gln Leu Thr Val  
 130 135 140

Leu Gly Val Ile Leu Leu Ile Ile Gly Gly Ser Gly Val Leu Ala Ser  
 145 150 155 160

Ile Leu Leu Gly Phe Ile Ile Ala Lys Glu Gly Leu Lys Pro Leu Ser  
 165 170 175

Lys Leu Gln Arg Ala Val Glu Glu Ile Glu Arg Thr Asp Glu Leu Arg  
 180 185 190

Ala Ile Pro Val Val Gly Asn Asp Glu Phe Ala Lys Leu Thr Arg Ser  
 195 200 205

Phe Asn Asp Met Leu Lys Ala Leu Arg Glu Ser Arg Thr Arg Gln Ser  
 210 215 220

Gln Leu Val Ala Asp Ala Gly His Glu Leu Lys Thr Pro Leu Thr Ser  
 225 230 235 240

Met Arg Thr Asn Ile Glu Leu Leu Leu Met Ala Thr Asn Ser Gly Gly  
 245 250 255

Ser Gly Ile Pro Lys Glu Glu Leu Asp Gly Leu Gln Arg Asp Val Leu  
 260 265 270

Ala Gln Met Thr Glu Met Ser Asp Leu Ile Gly Asp Leu Val Asp Leu

275					280					285					
Ala	Arg	Glu	Glu	Thr	Ala	Glu	Thr	Ser	Ser	Ile	Val	Asp	Leu	Asn	Gln
290					295					300					
Val	Leu	Glu	Ile	Ala	Leu	Asp	Arg	Met	Glu	Ser	Arg	Arg	Met	Thr	Val
305				310					315						320
Arg	Ile	Asp	Val	Ser	Glu	Thr	Val	Asp	Trp	Lys	Leu	Leu	Gly	Asp	Asp
			325					330						335	
Phe	Ser	Leu	Thr	Arg	Ala	Leu	Val	Asn	Val	Leu	Asp	Asn	Ala	Ile	Lys
			340					345					350		
Trp	Ser	Pro	Glu	Asn	Gly	Ile	Val	Arg	Val	Ser	Met	Ser	Gln	Ile	Asp
		355					360					365			
Lys	Ala	Thr	Val	Arg	Ile	Val	Ile	Asp	Asp	Ser	Gly	Pro	Gly	Ile	Ala
	370					375					380				
Glu	Lys	Glu	Arg	Gly	Leu	Val	Leu	Glu	Arg	Phe	Tyr	Arg	Ala	Val	Ser
385				390					395						400
Ser	Arg	Ser	Met	Pro	Gly	Ser	Gly	Leu	Gly	Leu	Ala	Ile	Val	Asn	Gln
			405					410						415	
Val	Val	Asn	Arg	His	Gly	Gly	Gln	Leu	Val	Val	Gly	Glu	Ser	Asp	Asp
		420					425						430		
Gly	Gly	Thr	Arg	Ile	Thr	Ile	Asp	Leu	Pro	Gly	Glu	Pro	Ile	Arg	Ser
		435					440					445			
Gly	Phe	Glu	Asn	Val	Asp	Asp									
	450					455									

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 <212> DNA  
 <213> Corynebacterium glutamicum

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 <223> RXA00609

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 Met Ser Lys Ile Leu  
 1 5  
 ctc gct gaa gat gac gcc ggc atc gca gat ttc atc gtt cgt ggc ctc 163  
 Leu Ala Glu Asp Asp Ala Gly Ile Ala Asp Phe Ile Val Arg Gly Leu  
 10 15 20  
 atc cgc gaa ggc ttc gaa tgc gag gtc acc gaa tcc ggc gcc gaa gct 211  
 Ile Arg Glu Gly Phe Glu Cys Glu Val Thr Glu Ser Gly Ala Glu Ala  
 25 30 35

ttc gcc cgc gca cat tcc ggc gat ttc gat ctc atg gtt tta gac ctc 259  
 Phe Ala Arg Ala His Ser Gly Asp Phe Asp Leu Met Val Leu Asp Leu  
                   40                                  45                                  50

ggc ctc ccc cac atg gac ggc acg gat gtc cta gag caa tta aga aat 307  
 Gly Leu Pro His Met Asp Gly Thr Asp Val Leu Glu Gln Leu Arg Asn  
                   55                                  60                                  65

ctg cag gtc acg cta cct atc att gtg ctc acg gca cgc acc aac atc 355  
 Leu Gln Val Thr Leu Pro Ile Ile Val Leu Thr Ala Arg Thr Asn Ile  
                   70                                  75                                  80                                  85

gag gac cgc ctc cgc acc ctc gag ggc ggc gcc gac gat tac atg ccc 403  
 Glu Asp Arg Leu Arg Thr Leu Glu Gly Gly Ala Asp Asp Tyr Met Pro  
                                   90                                  95                                  100

aaa cca ttc caa ttc gca gaa tta ctg gcc cgc atc aaa ctc cgc ctc 451  
 Lys Pro Phe Gln Phe Ala Glu Leu Leu Ala Arg Ile Lys Leu Arg Leu  
                                   105                                  110                                  115

gcc aaa cac act cct cag gaa acg ccg acc gat gcg cgc gtg cta cga 499  
 Ala Lys His Thr Pro Gln Glu Thr Pro Thr Asp Ala Arg Val Leu Arg  
                                   120                                  125                                  130

aac ggc gat ttg gag ctc gat ctt cgt acc cag cgt gtg ctc atc gac 547  
 Asn Gly Asp Leu Glu Leu Asp Leu Arg Thr Gln Arg Val Leu Ile Asp  
                   135                                  140                                  145

ggc tcc tgg cac gac ctt tcc cgc cgc gaa gtc gat ctg ctc gaa acc 595  
 Gly Ser Trp His Asp Leu Ser Arg Arg Glu Val Asp Leu Leu Glu Thr  
                   150                                  155                                  160                                  165

ctc atg cga cac cca ggg caa atc ctc tcc cga gtc caa ctc ctc cga 643  
 Leu Met Arg His Pro Gly Gln Ile Leu Ser Arg Val Gln Leu Leu Arg  
                                   170                                  175                                  180

ctg gtg tgg gac atg gat tgg gac ccc ggc tca aac gtg gtg gac gta 691  
 Leu Val Trp Asp Met Asp Trp Asp Pro Gly Ser Asn Val Val Asp Val  
                   185                                  190                                  195

tat atc cgc gcg ttg agg aag aaa atc ggt gcc cat cgg gtc gaa acc 739  
 Tyr Ile Arg Ala Leu Arg Lys Lys Ile Gly Ala His Arg Val Glu Thr  
                   200                                  205                                  210

atc cga gga tct ggc tac cgg ctg cgc taactgcaga acgagaccaa aaa 789  
 Ile Arg Gly Ser Gly Tyr Arg Leu Arg  
                   215                                  220

&lt;210&gt; 56

&lt;211&gt; 222

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 56

Met Ser Lys Ile Leu Leu Ala Glu Asp Asp Ala Gly Ile Ala Asp Phe  
           1                                  5                                  10                                  15

Ile Val Arg Gly Leu Ile Arg Glu Gly Phe Glu Cys Glu Val Thr Glu  
                   20                                  25                                  30

Ser Gly Ala Glu Ala Phe Ala Arg Ala His Ser Gly Asp Phe Asp Leu  
35 40 45

Met Val Leu Asp Leu Gly Leu Pro His Met Asp Gly Thr Asp Val Leu  
50 55 60

Glu Gln Leu Arg Asn Leu Gln Val Thr Leu Pro Ile Ile Val Leu Thr  
65 70 75 80

Ala Arg Thr Asn Ile Glu Asp Arg Leu Arg Thr Leu Glu Gly Gly Ala  
85 90 95

Asp Asp Tyr Met Pro Lys Pro Phe Gln Phe Ala Glu Leu Leu Ala Arg  
100 105 110

Ile Lys Leu Arg Leu Ala Lys His Thr Pro Gln Glu Thr Pro Thr Asp  
115 120 125

Ala Arg Val Leu Arg Asn Gly Asp Leu Glu Leu Asp Leu Arg Thr Gln  
130 135 140

Arg Val Leu Ile Asp Gly Ser Trp His Asp Leu Ser Arg Arg Glu Val  
145 150 155 160

Asp Leu Leu Glu Thr Leu Met Arg His Pro Gly Gln Ile Leu Ser Arg  
165 170 175

Val Gln Leu Leu Arg Leu Val Trp Asp Met Asp Trp Asp Pro Gly Ser  
180 185 190

Asn Val Val Asp Val Tyr Ile Arg Ala Leu Arg Lys Lys Ile Gly Ala  
195 200 205

His Arg Val Glu Thr Ile Arg Gly Ser Gly Tyr Arg Leu Arg  
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<211> 1188

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<223> RXA00284

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Met Ala Arg Lys Leu  
1 5

aag gac aaa ctt ccc cga agt ttt gac aaa atc gtc gaa tcg ggc gat 163  
Lys Asp Lys Leu Pro Arg Ser Phe Asp Lys Ile Val Glu Ser Gly Asp  
10 15 20

ttt gac gct ttc aaa gag gtc ttc acc gag cgc gcc ctc gac gcc aaa 211  
Phe Asp Ala Phe Lys Glu Val Phe Thr Glu Arg Ala Leu Asp Ala Lys



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Asn	Arg	His	Gly	Asn	Thr	Ala	Leu	His	Met	Arg	Gly	Val	Pro	Glu	Glu			
	40						45					50						
ttc	aag	att	tgg	atg	ctt	gac	cag	ggc	ctc	gat	gtg	gat	atc	cgc	aac	307		
Phe	Lys	Ile	Trp	Met	Leu	Asp	Gln	Gly	Leu	Asp	Val	Asp	Ile	Arg	Asn			
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gaa	gac	ggc	gac	acc	ccg	ctg	cac	gtg	cac	tcc	cat	gac	tgg	aac	tta	355		
Glu	Asp	Gly	Asp	Thr	Pro	Leu	His	Val	His	Ser	His	Asp	Trp	Asn	Leu			
	70				75					80					85			
agc	ccc	gat	ttt	ctg	ctc	aaa	cgc	ggc	gcc	gat	gtc	tgc	gca	gtc	aac	403		
Ser	Pro	Asp	Phe	Leu	Leu	Lys	Arg	Gly	Ala	Asp	Val	Cys	Ala	Val	Asn			
				90				95						100				
aat	gaa	ggc	gaa	tcg	gtt	gcc	tac	tcc	gct	gcc	ttc	ttc	cca	gaa	aac	451		
Asn	Glu	Gly	Glu	Ser	Val	Ala	Tyr	Ser	Ala	Ala	Phe	Phe	Pro	Glu	Asn			
			105				110						115					
ctc	aaa	aag	ctt	atc	gac	gcc	ggc	gcc	gac	ccc	tac	tcg	cgc	gcc	aac	499		
Leu	Lys	Lys	Leu	Ile	Asp	Ala	Gly	Ala	Asp	Pro	Tyr	Ser	Arg	Ala	Asn			
		120					125					130						
gac	ggc	acc	acg	ccg	ctg	atg	cgt	gtc	att	cga	agc	gcc	gac	acc	gga	547		
Asp	Gly	Thr	Thr	Pro	Leu	Met	Arg	Val	Ile	Arg	Ser	Ala	Asp	Thr	Gly			
	135					140					145							
caa	atc	atc	gaa	cta	gca	gaa	ata	acc	aag	cta	ctt	tcc	ggc	aca	gaa	595		
Gln	Ile	Ile	Glu	Leu	Ala	Glu	Ile	Thr	Lys	Leu	Leu	Ser	Gly	Thr	Glu			
	150				155					160					165			
ttc	acc	gac	gca	gaa	ttc	cga	gaa	acc	caa	gaa	cgc	atc	atc	gca	atg	643		
Phe	Thr	Asp	Ala	Glu	Phe	Arg	Glu	Thr	Gln	Glu	Arg	Ile	Ile	Ala	Met			
			170					175						180				
ggt	gaa	aga	ttc	gaa	gat	gtc	cgg	gaa	gtc	tac	aac	gaa	gaa	tcc	gtc	691		
Gly	Glu	Arg	Phe	Glu	Asp	Val	Arg	Glu	Val	Tyr	Asn	Glu	Glu	Ser	Val			
			185				190					195						
gac	caa	gca	tct	gcg	gac	atg	atc	tgg	ctc	tac	gat	cgt	ttc	gac	atc	739		
Asp	Gln	Ala	Ser	Ala	Asp	Met	Ile	Trp	Leu	Tyr	Asp	Arg	Phe	Asp	Ile			
		200				205						210						
ccc	gaa	gaa	ctc	cgc	gcc	aac	aca	cca	att	ttg	cac	gac	gga	gta	agc	787		
Pro	Glu	Glu	Leu	Arg	Ala	Asn	Thr	Pro	Ile	Leu	His	Asp	Gly	Val	Ser			
	215					220					225							
cca	ata	gaa	ctg	cct	ggg	gat	acc	tgg	caa	gaa	caa	ttc	atc	gaa	ggc	835		
Pro	Ile	Glu	Leu	Pro	Gly	Asp	Thr	Trp	Gln	Glu	Gln	Phe	Ile	Glu	Gly			
	230				235					240					245			
tac	gat	ctc	ctc	gtt	ccc	gca	atg	ggc	aaa	gcg	aaa	tcc	ctg	caa	ggc	883		
Tyr	Asp	Leu	Leu	Val	Pro	Ala	Met	Gly	Lys	Ala	Lys	Ser	Leu	Gln	Gly			
				250				255						260				
gaa	gcc	atc	cga	att	gcc	gga	cga	gta	tcc	aac	gaa	ttt	cac	ggc	aac	931		
Glu	Ala	Ile	Arg	Ile	Ala	Gly	Arg	Val	Ser	Asn	Glu	Phe	His	Gly	Asn			
			265				270						275					

ggt ggc gtc aac tgg gac aaa gac ttc aaa cgc atg gcc aaa tct ctc 979  
 Gly Gly Val Asn Trp Asp Lys Asp Phe Lys Arg Met Ala Lys Ser Leu  
 280 285 290  
 aac cac att tgt gag cag ggc gtt cct ttg ggt gag cca gaa tta gaa 1027  
 Asn His Ile Cys Glu Gln Gly Val Pro Leu Gly Glu Pro Glu Leu Glu  
 295 300 305  
 gaa ctg gct gcg gcc gtt aaa tca gtg cgc aaa gga gaa ccc acc gag 1075  
 Glu Leu Ala Ala Ala Val Lys Ser Val Arg Lys Gly Glu Pro Thr Glu  
 310 315 320 325  
 gag gag atc gac acc ctt cca cgg ttg gcc acc aaa tgg gtc gca caa 1123  
 Glu Glu Ile Asp Thr Leu Pro Arg Leu Ala Thr Lys Trp Val Ala Gln  
 330 335 340  
 aac cca caa ccg ctg cca ctg gga gag gtt gac tac aag cgc 1165  
 Asn Pro Gln Pro Leu Pro Leu Gly Glu Val Asp Tyr Lys Arg  
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 <213> Corynebacterium glutamicum

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 35 40 45  
 Gly Val Pro Glu Glu Phe Lys Ile Trp Met Leu Asp Gln Gly Leu Asp  
 50 55 60  
 Val Asp Ile Arg Asn Glu Asp Gly Asp Thr Pro Leu His Val His Ser  
 65 70 75 80  
 His Asp Trp Asn Leu Ser Pro Asp Phe Leu Leu Lys Arg Gly Ala Asp  
 85 90 95  
 Val Cys Ala Val Asn Asn Glu Gly Glu Ser Val Ala Tyr Ser Ala Ala  
 100 105 110  
 Phe Phe Pro Glu Asn Leu Lys Lys Leu Ile Asp Ala Gly Ala Asp Pro  
 115 120 125  
 Tyr Ser Arg Ala Asn Asp Gly Thr Thr Pro Leu Met Arg Val Ile Arg  
 130 135 140  
 Ser Ala Asp Thr Gly Gln Ile Ile Glu Leu Ala Glu Ile Thr Lys Leu  
 145 150 155 160  
 Leu Ser Gly Thr Glu Phe Thr Asp Ala Glu Phe Arg Glu Thr Gln Glu

ctg cag tgg atc atc gga cac ggt ggc atg tcc acc qta tgg ctc qca 211

Leu	Gln	Trp	Ile	Ile	Gly	His	Gly	Gly	Met	Ser	Thr	Val	Trp	Leu	Ala		
			25					30					35				
gat	gat	gtg	gtc	aat	gat	cgc	gaa	gta	gcc	atc	aag	gta	ctg	cgc	ccg	259	
Asp	Asp	Val	Val	Asn	Asp	Arg	Glu	Val	Ala	Ile	Lys	Val	Leu	Arg	Pro		
		40					45					50					
gaa	ttt	tcc	gac	aac	cag	gag	ttc	ttg	aac	cgt	ttc	cgc	aat	gaa	gcg	307	
Glu	Phe	Ser	Asp	Asn	Gln	Glu	Phe	Leu	Asn	Arg	Phe	Arg	Asn	Glu	Ala		
	55					60					65						
caa	gcg	gct	gag	aat	atc	gat	tct	gaa	cac	gtg	gtg	gcc	acc	tat	gac	355	
Gln	Ala	Ala	Glu	Asn	Ile	Asp	Ser	Glu	His	Val	Val	Ala	Thr	Tyr	Asp		
	70				75					80					85		
tac	cgt	gag	gtt	cca	gac	cct	gct	ggg	cat	act	ttc	tgc	ttc	atc	gtc	403	
Tyr	Arg	Glu	Val	Pro	Asp	Pro	Ala	Gly	His	Thr	Phe	Cys	Phe	Ile	Val		
				90					95					100			
atg	gaa	ttt	gtc	cgc	ggg	gaa	tcg	ctt	gcg	gat	ctt	cta	gag	cgc	gaa	451	
Met	Glu	Phe	Val	Arg	Gly	Glu	Ser	Leu	Ala	Asp	Leu	Leu	Glu	Arg	Glu		
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ggc	aga	ctg	ccg	gaa	gac	ctg	gct	ctt	gat	gtg	atg	gaa	cag	gcg	gca	499	
Gly	Arg	Leu	Pro	Glu	Asp	Leu	Ala	Leu	Asp	Val	Met	Glu	Gln	Ala	Ala		
		120					125					130					
cat	ggg	ttg	tcg	gtg	att	cac	cgg	atg	gac	atg	gtg	cac	cgc	gat	atc	547	
His	Gly	Leu	Ser	Val	Ile	His	Arg	Met	Asp	Met	Val	His	Arg	Asp	Ile		
	135					140					145						
aag	ccg	ggc	aac	atg	ctg	atc	aca	gcc	aat	ggc	att	gtg	aag	atc	acg	595	
Lys	Pro	Gly	Asn	Met	Leu	Ile	Thr	Ala	Asn	Gly	Ile	Val	Lys	Ile	Thr		
	150				155					160					165		
gac	ttt	ggg	atc	gct	aag	gct	gcc	gct	gct	gtg	cct	ttg	acc	cgc	acc	643	
Asp	Phe	Gly	Ile	Ala	Lys	Ala	Ala	Ala	Ala	Val	Pro	Leu	Thr	Arg	Thr		
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ggc	atg	gtg	gtg	ggg	act	gct	caa	tat	gtt	tca	cct	gag	caa	gcc	cag	691	
Gly	Met	Val	Val	Gly	Thr	Ala	Gln	Tyr	Val	Ser	Pro	Glu	Gln	Ala	Gln		
				185				190					195				
ggc	aag	gaa	gtc	acc	gcg	gct	tct	gat	att	tat	tct	ctc	ggg	gtg	gtc	739	
Gly	Lys	Glu	Val	Thr	Ala	Ala	Ser	Asp	Ile	Tyr	Ser	Leu	Gly	Val	Val		
		200					205					210					
ggc	tat	gag	atg	atg	gct	ggc	cgc	cgc	ccg	ttc	act	gga	gat	tct	tcg	787	
Gly	Tyr	Glu	Met	Met	Ala	Gly	Arg	Arg	Pro	Phe	Thr	Gly	Asp	Ser	Ser		
	215					220					225						
gtg	tct	gtg	gcg	atc	gcg	cac	atc	aac	caa	gct	ccg	ccg	cag	atg	ccc	835	
Val	Ser	Val	Ala	Ile	Ala	His	Ile	Asn	Gln	Ala	Pro	Pro	Gln	Met	Pro		
	230				235					240					245		
acc	agc	att	tcg	gca	cag	act	cgc	gag	ttg	att	ggc	att	gcg	ttg	cgc	883	
Thr	Ser	Ile	Ser	Ala	Gln	Thr	Arg	Glu	Leu	Ile	Gly	Ile	Ala	Leu	Arg		
				250					255					260			
aag	gat	ccg	ggg	cgc	cgt	ttc	cct	gat	gga	aat	gaa	atg	gcg	cta	gct	931	
Lys	Asp	Pro	Gly	Arg	Arg	Phe	Pro	Asp	Gly	Asn	Glu	Met	Ala	Leu	Ala		

265	270	275	
gtt tct gct gtg cgc ctt ggc aag cgc ccg cct caa ccg cgc acg agc			979
Val Ser Ala Val Arg Leu Gly Lys Arg Pro Pro Gln Pro Arg Thr Ser			
280	285	290	
gcg atg atg gcg cag gcg gag gcg ccg tcg cca agc gaa tca acg gcg			1027
Ala Met Met Ala Gln Ala Glu Ala Pro Ser Pro Ser Glu Ser Thr Ala			
295	300	305	
atg ctg ggc agg gtg gcc cgg cct gca aca atc acc caa gaa gcg gcc			1075
Met Leu Gly Arg Val Ala Arg Pro Ala Thr Ile Thr Gln Glu Ala Ala			
310	315	320	325
ccg aaa cgc ggt tcc ggc att ggc att ggt ctg ttc atc gca gct ttg			1123
Pro Lys Arg Gly Ser Gly Ile Gly Ile Gly Leu Phe Ile Ala Ala Leu			
	330	335	340
ctt gcc gtg att att ggc gcg gtg atc tat gcg ggc acc acc gga att			1171
Leu Ala Val Ile Ile Gly Ala Val Ile Tyr Ala Gly Thr Thr Gly Ile			
	345	350	355
ttg ttc aac gac act ccg gaa gaa acc acc aca cct gaa acc att acg			1219
Leu Phe Asn Asp Thr Pro Glu Glu Thr Thr Thr Pro Glu Thr Ile Thr			
	360	365	370
gaa aca tac acc cca acc gtg gag gaa acc acc tct cag tgg gta ccg			1267
Glu Thr Tyr Thr Pro Thr Val Glu Glu Thr Thr Ser Gln Trp Val Pro			
	375	380	385
cca acg cct cca aca cgg tca aca ttc acc gaa cct gaa aca act tca			1315
Pro Thr Pro Pro Thr Arg Ser Thr Phe Thr Glu Pro Glu Thr Thr Ser			
	390	395	400
cac cgt ccg acg aca agt gaa gag agc aca tcc gag gaa cca acc acg			1363
His Arg Pro Thr Thr Ser Glu Glu Ser Thr Ser Glu Glu Pro Thr Thr			
	410	415	420
gaa gct cca aca agt agc cga act gtg cct caa atc cct acc tct aca			1411
Glu Ala Pro Thr Ser Ser Arg Thr Val Pro Gln Ile Pro Thr Ser Thr			
	425	430	435
cct agg acg agt gct agc gtt cca gtt gag act aat gca ccg gct gat			1459
Pro Arg Thr Ser Ala Ser Val Pro Val Glu Thr Asn Ala Pro Ala Asp			
	440	445	450
gat tta atc gac gcc gta aat ggc cta ttg gat gta gga gga gcg cag			1507
Asp Leu Ile Asp Ala Val Asn Gly Leu Leu Asp Val Gly Gly Ala Gln			
	455	460	465
tgaccttcgt gatcgctgat cgc			1530

&lt;210&gt; 60

&lt;211&gt; 469

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 60

Met	Ser	Gln	Glu	Asp	Ile	Thr	Gly	Lys	Asp	Arg	Leu	Gln	Glu	Leu	Ile
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Gly Ala Asp Tyr Arg Leu Gln Trp Ile Ile Gly His Gly Gly Met Ser  
 20 25 30  
 Thr Val Trp Leu Ala Asp Asp Val Val Asn Asp Arg Glu Val Ala Ile  
 35 40 45  
 Lys Val Leu Arg Pro Glu Phe Ser Asp Asn Gln Glu Phe Leu Asn Arg  
 50 55 60  
 Phe Arg Asn Glu Ala Gln Ala Ala Glu Asn Ile Asp Ser Glu His Val  
 65 70 75 80  
 Val Ala Thr Tyr Asp Tyr Arg Glu Val Pro Asp Pro Ala Gly His Thr  
 85 90 95  
 Phe Cys Phe Ile Val Met Glu Phe Val Arg Gly Glu Ser Leu Ala Asp  
 100 105 110  
 Leu Leu Glu Arg Glu Gly Arg Leu Pro Glu Asp Leu Ala Leu Asp Val  
 115 120 125  
 Met Glu Gln Ala Ala His Gly Leu Ser Val Ile His Arg Met Asp Met  
 130 135 140  
 Val His Arg Asp Ile Lys Pro Gly Asn Met Leu Ile Thr Ala Asn Gly  
 145 150 155 160  
 Ile Val Lys Ile Thr Asp Phe Gly Ile Ala Lys Ala Ala Ala Ala Val  
 165 170 175  
 Pro Leu Thr Arg Thr Gly Met Val Val Gly Thr Ala Gln Tyr Val Ser  
 180 185 190  
 Pro Glu Gln Ala Gln Gly Lys Glu Val Thr Ala Ala Ser Asp Ile Tyr  
 195 200 205  
 Ser Leu Gly Val Val Gly Tyr Glu Met Met Ala Gly Arg Arg Pro Phe  
 210 215 220  
 Thr Gly Asp Ser Ser Val Ser Val Ala Ile Ala His Ile Asn Gln Ala  
 225 230 235 240  
 Pro Pro Gln Met Pro Thr Ser Ile Ser Ala Gln Thr Arg Glu Leu Ile  
 245 250 255  
 Gly Ile Ala Leu Arg Lys Asp Pro Gly Arg Arg Phe Pro Asp Gly Asn  
 260 265 270  
 Glu Met Ala Leu Ala Val Ser Ala Val Arg Leu Gly Lys Arg Pro Pro  
 275 280 285  
 Gln Pro Arg Thr Ser Ala Met Met Ala Gln Ala Glu Ala Pro Ser Pro  
 290 295 300  
 Ser Glu Ser Thr Ala Met Leu Gly Arg Val Ala Arg Pro Ala Thr Ile  
 305 310 315 320  
 Thr Gln Glu Ala Ala Pro Lys Arg Gly Ser Gly Ile Gly Ile Gly Leu  
 325 330 335

Phe Ile Ala Ala Leu Leu Ala Val Ile Ile Gly Ala Val Ile Tyr Ala  
 340 345 350  
 Gly Thr Thr Gly Ile Leu Phe Asn Asp Thr Pro Glu Glu Thr Thr Thr  
 355 360 365  
 Pro Glu Thr Ile Thr Glu Thr Tyr Thr Pro Thr Val Glu Glu Thr Thr  
 370 375 380  
 Ser Gln Trp Val Pro Pro Thr Pro Pro Thr Arg Ser Thr Phe Thr Glu  
 385 390 395 400  
 Pro Glu Thr Thr Ser His Arg Pro Thr Thr Ser Glu Glu Ser Thr Ser  
 405 410 415  
 Glu Glu Pro Thr Thr Glu Ala Pro Thr Ser Ser Arg Thr Val Pro Gln  
 420 425 430  
 Ile Pro Thr Ser Thr Pro Arg Thr Ser Ala Ser Val Pro Val Glu Thr  
 435 440 445  
 Asn Ala Pro Ala Asp Asp Leu Ile Asp Ala Val Asn Gly Leu Leu Asp  
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 Val Gly Gly Ala Gln  
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 <223> RXA00813

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 Met Thr Asp Ile Asp  
 1 5  
 ctg gtg gtg gaa aac gtc caa agg att atc gcc acc aaa gag aca ccg 163  
 Leu Val Val Glu Asn Val Gln Arg Ile Ile Ala Thr Lys Glu Thr Pro  
 10 15 20  
 ccg acc tct gcg gaa ata gcg agc ctg att cgg gaa caa gca ggc gtg 211  
 Pro Thr Ser Ala Glu Ile Ala Ser Leu Ile Arg Glu Gln Ala Gly Val  
 25 30 35  
 atc agt aac gag gac atc gtg atg gtg ttg cgt cga ctg cgc agt gat 259  
 Ile Ser Asn Glu Asp Ile Val Met Val Leu Arg Arg Leu Arg Ser Asp  
 40 45 50  
 tct gtg ggc gtg gga ccg ttg gaa tct ctg ctt gcg ctt cct ggc gtg 307  
 Ser Val Gly Val Gly Pro Leu Glu Ser Leu Leu Ala Leu Pro Gly Val  
 55 60 65

acg gat gtg ttg gtt aat gcc cat gac agc gtg tgg att gat cgc ggt	355
Thr Asp Val Leu Val Asn Ala His Asp Ser Val Trp Ile Asp Arg Gly	
70 75 80 85	
cag ggc gtg gag aaa gtc gac atg gat ctg ggc tca gag gag gcg gtg	403
Gln Gly Val Glu Lys Val Asp Met Asp Leu Gly Ser Glu Glu Ala Val	
90 95 100	
cgt cgc ctt gcc acc cgg ttg gcg ttg acc tgt ggc aga cgc tta gat	451
Arg Arg Leu Ala Thr Arg Leu Ala Leu Thr Cys Gly Arg Arg Leu Asp	
105 110 115	
gat gcg cag cct ttc gct gat ggc cga atc acc agg gac gac ggc agc	499
Asp Ala Gln Pro Phe Ala Asp Gly Arg Ile Thr Arg Asp Asp Gly Ser	
120 125 130	
gtg ttg cgc att cac gcg gtg ttg gca ccc ttg gcg gaa tcc ggc acg	547
Val Leu Arg Ile His Ala Val Leu Ala Pro Leu Ala Glu Ser Gly Thr	
135 140 145	
tgc atc agt gtg cga gta ctg cgt caa gca cgg ctg agc ctt gat gat	595
Cys Ile Ser Val Arg Val Leu Arg Gln Ala Arg Leu Ser Leu Asp Asp	
150 155 160 165	
ctt atc caa agc ggc acg gtg cct gag gac atc gcg cct gcg ctc cgg	643
Leu Ile Gln Ser Gly Thr Val Pro Glu Asp Ile Ala Pro Ala Leu Arg	
170 175 180	
aac atc atc aat caa cgg cgc tcg ttc ctt gtt gtc ggt ggc acc ggc	691
Asn Ile Ile Asn Gln Arg Arg Ser Phe Leu Val Val Gly Gly Thr Gly	
185 190 195	
aca ggg aaa acc aca ttg ctg tcc gcg atg ctc acc gaa gtt ccc gct	739
Thr Gly Lys Thr Thr Leu Leu Ser Ala Met Leu Thr Glu Val Pro Ala	
200 205 210	
gat caa cga atc atc tgc atc gag gac acc gca gag ctt cat ccc ggc	787
Asp Gln Arg Ile Ile Cys Ile Glu Asp Thr Ala Glu Leu His Pro Gly	
215 220 225	
cat cca agc acc atc aac ttg gtg tct cgc caa gca aac gtc gag ggc	835
His Pro Ser Thr Ile Asn Leu Val Ser Arg Gln Ala Asn Val Glu Gly	
230 235 240 245	
gcc ggc gcc gtg agc atg gcg gat ttg ttg aaa caa tcg ctg cgc atg	883
Ala Gly Ala Val Ser Met Ala Asp Leu Leu Lys Gln Ser Leu Arg Met	
250 255 260	
agg cct gac cgg att gtc gtc gga gag att cgc ggt gcg gaa gtc gtg	931
Arg Pro Asp Arg Ile Val Val Gly Glu Ile Arg Gly Ala Glu Val Val	
265 270 275	
gat ctt ttg gct gcg atg aat acc gga cac gac ggc ggt gct ggc acc	979
Asp Leu Leu Ala Ala Met Asn Thr Gly His Asp Gly Gly Ala Gly Thr	
280 285 290	
att cac gcg aac tcc atc tct gaa gtt ccc gcg cgc atg gaa gct ctt	1027
Ile His Ala Asn Ser Ile Ser Glu Val Pro Ala Arg Met Glu Ala Leu	
295 300 305	
gcg gcg acc ggc gga ttg gac cgc atg gca ttg cat tct caa ctc gcg	1075



Ala Ala Thr Gly Gly Leu Asp Arg Met Ala Leu His Ser Gln Leu Ala  
 310 315 320 325

gcc gca gtg gac att gtg ctg gtc atg aaa cac acc cct ttt ggc cgc 1123  
 Ala Ala Val Asp Ile Val Leu Val Met Lys His Thr Pro Phe Gly Arg  
 330 335 340

agg cta gct caa ctc ggg gtg ctc cgc gga aat cct gtg acc acg cag 1171  
 Arg Leu Ala Gln Leu Gly Val Leu Arg Gly Asn Pro Val Thr Thr Gln  
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gtg gtg tgg gat ttg gac cac ggc atg cac gaa ggg agc gaa gag gca 1219  
 Val Val Trp Asp Leu Asp His Gly Met His Glu Gly Ser Glu Glu Ala  
 360 365 370

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 Trp Phe Met Pro  
 375

&lt;210&gt; 62

&lt;211&gt; 377

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 62

Met Thr Asp Ile Asp Leu Val Val Glu Asn Val Gln Arg Ile Ile Ala  
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Thr Lys Glu Thr Pro Pro Thr Ser Ala Glu Ile Ala Ser Leu Ile Arg  
 20 25 30

Glu Gln Ala Gly Val Ile Ser Asn Glu Asp Ile Val Met Val Leu Arg  
 35 40 45

Arg Leu Arg Ser Asp Ser Val Gly Val Gly Pro Leu Glu Ser Leu Leu  
 50 55 60

Ala Leu Pro Gly Val Thr Asp Val Leu Val Asn Ala His Asp Ser Val  
 65 70 75 80

Trp Ile Asp Arg Gly Gln Gly Val Glu Lys Val Asp Met Asp Leu Gly  
 85 90 95

Ser Glu Glu Ala Val Arg Arg Leu Ala Thr Arg Leu Ala Leu Thr Cys  
 100 105 110

Gly Arg Arg Leu Asp Asp Ala Gln Pro Phe Ala Asp Gly Arg Ile Thr  
 115 120 125

Arg Asp Asp Gly Ser Val Leu Arg Ile His Ala Val Leu Ala Pro Leu  
 130 135 140

Ala Glu Ser Gly Thr Cys Ile Ser Val Arg Val Leu Arg Gln Ala Arg  
 145 150 155 160

Leu Ser Leu Asp Asp Leu Ile Gln Ser Gly Thr Val Pro Glu Asp Ile  
 165 170 175

Ala Pro Ala Leu Arg Asn Ile Ile Asn Gln Arg Arg Ser Phe Leu Val  
 180 185 190

Val Gly Gly Thr Gly Thr Gly Lys Thr Thr Leu Leu Ser Ala Met Leu  
 195 200 205  
 Thr Glu Val Pro Ala Asp Gln Arg Ile Ile Cys Ile Glu Asp Thr Ala  
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 Glu Leu His Pro Gly His Pro Ser Thr Ile Asn Leu Val Ser Arg Gln  
 225 230 235 240  
 Ala Asn Val Glu Gly Ala Gly Ala Val Ser Met Ala Asp Leu Leu Lys  
 245 250 255  
 Gln Ser Leu Arg Met Arg Pro Asp Arg Ile Val Val Gly Glu Ile Arg  
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 Gly Ala Glu Val Val Asp Leu Leu Ala Ala Met Asn Thr Gly His Asp  
 275 280 285  
 Gly Gly Ala Gly Thr Ile His Ala Asn Ser Ile Ser Glu Val Pro Ala  
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 Arg Met Glu Ala Leu Ala Ala Thr Gly Gly Leu Asp Arg Met Ala Leu  
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 His Ser Gln Leu Ala Ala Ala Val Asp Ile Val Leu Val Met Lys His  
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 Thr Pro Phe Gly Arg Arg Leu Ala Gln Leu Gly Val Leu Arg Gly Asn  
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 Val Thr Phe Val Ile  
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 Ala Asp Arg Tyr Glu Leu Asp Ala Val Ile Gly Ser Gly Gly Met Ser  
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 Glu Val Phe Ala Ala Thr Asp Thr Leu Ile Gly Arg Glu Val Ala Val

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ttc	cgc	agg	gaa	gcc	caa	aac	tcc	gga	agg	ttg	agc	cac	tct	tcg	atc	307
Phe	Arg	Arg	Glu	Ala	Gln	Asn	Ser	Gly	Arg	Leu	Ser	His	Ser	Ser	Ile	
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Val	Ala	Val	Phe	Asp	Thr	Gly	Glu	Val	Asp	Lys	Asp	Gly	Thr	Ser	Val	
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ccc	tac	att	gtg	atg	gaa	cgc	gtg	cag	ggt	cga	aac	ctg	cgc	gaa	gtt	403
Pro	Tyr	Ile	Val	Met	Glu	Arg	Val	Gln	Gly	Arg	Asn	Leu	Arg	Glu	Val	
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gtc	acc	gaa	gac	ggc	gta	ttc	acc	cca	gtt	gag	gca	gcc	aac	atc	ctc	451
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atc	cct	gtg	tgt	gaa	gcg	ctg	cag	gca	tcc	cat	gac	gcc	ggc	att	att	499
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cac	cgc	gat	gtg	aaa	ccc	gcc	aac	atc	atg	atc	acc	aac	acc	ggt	ggc	547
His	Arg	Asp	Val	Lys	Pro	Ala	Asn	Ile	Met	Ile	Thr	Asn	Thr	Gly	Gly	
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gtg	aaa	gtc	atg	gac	ttc	ggc	atc	gcc	cgc	gcg	gtc	aac	gat	tcc	acc	595
Val	Lys	Val	Met	Asp	Phe	Gly	Ile	Ala	Arg	Ala	Val	Asn	Asp	Ser	Thr	
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Tyr	Ala	Thr	Gly	Cys	Val	Met	Tyr	Glu	Leu	Val	Thr	Gly	Lys	Pro	Pro	
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Phe	Glu	Gly	Glu	Ser	Pro	Phe	Ala	Val	Ala	Tyr	Gln	His	Val	Gln	Glu	
215							220				225					
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Asp	Pro	Thr	Pro	Pro	Ser	Asp	Phe	Ile	Ala	Asp	Leu	Thr	Pro	Thr	Ser	
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gct	gtc	aac	gtg	gat	gcc	gtg	gta	ctc	acc	gcc	atg	gca	aaa	cac	ccc	883
Ala	Val	Asn	Val	Asp	Ala	Val	Val	Leu	Thr	Ala	Met	Ala	Lys	His	Pro	
250							255				260					
gcc	gac	cgc	tac	caa	aca	gcc	tcc	gaa	atg	gcc	gct	gac	ctg	ggc	cgg	931
Ala																

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Leu Ser Arg Asn Ala Val Ser His Ala Ala Arg Ala His Val Glu Thr	
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Glu Glu Thr Pro Glu Glu Pro Glu Thr Arg Phe Ser Thr Arg Thr Ser	
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acc caa gtg gcc ccc gcc gca ggc gtg gct gcg gcc agt acg ggg tca	1075
Thr Gln Val Ala Pro Ala Ala Gly Val Ala Ala Ala Ser Thr Gly Ser	
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Gly Ser Ser Ser Arg Lys Arg Gly Ser Arg Gly Leu Thr Ala Leu Ala	
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Ile Val Leu Ser Leu Gly Val Val Gly Val Ala Gly Ala Phe Thr Tyr	
345 350 355	
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Asp Tyr Phe Ala Asn Ser Ser Ser Thr Ala Thr Ser Ala Ile Pro Asn	
360 365 370	
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Val Glu Gly Leu Pro Gln Gln Glu Ala Leu Thr Glu Leu Gln Ala Ala	
375 380 385	
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Gly Phe Val Val Asn Ile Val Glu Glu Ala Ser Ala Asp Val Ala Glu	
390 395 400 405	
ggc ctc gtc atc cga gca aac cca agc gtt gga tcc gaa atc cgc caa	1363
Gly Leu Val Ile Arg Ala Asn Pro Ser Val Gly Ser Glu Ile Arg Gln	
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Gly Ala Thr Val Thr Ile Thr Val Ser Thr Gly Arg Glu Met Ile Asn	
425 430 435	
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Ile Pro Asp Val Ser Gly Met Thr Leu Glu Asp Ala Ala Arg Ala Leu	
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Glu Asp Val Gly Leu Ile Leu Asn Gln Asn Val Arg Glu Glu Thr Ser	
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Asp Asp Val Glu Ser Gly Leu Val Ile Asp Gln Asn Pro Glu Ala Gly	
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Gln Glu Val Val Val Gly Ser Ser Val Ser Leu Thr Met Ser Ser Gly	
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acc gag agc atc cga gtg ccc aac ctc acc ggc atg aac tgg tca caa	1651
Thr Glu Ser Ile Arg Val Pro Asn Leu Thr Gly Met Asn Trp Ser Gln	
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 Leu Asp Ser Ser Glu Pro Glu Gly Glu Val Leu Ser Val Ser Ser Gln  
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 Gly Thr Glu Leu Pro Lys Gly Ser Ser Ile Thr Val Glu Val Ser Asn  
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 Ala Ile Ser Ala Leu Arg Ala Ala Gly Trp Thr Ala Pro Asp Gln Ser  
 585 590 595  
 ctg atc gtc ggc gac ccc atc cac acc gca gcc ctc gtg gat caa aac 1939  
 Leu Ile Val Gly Asp Pro Ile His Thr Ala Ala Leu Val Asp Gln Asn  
 600 605 610  
 aaa atc gga ttc caa tcc cca acc cct gca acc ctc ttc cgc aaa gac 1987  
 Lys Ile Gly Phe Gln Ser Pro Thr Pro Ala Thr Leu Phe Arg Lys Asp  
 615 620 625  
 gcc caa gtg caa gtg cga ctc ttc gaa ttc gat ctc gct gca ctc gtg 2035  
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 caa tagccaacaa ggaaaccgtc aag 2061  
 Gln

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 <213> Corynebacterium glutamicum

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 Asn Phe Arg Glu Arg Phe Arg Arg Glu Ala Gln Asn Ser Gly Arg Leu  
 50 55 60  
 Ser His Ser Ser Ile Val Ala Val Phe Asp Thr Gly Glu Val Asp Lys  
 65 70 75 80  
 Asp Gly Thr Ser Val Pro Tyr Ile Val Met Glu Arg Val Gln Gly Arg  
 85 90 95

Asn Leu Arg Glu Val Val Thr Glu Asp Gly Val Phe Thr Pro Val Glu  
 100 105 110  
 Ala Ala Asn Ile Leu Ile Pro Val Cys Glu Ala Leu Gln Ala Ser His  
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 Asp Ala Gly Ile Ile His Arg Asp Val Lys Pro Ala Asn Ile Met Ile  
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 Thr Asn Thr Gly Gly Val Lys Val Met Asp Phe Gly Ile Ala Arg Ala  
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 Val Asn Asp Ser Thr Ser Ala Met Thr Gln Thr Ser Ala Val Ile Gly  
 165 170 175  
 Thr Ala Gln Tyr Leu Ser Pro Glu Gln Ala Arg Gly Lys Pro Ala Asp  
 180 185 190  
 Ala Arg Ser Asp Ile Tyr Ala Thr Gly Cys Val Met Tyr Glu Leu Val  
 195 200 205  
 Thr Gly Lys Pro Pro Phe Glu Gly Glu Ser Pro Phe Ala Val Ala Tyr  
 210 215 220  
 Gln His Val Gln Glu Asp Pro Thr Pro Pro Ser Asp Phe Ile Ala Asp  
 225 230 235 240  
 Leu Thr Pro Thr Ser Ala Val Asn Val Asp Ala Val Val Leu Thr Ala  
 245 250 255  
 Met Ala Lys His Pro Ala Asp Arg Tyr Gln Thr Ala Ser Glu Met Ala  
 260 265 270  
 Ala Asp Leu Gly Arg Leu Ser Arg Asn Ala Val Ser His Ala Ala Arg  
 275 280 285  
 Ala His Val Glu Thr Glu Glu Thr Pro Glu Glu Pro Glu Thr Arg Phe  
 290 295 300  
 Ser Thr Arg Thr Ser Thr Gln Val Ala Pro Ala Ala Gly Val Ala Ala  
 305 310 315 320  
 Ala Ser Thr Gly Ser Gly Ser Ser Ser Arg Lys Arg Gly Ser Arg Gly  
 325 330 335  
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 Gly Ala Phe Thr Tyr Asp Tyr Phe Ala Asn Ser Ser Ser Thr Ala Thr  
 355 360 365  
 Ser Ala Ile Pro Asn Val Glu Gly Leu Pro Gln Gln Glu Ala Leu Thr  
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 Glu Leu Gln Ala Ala Gly Phe Val Val Asn Ile Val Glu Glu Ala Ser  
 385 390 395 400  
 Ala Asp Val Ala Glu Gly Leu Val Ile Arg Ala Asn Pro Ser Val Gly  
 405 410 415  
 Ser Glu Ile Arg Gln Gly Ala Thr Val Thr Ile Thr Val Ser Thr Gly

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Arg	Glu	Met	Ile	Asn	Ile	Pro	Asp	Val	Ser	Gly	Met	Thr	Leu	Glu	Asp	
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Arg	Glu	Glu	Thr	Ser	Asp	Asp	Val	Glu	Ser	Gly	Leu	Val	Ile	Asp	Gln	
465					470					475					480	
Asn	Pro	Glu	Ala	Gly	Gln	Glu	Val	Val	Val	Gly	Ser	Ser	Val	Ser	Leu	
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Thr	Met	Ser	Ser	Gly	Thr	Glu	Ser	Ile	Arg	Val	Pro	Asn	Leu	Thr	Gly	
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Met	Asn	Trp	Ser	Gln	Ala	Glu	Gln	Asn	Leu	Ile	Ser	Met	Gly	Phe	Asn	
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Pro	Thr	Ala	Ser	Tyr	Leu	Asp	Ser	Ser	Glu	Pro	Glu	Gly	Glu	Val	Leu	
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Val	Glu	Val	Ser	Asn	Gly	Met	Leu	Ile	Gln	Ala	Pro	Asp	Leu	Ala	Arg	
565					570					575						
Met	Ser	Thr	Glu	Gln	Ala	Ile	Ser	Ala	Leu	Arg	Ala	Ala	Gly	Trp	Thr	
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Ala	Pro	Asp	Gln	Ser	Leu	Ile	Val	Gly	Asp	Pro	Ile	His	Thr	Ala	Ala	
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645																

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&lt;211&gt; 2271

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(2248)

&lt;223&gt; RXA02699

&lt;400&gt; 65

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Met Ser Thr Val Tyr

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Ala Ala Ala His Arg Ala Gly Met Val His Arg Asp Ile Lys Pro Asp	
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Asn Val Leu Ile Asn Ser Asp His Gln Val Lys Leu Ser Asp Phe Gly	
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Gly Thr Val Ala Tyr Leu Ser Pro Glu Gln Val Glu Gly Gly Glu Ile	
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Leu Thr Gly Thr Thr Pro Phe Ser Gly Glu Asp Asp Leu Asp His Ala	
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Tyr Ala Arg Leu Thr Glu Val Val Pro Ala Pro Ser Ser Leu Ile Asp	
200 205 210	
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215 220 225	
aat cct gag gat cgt ttc gat gat tct gga gag ttt ttg tcc gca ctg	835
Asn Pro Glu Asp Arg Phe Asp Asp Ser Gly Glu Phe Leu Ser Ala Leu	
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cct cag tat gac aat gag gtt ccc act ggt tcg att att ggg act gaa Pro Gln Tyr Asp Asn Glu Val Pro Thr Gly Ser Ile Ile Gly Thr Glu 425 430 435	1411
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Gln	Ile	His	Leu	Ser	Arg	Gly	Pro	Ala	Pro	Val	Glu	Ile	Pro	Asp	Val		
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Ser	Gly	Met	Gly	Val	Asp	Gln	Ala	Thr	Arg	Val	Leu	Glu	Arg	Ala	Gly		
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Leu	Ser	Val	Glu	Arg	Thr	Glu	Glu	Gly	Phe	Asp	Ala	Glu	Thr	Pro	Asn		
550					555					560					565		
ggg	gat	gtc	tac	ggg	act	tcg	ccc	aag	gta	tct	act	gag	gtc	aag	cgc	1843	
Gly	Asp	Val	Tyr	Gly	Thr	Ser	Pro	Lys	Val	Ser	Thr	Glu	Val	Lys	Arg		
			570					575						580			
gga	acc	tct	gtt	gtg	ctg	cag	gtg	tcc	aat	gct	att	tcg	gta	ccg	gat	1891	
Gly	Thr	Ser	Val	Val	Leu	Gln	Val	Ser	Asn	Ala	Ile	Ser	Val	Pro	Asp		
			585					590					595				
gtg	gtg	ggg	atg	acc	aag	gac	gaa	gcc	acc	gcg	gcg	ctt	gcg	gaa	gaa	1939	
Val	Val	Gly	Met	Thr	Lys	Asp	Glu	Ala	Thr	Ala	Ala	Leu	Ala	Glu	Glu		
		600					605					610					
gga	ttg	gtc	gtg	gcg	tcg	aca	agc	att	att	cct	ggg	gag	gcg	gcg	agc	1987	
Gly	Leu	Val	Val	Ala	Ser	Thr	Ser	Ile	Ile	Pro	Gly	Glu	Ala	Ala	Ser		
	615					620					625						
tcc	gct	gac	gcc	gtc	gtg	acc	gtc	gag	cct	gaa	tcc	ggc	agc	cgc	gtt	2035	
Ser	Ala	Asp	Ala	Val	Val	Thr	Val	Glu	Pro	Glu	Ser	Gly	Ser	Arg	Val		
630					635				640						645		
gat	cca	gcg	cat	ccg	cag	gtc	agc	ctc	ggg	tta	gct	ggg	gag	att	caa	2083	
Asp	Pro	Ala	His	Pro	Gln	Val	Ser	Leu	Gly	Leu	Ala	Gly	Glu	Ile	Gln		
				650				655						660			
gtt	cca	agc	gtg	gtt	gga	cgt	aag	gtt	agc	gat	gct	cga	agc	att	ctg	2131	
Val	Pro	Ser	Val	Val	Gly	Arg	Lys	Val	Ser	Asp	Ala	Arg	Ser	Ile	Leu		
			665				670						675				
gaa	gaa	gcc	ggg	tta	acg	ctg	aca	act	gat	gcg	gac	gac	aac	gat	cga	2179	
Glu	Glu	Ala	Gly	Leu	Thr	Leu	Thr	Thr	Asp	Ala	Asp	Asp	Asn	Asp	Arg		
		680					685					690					
att	tat	agt	caa	acc	cct	cgt	gca	cgc	agc	gaa	gtc	tcg	gta	ggg	gga	2227	
Ile	Tyr	Ser	Gln	Thr	Pro	Arg	Ala	Arg	Ser	Glu	Val	Ser	Val	Gly	Gly		
	695					700					705						
gaa	gtt	aca	gta	agg	gcg	ttt	tagtggttcc	ctcggttg	cag	caa						2271	
Glu	Val	Thr	Val	Arg	Ala	Phe											
710					715												

&lt;211&gt; 716

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 66

Met Ser Thr Val Tyr Arg Cys Leu Asp Leu Arg Leu Gly Arg Ser Met  
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Ala Leu Lys Val Met Glu Glu Asp Phe Val Asp Asp Pro Ile Phe Arg  
 20 25 30

Gln Arg Ser Arg Arg Glu Ala Arg Ser Met Ala Gln Leu Asn His Pro  
 35 40 45

Asn Leu Val Asn Val Tyr Asp Phe Ser Ala Thr Asp Gly Leu Val Tyr  
 50 55 60

Leu Val Met Glu Leu Ile Thr Gly Gly Thr Leu Arg Glu Leu Leu Ala  
 65 70 75 80

Glu Arg Gly Pro Met Pro Pro His Ala Ala Val Gly Val Met Arg Gly  
 85 90 95

Val Leu Thr Gly Leu Ala Ala Ala His Arg Ala Gly Met Val His Arg  
 100 105 110

Asp Ile Lys Pro Asp Asn Val Leu Ile Asn Ser Asp His Gln Val Lys  
 115 120 125

Leu Ser Asp Phe Gly Leu Val Arg Ala Ala His Ala Gly Gln Ser Gln  
 130 135 140

Asp Asn Gln Ile Val Gly Thr Val Ala Tyr Leu Ser Pro Glu Gln Val  
 145 150 155 160

Glu Gly Gly Glu Ile Gly Pro Ala Ser Asp Val Tyr Ser Ala Gly Ile  
 165 170 175

Val Leu Phe Glu Leu Leu Thr Gly Thr Thr Pro Phe Ser Gly Glu Asp  
 180 185 190

Asp Leu Asp His Ala Tyr Ala Arg Leu Thr Glu Val Val Pro Ala Pro  
 195 200 205

Ser Ser Leu Ile Asp Gly Val Pro Ser Leu Ile Asp Glu Leu Val Ala  
 210 215 220

Thr Ala Thr Ser Ile Asn Pro Glu Asp Arg Phe Asp Asp Ser Gly Glu  
 225 230 235 240

Phe Leu Ser Ala Leu Glu Asp Val Ala Thr Glu Leu Ser Leu Pro Ala  
 245 250 255

Phe Arg Val Pro Val Pro Val Asn Ser Ala Ala Asn Arg Ala Asn Ala  
 260 265 270

Gln Val Pro Asp Ala Gln Pro Thr Asp Met Phe Thr Thr His Ile Pro  
 275 280 285

Lys Thr Pro Glu Pro Asp His Thr Ala Ile Ile Pro Val Ala Ser Ala  
 290 295 300

Asn Glu Thr Ser Ile Leu Pro Ala Gln Asn Met Ala Gln Asn Met Ala  
 305 310 315 320  
 Gln Asn Pro Leu Gln Pro Pro Glu Pro Asp Phe Ala Pro Glu Pro Pro  
 325 330 335  
 Pro Asp Thr Ala Leu Asn Ile Gln Asp Gln Glu Leu Ala Arg Ala Asp  
 340 345 350  
 Glu Pro Glu Ile Asn Thr Val Ser Asn Arg Ser Lys Leu Lys Leu Thr  
 355 360 365  
 Leu Trp Ser Ile Phe Val Val Ala Val Ile Ala Ala Val Ala Val Gly  
 370 375 380  
 Gly Trp Trp Phe Gly Ser Gly Arg Tyr Gly Glu Ile Pro Gln Val Leu  
 385 390 395 400  
 Gly Met Asp Glu Val Gln Ala Val Ala Val Val Glu Glu Ala Gly Phe  
 405 410 415  
 Val Ala Val Ala Glu Pro Gln Tyr Asp Asn Glu Val Pro Thr Gly Ser  
 420 425 430  
 Ile Ile Gly Thr Glu Pro Ser Phe Gly Glu Arg Leu Pro Arg Gly Glu  
 435 440 445  
 Asp Val Ser Val Leu Val Ser Gln Gly Arg Pro Val Val Pro Asp Leu  
 450 455 460  
 Ser Glu Asp Arg Ser Leu Ser Thr Val Arg Glu Glu Leu Glu Gln Arg  
 465 470 475 480  
 Thr Phe Val Trp Val Asp Gly Pro Gly Glu Tyr Ser Asp Asp Val Pro  
 485 490 495  
 Glu Gly Gln Val Val Ser Phe Thr Pro Ser Ser Gly Thr Gln Leu Asp  
 500 505 510  
 Val Gly Glu Thr Val Gln Ile His Leu Ser Arg Gly Pro Ala Pro Val  
 515 520 525  
 Glu Ile Pro Asp Val Ser Gly Met Gly Val Asp Gln Ala Thr Arg Val  
 530 535 540  
 Leu Glu Arg Ala Gly Leu Ser Val Glu Arg Thr Glu Glu Gly Phe Asp  
 545 550 555 560  
 Ala Glu Thr Pro Asn Gly Asp Val Tyr Gly Thr Ser Pro Lys Val Ser  
 565 570 575  
 Thr Glu Val Lys Arg Gly Thr Ser Val Val Leu Gln Val Ser Asn Ala  
 580 585 590  
 Ile Ser Val Pro Asp Val Val Gly Met Thr Lys Asp Glu Ala Thr Ala  
 595 600 605  
 Ala Leu Ala Glu Glu Gly Leu Val Val Ala Ser Thr Ser Ile Ile Pro  
 610 615 620

Gly Glu Ala Ala Ser Ser Ala Asp Ala Val Val Thr Val Glu Pro Glu  
 625 630 635 640  
 Ser Gly Ser Arg Val Asp Pro Ala His Pro Gln Val Ser Leu Gly Leu  
 645 650 655  
 Ala Gly Glu Ile Gln Val Pro Ser Val Val Gly Arg Lys Val Ser Asp  
 660 665 670  
 Ala Arg Ser Ile Leu Glu Glu Ala Gly Leu Thr Leu Thr Thr Asp Ala  
 675 680 685  
 Asp Asp Asn Asp Arg Ile Tyr Ser Gln Thr Pro Arg Ala Arg Ser Glu  
 690 695 700  
 Val Ser Val Gly Gly Glu Val Thr Val Arg Ala Phe  
 705 710 715

<210> 67  
 <211> 549  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(526)  
 <223> RXA00319

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 aattgttttc gtatgcaccg gaaacatttg ccgatccccc atg tcg gaa gtc atc 115  
 Met Ser Glu Val Ile  
 1 5  
 gcg aag gca aaa gcg gaa gaa gct ggc ttg gaa gac aac gtc att ttc 163  
 Ala Lys Ala Lys Ala Glu Glu Ala Gly Leu Glu Asp Asn Val Ile Phe  
 10 15 20  
 tcc tcc tgt ggc atg ggc aat tgg cac gtt ggc caa cct gct gac aag 211  
 Ser Ser Cys Gly Met Gly Asn Trp His Val Gly Gln Pro Ala Asp Lys  
 25 30 35  
 cga gct ctc gcg gaa ctg aaa tca gcc ggt tac aac ggc gac acc cac 259  
 Arg Ala Leu Ala Glu Leu Lys Ser Ala Gly Tyr Asn Gly Asp Thr His  
 40 45 50  
 cgc gca gca caa ctt ggt ccc gag cac atg cgc gca gat ctc ttc gtc 307  
 Arg Ala Ala Gln Leu Gly Pro Glu His Met Arg Ala Asp Leu Phe Val  
 55 60 65  
 gcg cta gat tcc ggc cac gcc ggt gag ctc gcc gca acg ggt gtt ccc 355  
 Ala Leu Asp Ser Gly His Ala Gly Glu Leu Ala Ala Thr Gly Val Pro  
 70 75 80 85  
 aac gac aaa atc cgc ctc atg cgt tcc ttc gac cca gag tcc aac ccc 403  
 Asn Asp Lys Ile Arg Leu Met Arg Ser Phe Asp Pro Glu Ser Asn Pro  
 90 95 100  
 acc gac gat gtc gca gac cct tac tac ggc aca tcc cag gat ttc gtg 451

Thr Asp Asp Val Ala Asp Pro Tyr Tyr Gly Thr Ser Gln Asp Phe Val  
 105 110 115

ctc acc cgt gaa aac atc gaa gat gct atg ccg ggc ctt ttg gag tgg 499  
 Leu Thr Arg Glu Asn Ile Glu Asp Ala Met Pro Gly Leu Leu Glu Trp  
 120 125 130

gtc aga gat cac atc cgc act gat tct taggtctttg agctaaaaag 546  
 Val Arg Asp His Ile Arg Thr Asp Ser  
 135 140

tcc 549

<210> 68  
 <211> 142  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 68  
 Met Ser Glu Val Ile Ala Lys Ala Lys Ala Glu Glu Ala Gly Leu Glu  
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Asp Asn Val Ile Phe Ser Ser Cys Gly Met Gly Asn Trp His Val Gly  
 20 25 30

Gln Pro Ala Asp Lys Arg Ala Leu Ala Glu Leu Lys Ser Ala Gly Tyr  
 35 40 45

Asn Gly Asp Thr His Arg Ala Ala Gln Leu Gly Pro Glu His Met Arg  
 50 55 60

Ala Asp Leu Phe Val Ala Leu Asp Ser Gly His Ala Gly Glu Leu Ala  
 65 70 75 80

Ala Thr Gly Val Pro Asn Asp Lys Ile Arg Leu Met Arg Ser Phe Asp  
 85 90 95

Pro Glu Ser Asn Pro Thr Asp Asp Val Ala Asp Pro Tyr Tyr Gly Thr  
 100 105 110

Ser Gln Asp Phe Val Leu Thr Arg Glu Asn Ile Glu Asp Ala Met Pro  
 115 120 125

Gly Leu Leu Glu Trp Val Arg Asp His Ile Arg Thr Asp Ser  
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 <212> DNA  
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 <223> RXA01272

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                                         Met Ser Asn Ser Phe
                                         1                               5

act att ctc act gtc tgt act gga aac att tgc cgc tcc ccg tta gct 163
Thr Ile Leu Thr Val Cys Thr Gly Asn Ile Cys Arg Ser Pro Leu Ala
                        10                               15                               20

aag cag cta ctt gaa ctt gag ctt ccg ggg gca gat ata atc cgc gtt 211
Lys Gln Leu Leu Glu Leu Glu Leu Pro Gly Ala Asp Ile Ile Arg Val
                        25                               30                               35

gat tcc gcc ggt gtt cag gcg atg gtt gat tcg cct atg ccg gag caa 259
Asp Ser Ala Gly Val Gln Ala Met Val Asp Ser Pro Met Pro Glu Gln
                        40                               45                               50

tct tta gaa atc gca cgt aaa cag ggc ata gaa aac cct gag gag cac 307
Ser Leu Glu Ile Ala Arg Lys Gln Gly Ile Glu Asn Pro Glu Glu His
                        55                               60                               65

cga gct aag cag att act gag gag ctt gta aac caa tct gat ctg att 355
Arg Ala Lys Gln Ile Thr Glu Glu Leu Val Asn Gln Ser Asp Leu Ile
                        70                               75                               80                               85

ctt gcg atg gat ccg ggg cat cga aaa tcc att gtc cag cta agc ccg 403
Leu Ala Met Asp Arg Gly His Arg Lys Ser Ile Val Gln Leu Ser Pro
                        90                               95                               100

cgt gca acc cgt aag gtt ttc act gtt gtt gat ctt gcc agg tta att 451
Arg Ala Thr Arg Lys Val Phe Thr Val Val Asp Leu Ala Arg Leu Ile
                        105                               110                               115

gag gca aca act gat gct gat ctg cag gaa gag ctc aat ctg gca ggg 499
Glu Ala Thr Thr Asp Ala Asp Leu Gln Glu Glu Leu Asn Leu Ala Gly
                        120                               125                               130

gat tcc gtg atc gat agg ctg cat gcg aca gtt gag gct gct cgt ctt 547
Asp Ser Val Ile Asp Arg Leu His Ala Thr Val Glu Ala Ala Arg Leu
                        135                               140                               145

agc cgc agt gaa ttg aat cct ctg gat aac ctc gca gat gaa gat att 595
Ser Arg Ser Glu Leu Asn Pro Leu Asp Asn Leu Ala Asp Glu Asp Ile
                        150                               155                               160                               165

gtt gac ccg tac gga aag agt caa tcg gtt tat gag gca tcg gcg agt 643
Val Asp Pro Tyr Gly Lys Ser Gln Ser Val Tyr Glu Ala Ser Ala Ser
                        170                               175                               180

cag cta att cca gct att cgt ttg att gct tct tat ttg aac aaa gca 691
Gln Leu Ile Pro Ala Ile Arg Leu Ile Ala Ser Tyr Leu Asn Lys Ala
                        185                               190                               195

ctg gag tct gcg taatggcgag gaagtatcgg gtg 726
Leu Glu Ser Ala
                        200

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&lt;210&gt; 70

&lt;211&gt; 201

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 70

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Met Ser Asn Ser Phe Thr Ile Leu Thr Val Cys Thr Gly Asn Ile Cys
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Arg Ser Pro Leu Ala Lys Gln Leu Leu Glu Leu Glu Leu Pro Gly Ala
      20           25           30

Asp Ile Ile Arg Val Asp Ser Ala Gly Val Gln Ala Met Val Asp Ser
      35           40           45

Pro Met Pro Glu Gln Ser Leu Glu Ile Ala Arg Lys Gln Gly Ile Glu
      50           55           60

Asn Pro Glu Glu His Arg Ala Lys Gln Ile Thr Glu Glu Leu Val Asn
      65           70           75           80

Gln Ser Asp Leu Ile Leu Ala Met Asp Arg Gly His Arg Lys Ser Ile
      85           90           95

Val Gln Leu Ser Pro Arg Ala Thr Arg Lys Val Phe Thr Val Val Asp
      100          105          110

Leu Ala Arg Leu Ile Glu Ala Thr Thr Asp Ala Asp Leu Gln Glu Glu
      115          120          125

Leu Asn Leu Ala Gly Asp Ser Val Ile Asp Arg Leu His Ala Thr Val
      130          135          140

Glu Ala Ala Arg Leu Ser Arg Ser Glu Leu Asn Pro Leu Asp Asn Leu
      145          150          155          160

Ala Asp Glu Asp Ile Val Asp Pro Tyr Gly Lys Ser Gln Ser Val Tyr
      165          170          175

Glu Ala Ser Ala Ser Gln Leu Ile Pro Ala Ile Arg Leu Ile Ala Ser
      180          185          190

Tyr Leu Asn Lys Ala Leu Glu Ser Ala
      195          200

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&lt;210&gt; 71

&lt;211&gt; 1476

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1453)

&lt;223&gt; RXA01830

&lt;400&gt; 71

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acggcacttt tgtcgggtgtt acgcgcattg atcagcctga gcagattgcg gtgggacagg 60

atatccgtat tggtcgtaca gcagtgaggc ttgttcctg atg ttg aaa ctt aaa 115
                               Met Leu Lys Leu Lys
                               1           5

tat gcg gtg gca tct gac cga ggg tta gtg cgc ggg aac aat gag gat 163
Tyr Ala Val Ala Ser Asp Arg Gly Leu Val Arg Gly Asn Asn Glu Asp

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				10				15				20				
tcc	gct	tac	gct	ggc	ccg	cat	ttg	ttg	gcg	ctg	gct	gat	ggg	atg	ggc	211
Ser	Ala	Tyr	Ala	Gly	Pro	His	Leu	Leu	Ala	Leu	Ala	Asp	Gly	Met	Gly	
25				30				35								
ggc	cat	gct	gct	ggg	gag	atc	gct	tcc	caa	acc	atg	atc	aac	cat	ttg	259
Gly	His	Ala	Ala	Gly	Glu	Ile	Ala	Ser	Gln	Thr	Met	Ile	Asn	His	Leu	
40				45				50								
cgt	gcg	ctt	gat	gtt	gat	cct	ggg	gat	aac	gat	atg	ttg	gcg	ctg	gtg	307
Arg	Ala	Leu	Asp	Val	Asp	Pro	Gly	Asp	Asn	Asp	Met	Leu	Ala	Leu	Val	
55				60				65								
ggc	atg	gtg	gca	ggc	gaa	gcc	aac	gcg	gcg	att	gct	gag	ggc	atc	gcc	355
Gly	Met	Val	Ala	Gly	Glu	Ala	Asn	Ala	Ala	Ile	Ala	Glu	Gly	Ile	Ala	
70				75				80				85				
gaa	gac	ccg	gcg	cgc	gac	ggc	atg	ggc	act	acg	ttg	acg	gcg	ttc	atg	403
Glu	Asp	Pro	Ala	Arg	Asp	Gly	Met	Gly	Thr	Thr	Leu	Thr	Ala	Phe	Met	
90				95				100								
ttt	aac	ggg	cgt	gac	ctg	gca	atg	tgc	cac	gtc	ggc	gat	agt	cgt	ggg	451
Phe	Asn	Gly	Arg	Asp	Leu	Ala	Met	Cys	His	Val	Gly	Asp	Ser	Arg	Gly	
105				110				115								
tat	gtg	ctt	cgc	gac	gat	aag	ttg	gta	cag	gtt	aca	gtc	gac	gat	act	499
Tyr	Val	Leu	Arg	Asp	Asp	Lys	Leu	Val	Gln	Val	Thr	Val	Asp	Asp	Thr	
120				125				130								
ttt	gtg	cag	tcg	ttg	gtc	gct	gag	ggc	aag	ctt	gat	cca	gaa	gat	gtt	547
Phe	Val	Gln	Ser	Leu	Val	Ala	Glu	Gly	Lys	Leu	Asp	Pro	Glu	Asp	Val	
135				140				145								
tca	act	cac	cct	cag	cgt	tct	ttg	att	ctg	aag	gct	tac	acc	ggc	cat	595
Ser	Thr	His	Pro	Gln	Arg	Ser	Leu	Ile	Leu	Lys	Ala	Tyr	Thr	Gly	His	
150				155				160				165				
cct	gtg	gag	ccc	act	ctg	gag	caa	ttc	ccg	gcc	ttg	cct	ggg	gat	cgt	643
Pro	Val	Glu	Pro	Thr	Leu	Glu	Gln	Phe	Pro	Ala	Leu	Pro	Gly	Asp	Arg	
170				175				180								
ttg	ttg	ttg	tgc	tct	gat	ggg	cta	tca	gat	ccg	gtt	aca	cac	tcc	acg	691
Leu	Leu	Leu	Cys	Ser	Asp	Gly	Leu	Ser	Asp	Pro	Val	Thr	His	Ser	Thr	
185				190				195								
att	gaa	gaa	aca	gtg	cgt	gta	ggc	acc	ccg	cag	gat	gcg	tcc	acc	aag	739
Ile	Glu	Glu	Thr	Val	Arg	Val	Gly	Thr	Pro	Gln	Asp	Ala	Ser	Thr	Lys	
200				205				210								
ttg	gtg	gag	ttg	gcg	ctg	cgt	tct	ggc	ggg	ccg	gac	aat	gtg	acg	gtc	787
Leu	Val	Glu	Leu	Ala	Leu	Arg	Ser	Gly	Gly	Pro	Asp	Asn	Val	Thr	Val	
215				220				225								
att	gtg	gcc	gat	gtt	gta	gaa	gtc	acc	gag	gcg	gaa	gca	gca	gcg	gaa	835
Ile	Val	Ala	Asp	Val	Val	Glu	Val	Thr	Glu	Ala	Glu	Ala	Ala			

gat ccg cgg cct gat acc gct gcg gga cgc gct gcg gcg atc aca cgg	931
Asp Pro Arg Pro Asp Thr Ala Ala Gly Arg Ala Ala Ala Ile Thr Arg	
265 270 275	
cga gct caa gtg att gat ccg gca cca aag ata tct gat gct gga acg	979
Arg Ala Gln Val Ile Asp Pro Ala Pro Lys Ile Ser Asp Ala Gly Thr	
280 285 290	
gag gat att ccc aca att gag gag cca cca gag aaa agt tcc agc aaa	1027
Glu Asp Ile Pro Thr Ile Glu Glu Pro Pro Glu Lys Ser Ser Ser Lys	
295 300 305	
ctt gcg gta ttg atc gta gcc ctg gtc atc ctc atc ggt gta gtt gcc	1075
Leu Ala Val Leu Ile Val Ala Leu Val Ile Leu Ile Gly Val Val Ala	
310 315 320 325	
gca gga tgg tgg ggc tac tcc cgt att gac agc act ttt tac gtc gcg	1123
Ala Gly Trp Trp Gly Tyr Ser Arg Ile Asp Ser Thr Phe Tyr Val Ala	
330 335 340	
gtc aat gat gag gaa gcc atc acc gtg gaa cac ggt gtg gat tac cgc	1171
Val Asn Asp Glu Glu Ala Ile Thr Val Glu His Gly Val Asp Tyr Arg	
345 350 355	
atc ttt ggc aag gat tta cat tcg caa ttc cag gtg gcg tgc ctg aat	1219
Ile Phe Gly Lys Asp Leu His Ser Gln Phe Gln Val Ala Cys Leu Asn	
360 365 370	
gaa gct ggc acc ttg tca ctc aag gaa tcc tgt gaa aac ggt acg tct	1267
Glu Ala Gly Thr Leu Ser Leu Lys Glu Ser Cys Glu Asn Gly Thr Ser	
375 380 385	
ttc aaa ttg gat gat tta ccg gca tct gtt cgc ggt agt gtc gca gga	1315
Phe Lys Leu Asp Asp Leu Pro Ala Ser Val Arg Gly Ser Val Ala Gly	
390 395 400 405	
tta ccg tct ggg tcg tat gac gag gtc cag gcg caa atg caa cgg ctg	1363
Leu Pro Ser Gly Ser Tyr Asp Glu Val Gln Ala Gln Met Gln Arg Leu	
410 415 420	
gct gct caa gct ttg cca gtg tgc gtg aac tta gaa gta aca acc ggt	1411
Ala Ala Gln Ala Leu Pro Val Cys Val Asn Leu Glu Val Thr Thr Gly	
425 430 435	
ggc gat aga aac gaa ccc gga gtc aat tgt agg gag gtc tca	1453
Gly Asp Arg Asn Glu Pro Gly Val Asn Cys Arg Glu Val Ser	
440 445 450	
tgaacacgct tgaacgatta aag	1476

&lt;210&gt; 72

&lt;211&gt; 451

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 72

Met	Leu	Lys	Leu	Lys	Tyr	Ala	Val	Ala	Ser	Asp	Arg	Gly	Leu	Val	Arg
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Gly Asn Asn Glu Asp Ser Ala Tyr Ala Gly Pro His Leu Leu Ala Leu  
 20 25 30  
 Ala Asp Gly Met Gly Gly His Ala Ala Gly Glu Ile Ala Ser Gln Thr  
 35 40 45  
 Met Ile Asn His Leu Arg Ala Leu Asp Val Asp Pro Gly Asp Asn Asp  
 50 55 60  
 Met Leu Ala Leu Val Gly Met Val Ala Gly Glu Ala Asn Ala Ala Ile  
 65 70 75 80  
 Ala Glu Gly Ile Ala Glu Asp Pro Ala Arg Asp Gly Met Gly Thr Thr  
 85 90 95  
 Leu Thr Ala Phe Met Phe Asn Gly Arg Asp Leu Ala Met Cys His Val  
 100 105 110  
 Gly Asp Ser Arg Gly Tyr Val Leu Arg Asp Asp Lys Leu Val Gln Val  
 115 120 125  
 Thr Val Asp Asp Thr Phe Val Gln Ser Leu Val Ala Glu Gly Lys Leu  
 130 135 140  
 Asp Pro Glu Asp Val Ser Thr His Pro Gln Arg Ser Leu Ile Leu Lys  
 145 150 155 160  
 Ala Tyr Thr Gly His Pro Val Glu Pro Thr Leu Glu Gln Phe Pro Ala  
 165 170 175  
 Leu Pro Gly Asp Arg Leu Leu Leu Cys Ser Asp Gly Leu Ser Asp Pro  
 180 185 190  
 Val Thr His Ser Thr Ile Glu Glu Thr Val Arg Val Gly Thr Pro Gln  
 195 200 205  
 Asp Ala Ser Thr Lys Leu Val Glu Leu Ala Leu Arg Ser Gly Gly Pro  
 210 215 220  
 Asp Asn Val Thr Val Ile Val Ala Asp Val Val Glu Val Thr Glu Ala  
 225 230 235 240  
 Glu Ala Ala Ala Glu Ala Ser Val Pro Val Thr Ala Gly Ala Leu Asn  
 245 250 255  
 Gly Glu Gln Pro Glu Asp Pro Arg Pro Asp Thr Ala Ala Gly Arg Ala  
 260 265 270  
 Ala Ala Ile Thr Arg Arg Ala Gln Val Ile Asp Pro Ala Pro Lys Ile  
 275 280 285  
 Ser Asp Ala Gly Thr Glu Asp Ile Pro Thr Ile Glu Glu Pro Pro Glu  
 290 295 300  
 Lys Ser Ser Ser Lys Leu Ala Val Leu Ile Val Ala Leu Val Ile Leu  
 305 310 315 320  
 Ile Gly Val Val Ala Ala Gly Trp Trp Gly Tyr Ser Arg Ile Asp Ser  
 325 330 335  
 Thr Phe Tyr Val Ala Val Asn Asp Glu Glu Ala Ile Thr Val Glu His

340		345		350
Gly Val Asp Tyr Arg Ile Phe Gly Lys Asp Leu His Ser Gln Phe Gln				
355		360		365
Val Ala Cys Leu Asn Glu Ala Gly Thr Leu Ser Leu Lys Glu Ser Cys				
370		375		380
Glu Asn Gly Thr Ser Phe Lys Leu Asp Asp Leu Pro Ala Ser Val Arg				
385		390		395
				400
Gly Ser Val Ala Gly Leu Pro Ser Gly Ser Tyr Asp Glu Val Gln Ala				
		405		410
				415
Gln Met Gln Arg Leu Ala Ala Gln Ala Leu Pro Val Cys Val Asn Leu				
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				430
Glu Val Thr Thr Gly Gly Asp Arg Asn Glu Pro Gly Val Asn Cys Arg				
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				445
Glu Val Ser				
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<220>  
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 Met Asn Asn Pro Ala  
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 Gln Leu Arg Gln Asp Thr Glu Lys Glu Val Leu Ala Leu Leu Gly Ser  
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 Leu Val Leu Pro Ala Gly Thr Ala Leu Ala Ala Thr Gly Ser Leu Ala  
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 agg tcc gaa ctc acg ccg tat tcc gat ttg gac ctc att ttg atc cat 259  
 Arg Ser Glu Leu Thr Pro Tyr Ser Asp Leu Asp Leu Ile Leu Ile His  
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 Pro Pro Gly Ala Thr Pro Asp Gly Val Glu Asp Leu Trp Tyr Pro Ile  
 55 60 65  
 tgg gac gca aaa aag cgt ctc gac tac tcc gtg cgc acc cca gat gag 355  
 Trp Asp Ala Lys Lys Arg Leu Asp Tyr Ser Val Arg Thr Pro Asp Glu  
 70 75 80 85

tgt	gtg	gct	atg	att	tct	gcg	gat	tcc	act	gca	gcc	ctt	gcc	atg	ctt	403
Cys	Val	Ala	Met	Ile	Ser	Ala	Asp	Ser	Thr	Ala	Ala	Leu	Ala	Met	Leu	
				90					95					100		
gac	ctg	cgg	ttt	gtc	gct	ggc	gat	gag	gat	ctg	tgt	gcc	aaa	acg	cgc	451
Asp	Leu	Arg	Phe	Val	Ala	Gly	Asp	Glu	Asp	Leu	Cys	Ala	Lys	Thr	Arg	
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cgg	cgc	atc	gtg	gag	aag	tgg	cgc	cag	gaa	ctc	aac	aaa	aac	ttc	gat	499
Arg	Arg	Ile	Val	Glu	Lys	Trp	Arg	Gln	Glu	Leu	Asn	Lys	Asn	Phe	Asp	
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gcc	gtt	gtg	gac	acc	gcg	att	gcc	cgt	tgg	cgc	cgc	tcc	gga	ccc	gtc	547
Ala	Val	Val	Asp	Thr	Ala	Ile	Ala	Arg	Trp	Arg	Arg	Ser	Gly	Pro	Val	
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Val	Ala	Met	Thr	Arg	Pro	Asp	Leu	Lys	His	Gly	Arg	Gly	Gly	Leu	Arg	
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Asp	Phe	Glu	Leu	Ile	Lys	Ala	Leu	Ala	Leu	Gly	His	Leu	Cys	Asn	Leu	
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Pro	Gln	Leu	Asp	Ala	Gln	His	Gln	Leu	Leu	Leu	Asp	Ala	Arg	Thr	Leu	
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Leu	His	Val	His	Ala	Arg	Arg	Ser	Arg	Asp	Val	Leu	Asp	Pro	Glu	Phe	
		200					205					210				
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Ala	Val	Asp	Val	Ala	Met	Asp	Leu	Gly	Phe	Val	Asp	Arg	Tyr	His	Leu	
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ggc	cgg	gag	atc	gcc	gat	gca	gcc	cgc	gcc	att	gat	gat	ggc	ctg	acc	835
Gly	Arg	Glu	Ile	Ala	Asp	Ala	Ala	Arg	Ala	Ile	Asp	Asp	Gly	Leu	Thr	
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acc	gcg	ctg	gcc	acc	gcc	cgt	ggc	att	ttg	cca	cgt	cgc	aca	ggt	ttt	883
Thr	Ala	Leu	Ala	Thr	Ala	Arg	Gly	Ile	Leu	Pro	Arg	Arg	Thr	Gly	Phe	
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Ala	Phe	Arg	Asn	Ala	Ser	Arg	Arg	Pro	Leu	Asp	Leu	Asp	Val	Val	Asp	
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Ala	Asn	Gly	Thr	Ile	Glu	Leu	Ser	Lys	Lys	Pro	Asp	Leu	Asn	Asp	Pro	
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Ala	Leu	Pro	Leu	Arg	Val	Ala	Ala	Ala	Ala	Ala	Thr	Thr	Gly	Leu	Pro	
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Val	Ala	Glu	Ser	Thr	Trp	Val	Arg	Leu	Asn	Glu	Cys	Pro	Pro	Leu	Pro	
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Ser	Pro	Lys	Asn	Ser	Arg	Arg	Val	Val	Lys	Asn	Met	Asp	Arg	His	Gly		
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Pro	Arg	Glu	Pro	Ser	His	Ile	Ser	Thr	Ile	Asp	Glu	His	Ser	Leu	Asn		
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Thr	Val	Ala	Gly	Cys	Ala	Leu	Glu	Thr	Val	Thr	Val	Ala	Arg	Pro	Asp		
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Leu	Leu	Val	Leu	Gly	Ala	Leu	Tyr	His	Asp	Ile	Gly	Lys	Gly	Phe	Pro		
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cgt	cca	cac	gaa	caa	gta	ggt	gca	gag	atg	gtg	gcg	agg	gct	gca	agc	1411	
Arg	Pro	His	Glu	Gln	Val	Gly	Ala	Glu	Met	Val	Ala	Arg	Ala	Ala	Ser		
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Arg	Met	Gly	Leu	Asn	Leu	Arg	Asp	Arg	Ala	Ser	Val	Gln	Thr	Leu	Val		
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Ser	Glu	Gly	Ala	Val	Asp	Lys	Leu	Leu	Asp	Ala	Val	Arg	Tyr	Asp	Leu		
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Thr	Gly	Pro	Gly	Val	Trp	Thr	Ala	Arg	Leu	Glu	His	Ala	Leu	Arg	Ile		
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Arg Gly Ala Thr Leu Ile Ile Gln Ala Ala Leu Lys Pro Gly Phe Asp																				
665 670 675																				
cga gca acg gtg gaa cgc tcc gta gtc agg tcg ttg gca ggt agc	2176																			
Arg Ala Thr Val Glu Arg Ser Val Val Arg Ser Leu Ala Gly Ser																				
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&lt;210&gt; 74

&lt;211&gt; 692

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 74

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Thr Gly Ser Leu Ala Arg Ser Glu Leu Thr Pro Tyr Ser Asp Leu Asp
35 40 45

Leu Ile Leu Ile His Pro Pro Gly Ala Thr Pro Asp Gly Val Glu Asp
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Leu Trp Tyr Pro Ile Trp Asp Ala Lys Lys Arg Leu Asp Tyr Ser Val
65 70 75 80

Arg Thr Pro Asp Glu Cys Val Ala Met Ile Ser Ala Asp Ser Thr Ala
85 90 95

Ala Leu Ala Met Leu Asp Leu Arg Phe Val Ala Gly Asp Glu Asp Leu
100 105 110

Cys Ala Lys Thr Arg Arg Arg Ile Val Glu Lys Trp Arg Gln Glu Leu

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Arg	Gly	Gly	Leu	Arg	Asp	Phe	Glu	Leu	Ile	Lys	Ala	Leu	Ala	Leu	Gly
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His	Leu	Cys	Asn	Leu	Pro	Gln	Leu	Asp	Ala	Gln	His	Gln	Leu	Leu	Leu
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Asp	Ala	Arg	Thr	Leu	Leu	His	Val	His	Ala	Arg	Arg	Ser	Arg	Asp	Val
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Asp	Asp	Gly	Leu	Thr	Thr	Ala	Leu	Ala	Thr	Ala	Arg	Gly	Ile	Leu	Pro
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Arg	Arg	Thr	Gly	Phe	Ala	Phe	Arg	Asn	Ala	Ser	Arg	Arg	Pro	Leu	Asp
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Cys	Pro	Pro	Leu	Pro	Glu	Pro	Trp	Pro	Ala	Asn	Ala	Ala	Gly	Asp	Phe
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Phe	Arg	Ile	Leu	Ser	Ser	Pro	Lys	Asn	Ser	Arg	Arg	Val	Val	Lys	Asn
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Met	Asp	Arg	His	Gly	Leu	Trp	Ser	Arg	Phe	Val	Pro	Glu	Trp	Asp	Arg
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	370					375					380				
Glu	His	Ser	Leu	Asn	Thr	Val	Ala	Gly	Cys	Ala	Leu	Glu	Thr	Val	Thr
385					390					395					400
Val	Ala	Arg	Pro	Asp	Leu	Leu	Val	Leu	Gly	Ala	Leu	Tyr	His	Asp	Ile
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Gly	Lys	Gly	Phe	Pro	Arg	Pro	His	Glu	Gln	Val	Gly	Ala	Glu	Met	Val
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Ala	Arg	Ala	Ala	Ser	Arg	Met	Gly	Leu	Asn	Leu	Arg	Asp	Arg	Ala	Ser
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Val Gln Thr Leu Val Ala Glu His Thr Ala Val Ala Lys Ile Ala Ala  
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 Arg Leu Asp Pro Ser Ser Glu Gly Ala Val Asp Lys Leu Leu Asp Ala  
 465 470 475 480  
 Val Arg Tyr Asp Leu Val Thr Leu Asn Leu Leu Glu Val Leu Thr Glu  
 485 490 495  
 Ala Asp Ala Lys Ala Thr Gly Pro Gly Val Trp Thr Ala Arg Leu Glu  
 500 505 510  
 His Ala Leu Arg Ile Val Cys Lys Arg Ala Arg Asp Arg Leu Thr Asp  
 515 520 525  
 Ile Arg Pro Val Ala Pro Met Ile Ala Pro Arg Ser Glu Ile Gly Leu  
 530 535 540  
 Val Glu Arg Asp Gly Val Phe Thr Val Gln Trp His Gly Glu Asp Leu  
 545 550 555 560  
 His Arg Ile Leu Gly Val Ile Tyr Ala Lys Gly Trp Thr Ile Thr Ala  
 565 570 575  
 Ala Arg Met Leu Ala Asn Gly Gln Trp Ser Ala Glu Phe Asp Val Arg  
 580 585 590  
 Ala Asn Gly Pro Gln Asp Phe Asp Pro Gln His Phe Leu Gln Ala Tyr  
 595 600 605  
 Gln Ser Gly Val Phe Ser Glu Val Pro Ile Pro Ala Leu Gly Ile Thr  
 610 615 620  
 Ala Thr Phe Trp His Gly Asn Thr Leu Glu Val Arg Thr Glu Leu Arg  
 625 630 635 640  
 Thr Gly Ala Ile Phe Ala Leu Leu Arg Thr Leu Pro Asp Ala Leu Trp  
 645 650 655  
 Ile Asn Ala Val Thr Arg Gly Ala Thr Leu Ile Ile Gln Ala Ala Leu  
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 Lys Pro Gly Phe Asp Arg Ala Thr Val Glu Arg Ser Val Val Arg Ser  
 675 680 685  
 Leu Ala Gly Ser  
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 <223> RXA02210

<400> 75

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                                   Val Ser Val Ala Ala
                                   1 5
ggc gac aaa cca aca aat agc cgt caa gaa atc ctc gaa ggt gcc cga 163
Gly Asp Lys Pro Thr Asn Ser Arg Gln Glu Ile Leu Glu Gly Ala Arg
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Arg Cys Phe Ala Glu His Gly Tyr Glu Gly Ala Thr Val Arg Arg Leu
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gaa gaa gca aca ggt aaa tca cgc gga gcg atc ttt cat cac ttc ggt 259
Glu Glu Ala Thr Gly Lys Ser Arg Gly Ala Ile Phe His His Phe Gly
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gac aaa gaa aac ctg ttc cta gcc ctc gcg cgg gaa gat gca gcc cgc 307
Asp Lys Glu Asn Leu Phe Leu Ala Leu Ala Arg Glu Asp Ala Ala Arg
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Met Ala Glu Val Val Ser Glu Asn Gly Leu Val Glu Val Met Arg Gly
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atg ctg gaa gat cct gaa cga tat gac tgg atg tca gta cgc ctg gag 403
Met Leu Glu Asp Pro Glu Arg Tyr Asp Trp Met Ser Val Arg Leu Glu
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Ile Ser Lys Gln Leu Arg Thr Asp Pro Val Phe Arg Ala Lys Trp Ile
                                   105 110 115
gat cac caa agt gtt cta gac gaa gct gtc cgc gtg cgt ttg tcc cgc 499
Asp His Gln Ser Val Leu Asp Glu Ala Val Arg Val Arg Leu Ser Arg
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aac gtg gat aag gga caa atg cgc act gac gtc ccg atc gaa gtg ctg 547
Asn Val Asp Lys Gly Gln Met Arg Thr Asp Val Pro Ile Glu Val Leu
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cac acc ttc tta gag act gtt ctc gac ggt ttc atc tcc cgt ctt gct 595
His Thr Phe Leu Glu Thr Val Leu Asp Gly Phe Ile Ser Arg Leu Ala
                                   150 155 160 165
acc ggc gca tcc aca gaa gga ctg tcc gaa gta ttg gat ctg gtc gag 643
Thr Gly Ala Ser Thr Glu Gly Leu Ser Glu Val Leu Asp Leu Val Glu
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gga act gtc cgt aaa cgc gac taaacgaccc ctgattcaca ctt 687
Gly Thr Val Arg Lys Arg Asp
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&lt;210&gt; 76

&lt;211&gt; 188

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 76

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 Leu Glu Gly Ala Arg Arg Cys Phe Ala Glu His Gly Tyr Glu Gly Ala  
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 Thr Val Arg Arg Leu Glu Glu Ala Thr Gly Lys Ser Arg Gly Ala Ile  
 35 40 45  
 Phe His His Phe Gly Asp Lys Glu Asn Leu Phe Leu Ala Leu Ala Arg  
 50 55 60  
 Glu Asp Ala Ala Arg Met Ala Glu Val Val Ser Glu Asn Gly Leu Val  
 65 70 75 80  
 Glu Val Met Arg Gly Met Leu Glu Asp Pro Glu Arg Tyr Asp Trp Met  
 85 90 95  
 Ser Val Arg Leu Glu Ile Ser Lys Gln Leu Arg Thr Asp Pro Val Phe  
 100 105 110  
 Arg Ala Lys Trp Ile Asp His Gln Ser Val Leu Asp Glu Ala Val Arg  
 115 120 125  
 Val Arg Leu Ser Arg Asn Val Asp Lys Gly Gln Met Arg Thr Asp Val  
 130 135 140  
 Pro Ile Glu Val Leu His Thr Phe Leu Glu Thr Val Leu Asp Gly Phe  
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 165 170 175  
 Leu Asp Leu Val Glu Gly Thr Val Arg Lys Arg Asp  
 180 185

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 <212> DNA  
 <213> Corynebacterium glutamicum

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 <222> (101)..(319)  
 <223> RXA00221

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 Met Asn Ala Glu Glu  
 1 5  
 atc gga atg gcg ctg ctc aac gga cgc aaa gag cta ggc ctt aga caa 163  
 Ile Gly Met Ala Leu Leu Asn Gly Arg Lys Glu Leu Gly Leu Arg Gln  
 10 15 20  
 gga gag ctc gca gac tta gct gga gtt tct gaa cga ttc atc cgc gat 211  
 Gly Glu Leu Ala Asp Leu Ala Gly Val Ser Glu Arg Phe Ile Arg Asp  
 25 30 35

aca aaa ctc tac gtt ctc tat ttc cgc cgc tct gtg aat tct gac ctc 211  
Thr Lys Leu Tyr Val Leu Tyr Phe Arg Arg Ser Val Asn Ser Asp Leu  
25 30 35

tcg ggt cca cag ctc act att ttg agt cgc ctg gaa gaa aac ggc cca 259  
 Ser Gly Pro Gln Leu Thr Ile Leu Ser Arg Leu Glu Glu Asn Gly Pro  
           40                          45                          50

tcc cga att agt cgc atc gcg gaa ctt gaa gat att cgt atg cca acc 307  
 Ser Arg Ile Ser Arg Ile Ala Glu Leu Glu Asp Ile Arg Met Pro Thr  
           55                          60                          65

gct tcg aat gct ctg cat cag ctg gag caa ctc aac ctg gtt gag cgt 355  
 Ala Ser Asn Ala Leu His Gln Leu Glu Gln Leu Asn Leu Val Glu Arg  
           70                          75                          80                          85

atc cgc gac acc aaa gac cgc cga ggc gtg cag gtt cag ctc act gat 403  
 Ile Arg Asp Thr Lys Asp Arg Arg Gly Val Gln Val Gln Leu Thr Asp  
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 His Gly Arg Glu Glu Leu Glu Arg Val Asn Asn Glu Arg Asn Ala Glu  
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 Met Ala Arg Leu Leu Glu Met Leu Thr Pro Glu Gln Leu Glu Arg Thr  
           120                          125                          130

gaa gac ctg gtg gat atc att act gag ctt gca gag gtg tac ggt agc 547  
 Glu Asp Leu Val Asp Ile Ile Thr Glu Leu Ala Glu Val Tyr Gly Ser  
           135                          140                          145

tgg aaa gag acc gac agc ggt tct taacagtttt ctccatctca act 594  
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&lt;210&gt; 80

&lt;211&gt; 157

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 80

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Val Arg Pro Ala Leu Thr Lys Leu Tyr Val Leu Tyr Phe Arg Arg Ser  
           20                          25                          30

Val Asn Ser Asp Leu Ser Gly Pro Gln Leu Thr Ile Leu Ser Arg Leu  
           35                          40                          45

Glu Glu Asn Gly Pro Ser Arg Ile Ser Arg Ile Ala Glu Leu Glu Asp  
           50                          55                          60

Ile Arg Met Pro Thr Ala Ser Asn Ala Leu His Gln Leu Glu Gln Leu  
           65                          70                          75                          80

Asn Leu Val Glu Arg Ile Arg Asp Thr Lys Asp Arg Arg Gly Val Gln  
                           85                          90                          95

Val Gln Leu Thr Asp His Gly Arg Glu Glu Leu Glu Arg Val Asn Asn  
           100                          105                          110

Glu Arg Asn Ala Glu Met Ala Arg Leu Leu Glu Met Leu Thr Pro Glu

115		120		125
Gln Leu Glu Arg Thr Glu Asp Leu Val Asp Ile Ile Thr Glu Leu Ala				
130		135		140
Glu Val Tyr Gly Ser Trp Lys Glu Thr Asp Ser Gly Ser				
145		150		155

<210> 81  
 <211> 448  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(448)  
 <223> FRXA00551

<400> 81  
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 tagataggtt atcgaacgga aattacttgg caataccgct atg ctg gca ggc atg 115  
 Met Leu Ala Gly Met  
 1 5  
 cct aat tta aac gct gag gag cta gca gtc cgc gtg cga ccc gcg ctg 163  
 Pro Asn Leu Asn Ala Glu Glu Leu Ala Val Arg Val Arg Pro Ala Leu  
 10 15 20  
 aca aaa ctc tac gtt ctc tat ttc cgc cgc tct gtg aat tct gac ctc 211  
 Thr Lys Leu Tyr Val Leu Tyr Phe Arg Arg Ser Val Asn Ser Asp Leu  
 25 30 35  
 tcg ggt cca cag ctc act att ttg agt cgc ctg gaa gaa aac ggc cca 259  
 Ser Gly Pro Gln Leu Thr Ile Leu Ser Arg Leu Glu Glu Asn Gly Pro  
 40 45 50  
 tcc cga att agt cgc atc gcg gaa ctt gaa gat att cgt atg cca acc 307  
 Ser Arg Ile Ser Arg Ile Ala Glu Leu Glu Asp Ile Arg Met Pro Thr  
 55 60 65  
 gct tcg aat gct ctg cat cag ctg gag caa ctc aac ctg gtt gag cgt 355  
 Ala Ser Asn Ala Leu His Gln Leu Glu Gln Leu Asn Leu Val Glu Arg  
 70 75 80 85  
 atc cgc gac acc aaa gac cgc cga ggc gtg cag gtt cag ctc act gat 403  
 Ile Arg Asp Thr Lys Asp Arg Arg Gly Val Gln Val Gln Leu Thr Asp  
 90 95 100  
 cat gga cgc gaa gag ctt gag cgc gtg aac aat gaa cga aac gca 448  
 His Gly Arg Glu Glu Leu Glu Arg Val Asn Asn Glu Arg Asn Ala  
 105 110 115

<210> 82  
 <211> 116  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 82

Met Leu Ala Gly Met Pro Asn Leu Asn Ala Glu Glu Leu Ala Val Arg  
 1 5 10 15  
 Val Arg Pro Ala Leu Thr Lys Leu Tyr Val Leu Tyr Phe Arg Arg Ser  
 20 25 30  
 Val Asn Ser Asp Leu Ser Gly Pro Gln Leu Thr Ile Leu Ser Arg Leu  
 35 40 45  
 Glu Glu Asn Gly Pro Ser Arg Ile Ser Arg Ile Ala Glu Leu Glu Asp  
 50 55 60  
 Ile Arg Met Pro Thr Ala Ser Asn Ala Leu His Gln Leu Glu Gln Leu  
 65 70 75 80  
 Asn Leu Val Glu Arg Ile Arg Asp Thr Lys Asp Arg Arg Gly Val Gln  
 85 90 95  
 Val Gln Leu Thr Asp His Gly Arg Glu Glu Leu Glu Arg Val Asn Asn  
 100 105 110  
 Glu Arg Asn Ala  
 115

<210> 83  
 <211> 588  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(565)  
 <223> RXA01763

<400> 83  
 attttgaaaaa cttacatcgt tcgcttgacg cacagaatgc atgcatgttc aaatgattga 60  
 agatcgaaac tatttttcag ccagttcaca tggagccact atg acc acc agc aac 115  
 Met Thr Thr Ser Asn  
 1 5  
 ccc acc gcc gag atc att ggc gga cca gaa cga ttc ctc gag gcc gaa 163  
 Pro Thr Ala Glu Ile Ile Gly Gly Pro Glu Arg Phe Leu Glu Ala Glu  
 10 15 20  
 ttg tcc cag cag att caa ttc ctc act gcc cgc gca cga gcc aag gga 211  
 Leu Ser Gln Gln Ile Gln Phe Leu Thr Ala Arg Ala Arg Ala Lys Gly  
 25 30 35  
 tcc gcc aaa gga aac gaa gcc tta gtc gac ctc gga ctt aaa gtt cgc 259  
 Ser Ala Lys Gly Asn Glu Ala Leu Val Asp Leu Gly Leu Lys Val Arg  
 40 45 50  
 caa tac tcc aca ctg tcc cta gcg gcc agc gga tta aaa cca acc caa 307  
 Gln Tyr Ser Thr Leu Ser Leu Ala Ala Ser Gly Leu Lys Pro Thr Gln  
 55 60 65  
 cga gaa ttg gga gca ttt ctc gac cta gac cca agt cag att gtt gcc 355  
 Arg Glu Leu Gly Ala Phe Leu Asp Leu Asp Pro Ser Gln Ile Val Ala  
 70 75 80 85

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ttg gtc gat ttc cta gaa aag cgc gga tta gtg gcc cgg gaa gtt gac 403
Leu Val Asp Phe Leu Glu Lys Arg Gly Leu Val Ala Arg Glu Val Asp
          90                      95                      100

ccc cgg gat agg cgc tcg aag atc atc atc gcc acc gaa aaa ggt ctg 451
Pro Arg Asp Arg Arg Ser Lys Ile Ile Ile Ala Thr Glu Lys Gly Leu
          105                      110                      115

gaa att cac gac gaa gcc acc aaa cgc ctc ctc atc gcc gag ggt gaa 499
Glu Ile His Asp Glu Ala Thr Lys Arg Leu Leu Ile Ala Glu Gly Glu
          120                      125                      130

tct cta aaa aac ctc acc tcc gac gag caa gaa caa cta agg gaa ctg 547
Ser Leu Lys Asn Leu Thr Ser Asp Glu Gln Glu Gln Leu Arg Glu Leu
          135                      140                      145

ctg ctc aaa atc gcc ttt taagtctctt aaccacgccg gcc 588
Leu Leu Lys Ile Ala Phe
150                      155

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<210> 84  
 <211> 155  
 <212> PRT  
 <213> Corynebacterium glutamicum

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<400> 84
Met Thr Thr Ser Asn Pro Thr Ala Glu Ile Ile Gly Gly Pro Glu Arg
  1              5              10              15

Phe Leu Glu Ala Glu Leu Ser Gln Gln Ile Gln Phe Leu Thr Ala Arg
      20              25              30

Ala Arg Ala Lys Gly Ser Ala Lys Gly Asn Glu Ala Leu Val Asp Leu
      35              40              45

Gly Leu Lys Val Arg Gln Tyr Ser Thr Leu Ser Leu Ala Ala Ser Gly
      50              55              60

Leu Lys Pro Thr Gln Arg Glu Leu Gly Ala Phe Leu Asp Leu Asp Pro
      65              70              75              80

Ser Gln Ile Val Ala Leu Val Asp Phe Leu Glu Lys Arg Gly Leu Val
      85              90              95

Ala Arg Glu Val Asp Pro Arg Asp Arg Arg Ser Lys Ile Ile Ile Ala
      100              105              110

Thr Glu Lys Gly Leu Glu Ile His Asp Glu Ala Thr Lys Arg Leu Leu
      115              120              125

Ile Ala Glu Gly Glu Ser Leu Lys Asn Leu Thr Ser Asp Glu Gln Glu
      130              135              140

Gln Leu Arg Glu Leu Leu Leu Lys Ile Ala Phe
145              150              155

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<210> 85  
 <211> 717



&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(694)

&lt;223&gt; RXA02667

&lt;400&gt; 85

gcgcagcagg gtgaagtatt aaataggctcg cttgcatgga caatgcgggc gccaccggct 60

ggttctagca aaaatggaac cgccattaga aggagtggga atg gaa ttc aag gtc 115  
 Met Glu Phe Lys Val  
 1 5

gga gat acc gtc gtt tac ccg cac cac gga gct gca att att tca gcc 163  
 Gly Asp Thr Val Val Tyr Pro His His Gly Ala Ala Ile Ile Ser Ala  
 10 15 20

ctg gag cag cgt gaa atg aat ggt gag acg gtg gac tac ctg gtt ctc 211  
 Leu Glu Gln Arg Glu Met Asn Gly Glu Thr Val Asp Tyr Leu Val Leu  
 25 30 35

cag atc aat cat tcc gat ctc gtc gtt cgc gtt cca gca aag aac gct 259  
 Gln Ile Asn His Ser Asp Leu Val Arg Val Pro Ala Lys Asn Ala  
 40 45 50

gaa ctc gtt ggc gtg cgt gac gtt gtc ggc gag gag ggc ctg cag aag 307  
 Glu Leu Val Gly Val Arg Asp Val Val Gly Glu Glu Gly Leu Gln Lys  
 55 60 65

gtt ttc tct gtt ctt cgt gaa att gac gtc gaa gaa gcc ggc aac tgg 355  
 Val Phe Ser Val Leu Arg Glu Ile Asp Val Glu Glu Ala Gly Asn Trp  
 70 75 80 85

tcc cgc cgt tac aag gct aac cag gag cgt ttg gct tcc ggt gac gtg 403  
 Ser Arg Arg Tyr Lys Ala Asn Gln Glu Arg Leu Ala Ser Gly Asp Val  
 90 95 100

aac aag gtc gct gag gtt gtc cgt gac ctg tgg cgt cgt gat cag gat 451  
 Asn Lys Val Ala Glu Val Val Arg Asp Leu Trp Arg Arg Asp Gln Asp  
 105 110 115

cgt ggc ctt tcc gct ggt gag aag cgc atg ctc tcc aag gcg cgt cag 499  
 Arg Gly Leu Ser Ala Gly Glu Lys Arg Met Leu Ser Lys Ala Arg Gln  
 120 125 130

gtt ctt gtt ggt gag ctc gcg ctc gcc gaa acc gtg gac gat gag aag 547  
 Val Leu Val Gly Glu Leu Ala Leu Ala Glu Thr Val Asp Asp Glu Lys  
 135 140 145

gcg gat gct ttc ctc agc cag gtc gat gag acc att gct cgc cac cgc 595  
 Ala Asp Ala Phe Leu Ser Gln Val Asp Glu Thr Ile Ala Arg His Arg  
 150 155 160 165

gct gac ctg ctc ggc gac gag gaa gag aag aag gac gca ttc gac gac 643  
 Ala Asp Leu Leu Gly Asp Glu Glu Glu Lys Lys Asp Ala Phe Asp Asp  
 170 175 180

ttc gac gat tcc gac gtg gat ctt gac gat ctg agc ttc gac gac gaa 691  
 Phe Asp Asp Ser Asp Val Asp Leu Asp Asp Leu Ser Phe Asp Asp Glu

185

190

195

gat tagacgccca tgtcgtctac acg  
Asp

717

&lt;210&gt; 86

&lt;211&gt; 198

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 86

Met Glu Phe Lys Val Gly Asp Thr Val Val Tyr Pro His His Gly Ala  
1 5 10 15

Ala Ile Ile Ser Ala Leu Glu Gln Arg Glu Met Asn Gly Glu Thr Val  
20 25 30

Asp Tyr Leu Val Leu Gln Ile Asn His Ser Asp Leu Val Val Arg Val  
35 40 45

Pro Ala Lys Asn Ala Glu Leu Val Gly Val Arg Asp Val Val Gly Glu  
50 55 60

Glu Gly Leu Gln Lys Val Phe Ser Val Leu Arg Glu Ile Asp Val Glu  
65 70 75 80

Glu Ala Gly Asn Trp Ser Arg Arg Tyr Lys Ala Asn Gln Glu Arg Leu  
85 90 95

Ala Ser Gly Asp Val Asn Lys Val Ala Glu Val Val Arg Asp Leu Trp  
100 105 110

Arg Arg Asp Gln Asp Arg Gly Leu Ser Ala Gly Glu Lys Arg Met Leu  
115 120 125

Ser Lys Ala Arg Gln Val Leu Val Gly Glu Leu Ala Leu Ala Glu Thr  
130 135 140

Val Asp Asp Glu Lys Ala Asp Ala Phe Leu Ser Gln Val Asp Glu Thr  
145 150 155 160

Ile Ala Arg His Arg Ala Asp Leu Leu Gly Asp Glu Glu Glu Lys Lys  
165 170 175

Asp Ala Phe Asp Asp Phe Asp Asp Ser Asp Val Asp Leu Asp Asp Leu  
180 185 190

Ser Phe Asp Asp Glu Asp  
195

&lt;210&gt; 87

&lt;211&gt; 479

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(456)

&lt;223&gt; RXA00348

&lt;400&gt; 87

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acc cgc gag cgc ctc gaa aac gcc caa tac cag gta caa cgc gac cga      48
Thr Arg Glu Arg Leu Glu Asn Ala Gln Tyr Gln Val Gln Arg Asp Arg
   1             5             10             15

gtc agg ggt gcc atg gaa gtc ttt atc gaa gcg gga atc gat ccc ggc      96
Val Arg Gly Ala Met Glu Val Phe Ile Glu Ala Gly Ile Asp Pro Gly
             20             25             30

acc gtg ccg atc atg gaa tgc tgg atc aac aac cgc caa cac aac ttc      144
Thr Val Pro Ile Met Glu Cys Trp Ile Asn Asn Arg Gln His Asn Phe
             35             40             45

gaa gtg gcc aaa gaa ctt cta gaa aca cac cca gac ctc acc gca gta      192
Glu Val Ala Lys Glu Leu Leu Glu Thr His Pro Asp Leu Thr Ala Val
             50             55             60

ctc tgt acc gtc gat gca ctg gca ttc ggc gtt ctg gaa tac ctt aaa      240
Leu Cys Thr Val Asp Ala Leu Ala Phe Gly Val Leu Glu Tyr Leu Lys
             65             70             75             80

agc gta ggt aaa tca gcg cct gca gat cta tcc ctc act ggt ttc gat      288
Ser Val Gly Lys Ser Ala Pro Ala Asp Leu Ser Leu Thr Gly Phe Asp
             85             90             95

ggc acc cac atg gca ctc gca cgg gat ctc acc acc gtc atc caa ccc      336
Gly Thr His Met Ala Leu Ala Arg Asp Leu Thr Thr Val Ile Gln Pro
             100             105             110

aac aaa ctc aaa ggg ttc aaa gcc ggc gaa aca ctg ttg aaa atg att      384
Asn Lys Leu Lys Gly Phe Lys Ala Gly Glu Thr Leu Leu Lys Met Ile
             115             120             125

gac aaa gaa tac gtg gaa cca gaa gtg gaa ttg gaa act tcc ttc cac      432
Asp Lys Glu Tyr Val Glu Pro Glu Val Glu Leu Glu Thr Ser Phe His
             130             135             140

cca ggt tcc acg gtt gcg cca atc taggcttgtg gcacttttcg tgc      479
Pro Gly Ser Thr Val Ala Pro Ile
             145             150

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&lt;210&gt; 88

&lt;211&gt; 152

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 88

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Thr Arg Glu Arg Leu Glu Asn Ala Gln Tyr Gln Val Gln Arg Asp Arg
   1             5             10             15

Val Arg Gly Ala Met Glu Val Phe Ile Glu Ala Gly Ile Asp Pro Gly
             20             25             30

Thr Val Pro Ile Met Glu Cys Trp Ile Asn Asn Arg Gln His Asn Phe
             35             40             45

Glu Val Ala Lys Glu Leu Leu Glu Thr His Pro Asp Leu Thr Ala Val
             50             55             60

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Leu Cys Thr Val Asp Ala Leu Ala Phe Gly Val Leu Glu Tyr Leu Lys  
 65 70 75 80  
 Ser Val Gly Lys Ser Ala Pro Ala Asp Leu Ser Leu Thr Gly Phe Asp  
 85 90 95  
 Gly Thr His Met Ala Leu Ala Arg Asp Leu Thr Thr Val Ile Gln Pro  
 100 105 110  
 Asn Lys Leu Lys Gly Phe Lys Ala Gly Glu Thr Leu Leu Lys Met Ile  
 115 120 125  
 Asp Lys Glu Tyr Val Glu Pro Glu Val Glu Leu Glu Thr Ser Phe His  
 130 135 140  
 Pro Gly Ser Thr Val Ala Pro Ile  
 145 150

<210> 89  
 <211> 567  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(544)  
 <223> RXA01500

<400> 89  
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 tgtttcgcga agtcccattg ttggagtttag gcttataccc atg gct acg cat cca 115  
 Met Ala Thr His Pro  
 1 5  
 gat att ccc aca gag ttg ctt gaa tct ccg agc tat caa ctt gaa cga 163  
 Asp Ile Pro Thr Glu Leu Leu Glu Ser Pro Ser Tyr Gln Leu Glu Arg  
 10 15 20  
 ctt cga cga cgc act cgt gac cat gtt gag gcc gaa ttg gcc aag cat 211  
 Leu Arg Arg Arg Thr Arg Asp His Val Glu Ala Glu Leu Ala Lys His  
 25 30 35  
 gag acc acg atg agg gaa ttc tgg acg ctt aca tgt ctg gtt cat tcc 259  
 Glu Thr Thr Met Arg Glu Phe Trp Thr Leu Thr Cys Leu Val His Ser  
 40 45 50  
 gac gct gca agc cag tca gtt ctg tgt gag ctg ctg gcc att gat gca 307  
 Asp Ala Ala Ser Gln Ser Val Leu Cys Glu Leu Leu Ala Ile Asp Ala  
 55 60 65  
 tcg gat atg gtc aga ctc gtt gac tca ctt gag gta cgc ggc tgg gcg 355  
 Ser Asp Met Val Arg Leu Val Asp Ser Leu Glu Val Arg Gly Trp Ala  
 70 75 80 85  
 aaa agg gaa cgt gat ccc aaa gac cgt cgt cgc caa att gtt gcg tca 403  
 Lys Arg Glu Arg Asp Pro Lys Asp Arg Arg Arg Gln Ile Val Ala Ser  
 90 95 100

acg aag aag gga aaa aac gcc cag gcg gat ctg cac aaa gtt gtg ctt 451  
 Thr Lys Lys Gly Lys Asn Ala Gln Ala Asp Leu His Lys Val Val Leu  
 105 110 115  
 gag gca gag gat gct gcg ttg gat gag tct acg tcc aag cag ttg aag 499  
 Glu Ala Glu Asp Ala Ala Leu Asp Glu Ser Thr Ser Lys Gln Leu Lys  
 120 125 130  
 cac ctt cgt aaa ttg gcc gca gca att atc tcc acc gaa gag gac 544  
 His Leu Arg Lys Leu Ala Ala Ala Ile Ile Ser Thr Glu Glu Asp  
 135 140 145  
 taaatataac gtggcattga gca 567

<210> 90  
 <211> 148  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 90  
 Met Ala Thr His Pro Asp Ile Pro Thr Glu Leu Leu Glu Ser Pro Ser  
 1 5 10 15  
 Tyr Gln Leu Glu Arg Leu Arg Arg Arg Thr Arg Asp His Val Glu Ala  
 20 25 30  
 Glu Leu Ala Lys His Glu Thr Thr Met Arg Glu Phe Trp Thr Leu Thr  
 35 40 45  
 Cys Leu Val His Ser Asp Ala Ala Ser Gln Ser Val Leu Cys Glu Leu  
 50 55 60  
 Leu Ala Ile Asp Ala Ser Asp Met Val Arg Leu Val Asp Ser Leu Glu  
 65 70 75 80  
 Val Arg Gly Trp Ala Lys Arg Glu Arg Asp Pro Lys Asp Arg Arg Arg  
 85 90 95  
 Gln Ile Val Ala Ser Thr Lys Lys Gly Lys Asn Ala Gln Ala Asp Leu  
 100 105 110  
 His Lys Val Val Leu Glu Ala Glu Asp Ala Ala Leu Asp Glu Ser Thr  
 115 120 125  
 Ser Lys Gln Leu Lys His Leu Arg Lys Leu Ala Ala Ala Ile Ile Ser  
 130 135 140  
 Thr Glu Glu Asp  
 145

<210> 91  
 <211> 272  
 <212> DNA  
 <213> Corynebacterium glutamicum  
 <220>  
 <221> CDS  
 <222> (37)..(249)  
 <223> RXA01125

<400> 93  
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cggactcaaa	caagatgtgt	gcagatgaag	gagaaaagca	gtg	gaa	ggt	gta	cag		115
				Val	Glu	Gly	Val	Gln		
				1				5		
gag atc ctg tcg cgc gcc gga att ttt caa ggc gtt gac cca acg gca										163
Glu Ile Leu Ser Arg Ala Gly Ile Phe Gln Gly Val Asp Pro Thr Ala										
	10			15				20		
gtc aat aac ctc atc cag gat atg gag acc gtt cgc ttc cca cgc gga										211
Val Asn Asn Leu Ile Gln Asp Met Glu Thr Val Arg Phe Pro Arg Gly										
	25			30				35		
gca acc atc ttc gac gag ggc gag cca ggt gac cgc ctt tac atc atc										259
Ala Thr Ile Phe Asp Glu Gly Glu Pro Gly Asp Arg Leu Tyr Ile Ile										
	40			45				50		
acc tcc ggc aaa gtg aag ctt gcg cgc cac gca ccg gac ggc cgc gaa										307
Thr Ser Gly Lys Val Lys Leu Ala Arg His Ala Pro Asp Gly Arg Glu										
	55			60				65		
aac ctg ctg acc atc atg ggt cct tcc gac atg ttc ggt gag ctc tcc										355
Asn Leu Leu Thr Ile Met Gly Pro Ser Asp Met Phe Gly Glu Leu Ser										
	70			75				80		85
atc ttc gac cca ggc cca cgc acc tcc tct gca gtg tgt gtc acc gaa										403
Ile Phe Asp Pro Gly Pro Arg Thr Ser Ser Ala Val Cys Val Thr Glu										
	90			95				100		
gtt cat gca gca acc atg aac tct gac atg ctg cgc aac tgg gta gct										451
Val His Ala Ala Thr Met Asn Ser Asp Met Leu Arg Asn Trp Val Ala										
	105			110				115		
gac cac cca gct atc gct gag cag ctc ctg cgc gtt ctg gct cgt cgt										499
Asp His Pro Ala Ile Ala Glu Gln Leu Leu Arg Val Leu Ala Arg Arg										
	120			125				130		
ctg cgt cgc acc aac gct tcc ctg gct gac ctc atc ttc acc gac gtc										547
Leu Arg Arg Thr Asn Ala Ser Leu Ala Asp Leu Ile Phe Thr Asp Val										
	135			140				145		
cca ggc cgc gtt gct aag acc ctt ctg cag ctg gct aac cgc ttc ggc										595
Pro Gly Arg Val Ala Lys Thr Leu Leu Gln Leu Ala Asn Arg Phe Gly										
	150			155				160		165
acc caa gaa gct ggc gcg ctg cgc gtg aac cac gac ctc act cag gaa										643
Thr Gln Glu Ala Gly Ala Leu Arg Val Asn His Asp Leu Thr Gln Glu										
	170			175				180		
gaa atc gca cag ctc gtc ggt gct tcc cgt gaa act gtg aat aag gct										691
Glu Ile Ala Gln Leu Val Gly Ala Ser Arg Glu Thr Val Asn Lys Ala										
	185			190				195		
ctt gca acg ttc gca cac cgt ggc tgg atc cgc ctc gag ggc aag tcc										739
Leu Ala Thr Phe Ala His Arg Gly Trp Ile Arg Leu Glu Gly Lys Ser										
	200			205				210		
gtc ctc att gtg gac acc gag cat ttg gca cgt cgc gct cga										781
Val Leu Ile Val Asp Thr Glu His Leu Ala Arg Arg Ala Arg										
	215			220				225		

taatcaccaa agcgctaaaa agc

804

<210> 94  
 <211> 227  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 94  
 Val Glu Gly Val Gln Glu Ile Leu Ser Arg Ala Gly Ile Phe Gln Gly  
     1                    5                    10                    15  
 Val Asp Pro Thr Ala Val Asn Asn Leu Ile Gln Asp Met Glu Thr Val  
           20                    25                    30  
 Arg Phe Pro Arg Gly Ala Thr Ile Phe Asp Glu Gly Glu Pro Gly Asp  
           35                    40                    45  
 Arg Leu Tyr Ile Ile Thr Ser Gly Lys Val Lys Leu Ala Arg His Ala  
           50                    55                    60  
 Pro Asp Gly Arg Glu Asn Leu Leu Thr Ile Met Gly Pro Ser Asp Met  
           65                    70                    75                    80  
 Phe Gly Glu Leu Ser Ile Phe Asp Pro Gly Pro Arg Thr Ser Ser Ala  
                     85                    90                    95  
 Val Cys Val Thr Glu Val His Ala Ala Thr Met Asn Ser Asp Met Leu  
                     100                    105                    110  
 Arg Asn Trp Val Ala Asp His Pro Ala Ile Ala Glu Gln Leu Leu Arg  
           115                    120                    125  
 Val Leu Ala Arg Arg Leu Arg Arg Thr Asn Ala Ser Leu Ala Asp Leu  
           130                    135                    140  
 Ile Phe Thr Asp Val Pro Gly Arg Val Ala Lys Thr Leu Leu Gln Leu  
           145                    150                    155                    160  
 Ala Asn Arg Phe Gly Thr Gln Glu Ala Gly Ala Leu Arg Val Asn His  
                     165                    170                    175  
 Asp Leu Thr Gln Glu Glu Ile Ala Gln Leu Val Gly Ala Ser Arg Glu  
           180                    185                    190  
 Thr Val Asn Lys Ala Leu Ala Thr Phe Ala His Arg Gly Trp Ile Arg  
           195                    200                    205  
 Leu Glu Gly Lys Ser Val Leu Ile Val Asp Thr Glu His Leu Ala Arg  
           210                    215                    220  
 Arg Ala Arg  
 225

<210> 95  
 <211> 804  
 <212> DNA  
 <213> Corynebacterium glutamicum  
 <220>



&lt;221&gt; CDS

&lt;222&gt; (101)..(781)

&lt;223&gt; FRXA00822

&lt;400&gt; 95

cagttagggtg tcatccggat tttatctcaa accctaacac cccaggtggt gccactcatc 60

cggactcaaa caagatgtgt gcagatgaag gagaaaagca gtg gaa ggt gta cag 115  
 Val Glu Gly Val Gln  
 1 5

gag atc ctg tcg cgc gcc gga att ttt caa ggc gtt gac cca acg gca 163  
 Glu Ile Leu Ser Arg Ala Gly Ile Phe Gln Gly Val Asp Pro Thr Ala  
 10 15 20

gtc aat aac ctg atc cag gat atg gag acc gtt cgc ttc cca cgc gga 211  
 Val Asn Asn Leu Ile Gln Asp Met Glu Thr Val Arg Phe Pro Arg Gly  
 25 30 35

gca acc atc ttc gac gag ggc gag cca ggt gac cgc ctt tac atc atc 259  
 Ala Thr Ile Phe Asp Glu Gly Glu Pro Gly Asp Arg Leu Tyr Ile Ile  
 40 45 50

acc tcc ggc aaa gtg aag ctt gcg cgc cac gca ccg gac ggc cgc gaa 307  
 Thr Ser Gly Lys Val Lys Leu Ala Arg His Ala Pro Asp Gly Arg Glu  
 55 60 65

aac ctg ctg acc atc atg ggt cct tcc gac atg ttc ggt gag ctg tcc 355  
 Asn Leu Leu Thr Ile Met Gly Pro Ser Asp Met Phe Gly Glu Leu Ser  
 70 75 80 85

atc ttc gac cca ggc cca cgc acc tcc tct gca gtg tgt gtc acc gaa 403  
 Ile Phe Asp Pro Gly Pro Arg Thr Ser Ser Ala Val Cys Val Thr Glu  
 90 95 100

gtt cat gca gca acc atg aac tct gac atg ctg cgc aac tgg gta gct 451  
 Val His Ala Ala Thr Met Asn Ser Asp Met Leu Arg Asn Trp Val Ala  
 105 110 115

gac cac cca gct atc gct gag cag ctg ctg cgc gtt ctg gct cgt cgt 499  
 Asp His Pro Ala Ile Ala Glu Gln Leu Leu Arg Val Leu Ala Arg Arg  
 120 125 130

ctg cgt cgc acc aac gct tcc ctg gct gac ctg atc ttc acc gac gtc 547  
 Leu Arg Arg Thr Asn Ala Ser Leu Ala Asp Leu Ile Phe Thr Asp Val  
 135 140 145

cca ggc cgc gtt gct aag acc ctt ctg cag ctg gct aac cgc ttc ggc 595  
 Pro Gly Arg Val Ala Lys Thr Leu Leu Gln Leu Ala Asn Arg Phe Gly  
 150 155 160 165

acc caa gaa gct ggc gcg ctg cgc gtg aac cac gac ctg act cag gaa 643  
 Thr Gln Glu Ala Gly Ala Leu Arg Val Asn His Asp Leu Thr Gln Glu  
 170 175 180

gaa atc gca cag ctg gtc ggt gct tcc cgt gaa act gtg aat aag gct 691  
 Glu Ile Ala Gln Leu Val Gly Ala Ser Arg Glu Thr Val Asn Lys Ala  
 185 190 195

ctt gca acg ttc gca cac cgt ggc tgg atc cgc ctg gag ggc aag tcc 739  
 Leu Ala Thr Phe Ala His Arg Gly Trp Ile Arg Leu Glu Gly Lys Ser

200	205	210	
gtc ctc att gtg gac acc gag cat ttg gca cgt cgc gct cga			781
Val Leu Ile Val Asp Thr Glu His Leu Ala Arg Arg Ala Arg			
215	220	225	

taatcaccaa agcgctaaaa agc	804
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<210> 96  
 <211> 227  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 96	
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Val Asp Pro Thr Ala Val Asn Asn Leu Ile Gln Asp Met Glu Thr Val	
20 25 30	
Arg Phe Pro Arg Gly Ala Thr Ile Phe Asp Glu Gly Glu Pro Gly Asp	
35 40 45	
Arg Leu Tyr Ile Ile Thr Ser Gly Lys Val Lys Leu Ala Arg His Ala	
50 55 60	
Pro Asp Gly Arg Glu Asn Leu Leu Thr Ile Met Gly Pro Ser Asp Met	
65 70 75 80	
Phe Gly Glu Leu Ser Ile Phe Asp Pro Gly Pro Arg Thr Ser Ser Ala	
85 90 95	
Val Cys Val Thr Glu Val His Ala Ala Thr Met Asn Ser Asp Met Leu	
100 105 110	
Arg Asn Trp Val Ala Asp His Pro Ala Ile Ala Glu Gln Leu Leu Arg	
115 120 125	
Val Leu Ala Arg Arg Leu Arg Arg Thr Asn Ala Ser Leu Ala Asp Leu	
130 135 140	
Ile Phe Thr Asp Val Pro Gly Arg Val Ala Lys Thr Leu Leu Gln Leu	
145 150 155 160	
Ala Asn Arg Phe Gly Thr Gln Glu Ala Gly Ala Leu Arg Val Asn His	
165 170 175	
Asp Leu Thr Gln Glu Glu Ile Ala Gln Leu Val Gly Ala Ser Arg Glu	
180 185 190	
Thr Val Asn Lys Ala Leu Ala Thr Phe Ala His Arg Gly Trp Ile Arg	
195 200 205	
Leu Glu Gly Lys Ser Val Leu Ile Val Asp Thr Glu His Leu Ala Arg	
210 215 220	
Arg Ala Arg	
225	

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<400> 98
Met Val Thr Tyr Thr Thr Leu Leu Asp Lys Pro Ile Ser Glu Ser Ala
  1             5             10             15

Pro Arg Lys Ala Pro Glu Pro Leu Leu Arg Glu Ala Leu Gly Ala Ala
      20             25             30

Leu Arg Ser Phe Arg Ala Asp Lys Gly Val Thr Leu Arg Glu Leu Ala
    35             40             45

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Glu Ala Ser Arg Val Ser Pro Gly Tyr Leu Ser Glu Leu Glu Arg Gly  
 50 55 60  
 Arg Lys Glu Val Ser Ser Glu Leu Leu Ala Ser Val Cys His Ala Leu  
 65 70 75 80  
 Gly Ala Ser Val Ala Asp Val Leu Ile Glu Ala Ala Gly Ser Met Ala  
 85 90 95  
 Leu Gln Ala Ala Gln Glu Asp Leu Ala Arg Val  
 100 105

<210> 99  
 <211> 444  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(421)  
 <223> FRXA00849

<400> 99  
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 actgggaaca aattttaggg aaagggagtt gaacctaacg atg gtt act tat aca 115  
 Met Val Thr Tyr Thr  
 1 5  
 acc ctt cta gac aag ccg att tca gaa tct gcc cca cgg aaa gct cca 163  
 Thr Leu Leu Asp Lys Pro Ile Ser Glu Ser Ala Pro Arg Lys Ala Pro  
 10 15 20  
 gag cca ctt ctc cgc gaa gct ctg ggt gca gct ctt cgt tct ttc cgt 211  
 Glu Pro Leu Leu Arg Glu Ala Leu Gly Ala Ala Leu Arg Ser Phe Arg  
 25 30 35  
 gct gac aag ggc gtt act ttg cgt gag ctg gcg gaa gct tca cgt gtg 259  
 Ala Asp Lys Gly Val Thr Leu Arg Glu Leu Ala Glu Ala Ser Arg Val  
 40 45 50  
 tca cct ggt tat ctt tca gaa ttg gaa cgc ggc cgc aaa gag gtg tcc 307  
 Ser Pro Gly Tyr Leu Ser Glu Leu Glu Arg Gly Arg Lys Glu Val Ser  
 55 60 65  
 tct gag ctt ctt gcc tcc gtg tgc cac gct ttg ggg gcc agc gtt gcg 355  
 Ser Glu Leu Leu Ala Ser Val Cys His Ala Leu Gly Ala Ser Val Ala  
 70 75 80 85  
 gat gtg ttg atc gaa gct gca ggt tcc atg gcg ctg caa gca gcg cag 403  
 Asp Val Leu Ile Glu Ala Ala Gly Ser Met Ala Leu Gln Ala Ala Gln  
 90 95 100  
 gaa gac ctc gct cgc gtc taagcgcatt ggtgggcgtc gaa 444  
 Glu Asp Leu Ala Arg Val  
 105

<210> 100  
 <211> 107

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 100

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Met Val Thr Tyr Thr Thr Leu Leu Asp Lys Pro Ile Ser Glu Ser Ala
 1             5             10             15

Pro Arg Lys Ala Pro Glu Pro Leu Leu Arg Glu Ala Leu Gly Ala Ala
          20             25             30

Leu Arg Ser Phe Arg Ala Asp Lys Gly Val Thr Leu Arg Glu Leu Ala
          35             40             45

Glu Ala Ser Arg Val Ser Pro Gly Tyr Leu Ser Glu Leu Glu Arg Gly
          50             55             60

Arg Lys Glu Val Ser Ser Glu Leu Leu Ala Ser Val Cys His Ala Leu
          65             70             75             80

Gly Ala Ser Val Ala Asp Val Leu Ile Glu Ala Ala Gly Ser Met Ala
          85             90             95

Leu Gln Ala Ala Gln Glu Asp Leu Ala Arg Val
          100             105

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&lt;210&gt; 101

&lt;211&gt; 492

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(469)

&lt;223&gt; RXA02698

&lt;400&gt; 101

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catcctgttt tcaaagggtca agaagggtgct ttcattcccgc gcacgcgcag aaatacccta 60

aagattctcc attagagctc gaaccagcta aattaagact gtg agt tcc aac aat 115
          Val Ser Ser Asn Asn
          1             5

gaa tct tcc ttc gcc ctg ccc gac aat gaa cca ttg ctg acc ctt ccg 163
Glu Ser Ser Phe Ala Leu Pro Asp Asn Glu Pro Leu Leu Thr Leu Pro
          10             15             20

gag aca gcc gag cgc ctc ggc gtt gtt gtc acc aag gtg atg gat ctg 211
Glu Thr Ala Glu Arg Leu Gly Val Val Val Thr Lys Val Met Asp Leu
          25             30             35

gtc aat gaa cac aaa ttg atc gtg gtc cgg cgc gac ggt att cgc tac 259
Val Asn Glu His Lys Leu Ile Val Val Arg Arg Asp Gly Ile Arg Tyr
          40             45             50

att cca gaa gct ttc ctg agc acc aag aag gaa aac acc aac cgt ttc 307
Ile Pro Glu Ala Phe Leu Ser Thr Lys Lys Glu Asn Thr Asn Arg Phe
          55             60             65

atc cct gga gtt att gcc ttg ctt gcc gac ggt ggc ttc agc gac gag 355
Ile Pro Gly Val Ile Ala Leu Leu Ala Asp Gly Gly Phe Ser Asp Glu

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<400> 103
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gaatatcggg tcgategctt ttaaacactc aggaggatcc ttg ccg gcc aaa atc    115
                               Leu Pro Ala Lys Ile

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	1	5	
acg gac act cgt ccc acc cca gaa tcc ctt cac gct gtt gaa gag gaa			163
Thr Asp Thr Arg Pro Thr Pro Glu Ser Leu His Ala Val Glu Glu Glu			
	10	15	20
acc gca gcc ggt gcc cgc agg att gtt gcc acc tat tct aag gac ttc			211
Thr Ala Ala Gly Ala Arg Arg Ile Val Ala Thr Tyr Ser Lys Asp Phe			
	25	30	35
ttc gac ggc gtc act ttg atg tgc atg ctc ggc gtt gaa cct cag ggc			259
Phe Asp Gly Val Thr Leu Met Cys Met Leu Gly Val Glu Pro Gln Gly			
	40	45	50
ctg cgt tac acc aag gtc gct tct gaa cac gag gaa gct cag cca aag			307
Leu Arg Tyr Thr Lys Val Ala Ser Glu His Glu Ala Gln Pro Lys			
	55	60	65
aag gct aca aag cgg act cgt aag gca cca gct aag aag gct gct gct			355
Lys Ala Thr Lys Arg Thr Arg Lys Ala Pro Ala Lys Lys Ala Ala Ala			
	70	75	80
aag aaa acg acc aag aag acc act aag aaa act act aaa aag acc acc			403
Lys Lys Thr Thr Lys Lys Thr Thr Lys Lys Thr Thr Lys Lys Thr Thr			
	90	95	100
gca aag aag acc aca aag aag tct taagccggat cttatatgga tga			450
Ala Lys Lys Thr Thr Lys Lys Ser			
	105		

&lt;210&gt; 104

&lt;211&gt; 109

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 104

Leu Pro Ala Lys Ile Thr Asp Thr Arg Pro Thr Pro Glu Ser Leu His			
1	5	10	15
Ala Val Glu Glu Glu Thr Ala Ala Gly Ala Arg Arg Ile Val Ala Thr			
	20	25	30
Tyr Ser Lys Asp Phe Phe Asp Gly Val Thr Leu Met Cys Met Leu Gly			
	35	40	45
Val Glu Pro Gln Gly Leu Arg Tyr Thr Lys Val Ala Ser Glu His Glu			
	50	55	60
Glu Ala Gln Pro Lys Lys Ala Thr Lys Arg Thr Arg Lys Ala Pro Ala			
	65	70	75
Lys Lys Ala Ala Ala Lys Lys Thr Thr Lys Lys Thr Thr Lys Lys Thr			
	85	90	95
Thr Lys Lys Thr Thr Ala Lys Lys Thr Thr Lys Lys Ser			
	100	105	

&lt;210&gt; 105

&lt;211&gt; 495

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(495)

&lt;223&gt; RXA02830

&lt;400&gt; 105

ctg gaa gac agc ctt ggc gtg tcg ctg ttt gaa cgg gcc ggg cgc ggg	48
Leu Glu Asp Ser Leu Gly Val Ser Leu Phe Glu Arg Ala Gly Arg Gly	
1 5 10 15	

ctg gcg ctg aca ggg gcg ggc gat cag ctt ttg tcg cag gcg cgc cgc	96
Leu Ala Leu Thr Gly Ala Gly Asp Gln Leu Leu Ser Gln Ala Arg Arg	
20 25 30	

ctg atc gcc ctg aac gac gag gta tac gcc cgc ttg aac gcc ggt gcc	144
Leu Ile Ala Leu Asn Asp Glu Val Tyr Ala Arg Leu Asn Ala Gly Ala	
35 40 45	

tac gag ggc gag gtg acg ctg ggc gtg cct caa gac gtg atc tac ccc	192
Tyr Glu Gly Glu Val Thr Leu Gly Val Pro Gln Asp Val Ile Tyr Pro	
50 55 60	

gtc atc ccg cgc gtc ttg cag caa ttc gcc cgc gat ttt ccc cgc gtg	240
Val Ile Pro Arg Val Leu Gln Gln Phe Ala Arg Asp Phe Pro Arg Val	
65 70 75 80	

caa att cac ctg atc tcg aac ttc acg ctg atg ctg aaa gaa cag ttc	288
Gln Ile His Leu Ile Ser Asn Phe Thr Leu Met Leu Lys Glu Gln Phe	
85 90 95	

cgc cgc ggc gaa atc gac gtg atg ctg acg acc gag gac gag ctg ggc	336
Arg Arg Gly Glu Ile Asp Val Met Leu Thr Thr Glu Asp Glu Leu Gly	
100 105 110	

gag ggc ggc gag acg ctg gcc cag cgc gag ctg atc tgg gtc ggc gca	384
Glu Gly Gly Glu Thr Leu Ala Gln Arg Glu Leu Ile Trp Val Gly Ala	
115 120 125	

ccg ggc ggg tcg gcg tgg acc cgc agg ccg ctg ccc ttg gcg ttt gaa	432
Pro Gly Gly Ser Ala Trp Thr Arg Arg Pro Leu Pro Leu Ala Phe Glu	
130 135 140	

cgc gcc tgc att ttc cgg tct ttc ttg cag cgc cgc ttg gat gcc aac	480
Arg Ala Cys Ile Phe Arg Ser Phe Leu Gln Arg Arg Leu Asp Ala Asn	
145 150 155 160	

agc atc tat tgg caa	495
Ser Ile Tyr Trp Gln	
165	

&lt;210&gt; 106

&lt;211&gt; 165

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 106

Leu Glu Asp Ser Leu Gly Val Ser Leu Phe Glu Arg Ala Gly Arg Gly
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1	5	10	15
Leu Ala Leu Thr Gly Ala Gly Asp Gln Leu Leu Ser Gln Ala Arg Arg	20	25	30
Leu Ile Ala Leu Asn Asp Glu Val Tyr Ala Arg Leu Asn Ala Gly Ala	35	40	45
Tyr Glu Gly Glu Val Thr Leu Gly Val Pro Gln Asp Val Ile Tyr Pro	50	55	60
Val Ile Pro Arg Val Leu Gln Gln Phe Ala Arg Asp Phe Pro Arg Val	65	70	75
Gln Ile His Leu Ile Ser Asn Phe Thr Leu Met Leu Lys Glu Gln Phe	85	90	95
Arg Arg Gly Glu Ile Asp Val Met Leu Thr Thr Glu Asp Glu Leu Gly	100	105	110
Glu Gly Gly Glu Thr Leu Ala Gln Arg Glu Leu Ile Trp Val Gly Ala	115	120	125
Pro Gly Gly Ser Ala Trp Thr Arg Arg Pro Leu Pro Leu Ala Phe Glu	130	135	140
Arg Ala Cys Ile Phe Arg Ser Phe Leu Gln Arg Arg Leu Asp Ala Asn	145	150	155
Ser Ile Tyr Trp Gln	165		

<210> 107  
 <211> 459  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(436)  
 <223> RXA00947

<400> 107  
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 taaattcaat actgttttac gagatcattt ggagggtgtc atg gcc cgc aaa ttg 115  
 Met Ala Arg Lys Leu  
 1 5  
 gaa cat cca tct ttg gcc gag atg aat tta aat gcc atc atg ttt gcg 163  
 Glu His Pro Ser Leu Ala Glu Met Asn Leu Asn Ala Ile Met Phe Ala  
 10 15 20  
 ctg tcg gat cct att agg cga caa atc ctg tcg cag ctg tcg tgc gga 211  
 Leu Ser Asp Pro Ile Arg Arg Gln Ile Leu Ser Gln Leu Ser Cys Gly  
 25 30 35  
 cat aat gat cag gca tgt gtt gcc ttc gag ctt cca gta tct aaa tcc 259  
 His Asn Asp Gln Ala Cys Val Ala Phe Glu Leu Pro Val Ser Lys Ser  
 40 45 50

acc tca acg cac cac ttc cgc gta ctc cgt gag gcg ggt ctg att act 307  
 Thr Ser Thr His His Phe Arg Val Leu Arg Glu Ala Gly Leu Ile Thr  
           55                                60                                65

cag cgc tat gaa gga act gcc att cta agt gcg ctg cgc agc gaa gat 355  
 Gln Arg Tyr Glu Gly Thr Ala Ile Leu Ser Ala Leu Arg Ser Glu Asp  
           70                                75                                80                                85

atg gaa gcg cgt ttt ccg gga ctg ctg act tct gtc atg cga gcg gaa 403  
 Met Glu Ala Arg Phe Pro Gly Leu Leu Thr Ser Val Met Arg Ala Glu  
                                 90                                95                                100

gtg gaa gag cgc aac gca gct gac ttg ccc gtt taggacgggtt agcaagtatt 456  
 Val Glu Glu Arg Asn Ala Ala Asp Leu Pro Val  
                                 105                                110

atc 459

<210> 108  
 <211> 112  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 108  
 Met Ala Arg Lys Leu Glu His Pro Ser Leu Ala Glu Met Asn Leu Asn  
           1                                5                                10                                15

Ala Ile Met Phe Ala Leu Ser Asp Pro Ile Arg Arg Gln Ile Leu Ser  
                                 20                                25                                30

Gln Leu Ser Cys Gly His Asn Asp Gln Ala Cys Val Ala Phe Glu Leu  
                                 35                                40                                45

Pro Val Ser Lys Ser Thr Ser Thr His His Phe Arg Val Leu Arg Glu  
                                 50                                55                                60

Ala Gly Leu Ile Thr Gln Arg Tyr Glu Gly Thr Ala Ile Leu Ser Ala  
                                 65                                70                                75                                80

Leu Arg Ser Glu Asp Met Glu Ala Arg Phe Pro Gly Leu Leu Thr Ser  
                                 85                                90                                95

Val Met Arg Ala Glu Val Glu Glu Arg Asn Ala Ala Asp Leu Pro Val  
                                 100                                105                                110

<210> 109  
 <211> 828  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(805)  
 <223> RXA01836

&lt;400&gt; 109

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cttcaccacg tctcattggg tgaaatgcta aattcaagggt atg gga cag caa gaa 115
Met Gly Gln Gln Glu
1 5

att atc gag gac tcc acc gag agc ggt att aag gtt tta gac cgc act 163
Ile Ile Glu Asp Ser Thr Glu Ser Gly Ile Lys Val Leu Asp Arg Thr
10 15 20

gta tta atc ctc aat gtc atc gca gaa cag cct cga tcg ttg gca gag 211
Val Leu Ile Leu Asn Val Ile Ala Glu Gln Pro Arg Ser Leu Ala Glu
25 30 35

ctc gca gct gcc acc gat ctg ccc agg gct aca gcc cac cgc ctc gcc 259
Leu Ala Ala Ala Thr Asp Leu Pro Arg Ala Thr Ala His Arg Leu Ala
40 45 50

tca gcg ctt gag gta cac ggc atg ttg gca cgc tcc cgc gat aat aga 307
Ser Ala Leu Glu Val His Gly Met Leu Ala Arg Ser Arg Asp Asn Arg
55 60 65

tgg acc atc ggc gca cgg ctt gcc tca ttg ggt gca cgc ggc gct gac 355
Trp Thr Ile Gly Ala Arg Leu Ala Ser Leu Gly Ala Arg Gly Ala Asp
70 75 80 85

acc ctc atc gat acg gcc gta cca att atg gcc gac ctt atg gag cgc 403
Thr Leu Ile Asp Thr Ala Val Pro Ile Met Ala Asp Leu Met Glu Arg
90 95 100

acc ggc gaa tcc gtt cag ctt tat cgc ctc acc ggc acc acc cgc acg 451
Thr Gly Glu Ser Val Gln Leu Tyr Arg Leu Thr Gly Thr Thr Arg Thr
105 110 115

tgt gtg gcc agc caa gag ccc agc tcc ggg cta aaa aac gtg gtt ccc 499
Cys Val Ala Ser Gln Glu Pro Ser Ser Gly Leu Lys Asn Val Val Pro
120 125 130

gtg ggc act cgc atg cct tta aat gca ggg tca gca gcg cgc gtt ttt 547
Val Gly Thr Arg Met Pro Leu Asn Ala Gly Ser Ala Ala Arg Val Phe
135 140 145

gcc gcc tac ctc ccc atc ccc tct gcc agc gtc ttt tcc cgc gag gag 595
Ala Ala Tyr Leu Pro Ile Pro Ser Ala Ser Val Phe Ser Arg Glu Glu
150 155 160 165

ctt gac cag gtg cgc gcc agc ggc tta gcg gag tcc gtg ggc gag cgt 643
Leu Asp Gln Val Arg Ala Ser Gly Leu Ala Glu Ser Val Gly Glu Arg
170 175 180

gag ctc ggc ctt gct agc ctc tcc tcc cct gtt ttt gat tcc aac gga 691
Glu Leu Gly Leu Ala Ser Leu Ser Ser Pro Val Phe Asp Ser Asn Gly
185 190 195

tcc atg atc gcg gca ctg tcc atc tcc ggc gtg gcc gag cgc ctc aag 739
Ser Met Ile Ala Ala Leu Ser Ile Ser Gly Val Ala Glu Arg Leu Lys
200 205 210

ccc cac ccc gcc gcc atg tgg ggc acc gag ctt atc gac gcc gcc gag 787
Pro His Pro Ala Ala Met Trp Gly Thr Glu Leu Ile Asp Ala Ala Glu

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215 220 225 828  
 cgc cta ggc gct ttg ctt taagagcttt tcgacgcaca acc  
 Arg Leu Gly Ala Leu Leu  
 230 235

<210> 110  
 <211> 235  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 110  
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 Val Leu Asp Arg Thr Val Leu Ile Leu Asn Val Ile Ala Glu Gln Pro  
 20 25 30  
 Arg Ser Leu Ala Glu Leu Ala Ala Ala Thr Asp Leu Pro Arg Ala Thr  
 35 40 45  
 Ala His Arg Leu Ala Ser Ala Leu Glu Val His Gly Met Leu Ala Arg  
 50 55 60  
 Ser Arg Asp Asn Arg Trp Thr Ile Gly Ala Arg Leu Ala Ser Leu Gly  
 65 70 75 80  
 Ala Arg Gly Ala Asp Thr Leu Ile Asp Thr Ala Val Pro Ile Met Ala  
 85 90 95  
 Asp Leu Met Glu Arg Thr Gly Glu Ser Val Gln Leu Tyr Arg Leu Thr  
 100 105 110  
 Gly Thr Thr Arg Thr Cys Val Ala Ser Gln Glu Pro Ser Ser Gly Leu  
 115 120 125  
 Lys Asn Val Val Pro Val Gly Thr Arg Met Pro Leu Asn Ala Gly Ser  
 130 135 140  
 Ala Ala Arg Val Phe Ala Ala Tyr Leu Pro Ile Pro Ser Ala Ser Val  
 145 150 155 160  
 Phe Ser Arg Glu Glu Leu Asp Gln Val Arg Ala Ser Gly Leu Ala Glu  
 165 170 175  
 Ser Val Gly Glu Arg Glu Leu Gly Leu Ala Ser Leu Ser Ser Pro Val  
 180 185 190  
 Phe Asp Ser Asn Gly Ser Met Ile Ala Ala Leu Ser Ile Ser Gly Val  
 195 200 205  
 Ala Glu Arg Leu Lys Pro His Pro Ala Ala Met Trp Gly Thr Glu Leu  
 210 215 220  
 Ile Asp Ala Ala Glu Arg Leu Gly Ala Leu Leu  
 225 230 235

<210> 111  
 <211> 777

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(754)

&lt;223&gt; RXA00292

&lt;400&gt; 111

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gcgctgtatt tggagtgaaa ctaccgggag taatggagta atg gat caa aca ctt 115  
 Met Asp Gln Thr Leu  
 1 5

aaa gtt tta gta att gat gat gat ttc cgc gtc gcc ggc att cac gcc 163  
 Lys Val Leu Val Ile Asp Asp Asp Phe Arg Val Ala Gly Ile His Ala  
 10 15 20

tcc atc gtt gat gcg tcc cct gga ttt tgc gtg gtc ggt acc gcg cgt 211  
 Ser Ile Val Asp Ala Ser Pro Gly Phe Ser Val Val Gly Thr Ala Arg  
 25 30 35

acc ctc gca gag gca aaa acc ctg atc gcc aca ttt tcc ccg gat ctc 259  
 Thr Leu Ala Glu Ala Lys Thr Leu Ile Ala Thr Phe Ser Pro Asp Leu  
 40 45 50

cta ctt gtt gat gtc tac ctc ccc gac ggc gat ggc att gac ctc gtg 307  
 Leu Leu Val Asp Val Tyr Leu Pro Asp Gly Asp Gly Ile Asp Leu Val  
 55 60 65

ggc acc tcc aat att gat gcg ttt gtg ctc agc gca gcc gat gac atc 355  
 Gly Thr Ser Asn Ile Asp Ala Phe Val Leu Ser Ala Ala Asp Asp Ile  
 70 75 80 85

aaa aca gtt cga cgc gcc atg cgt gcc ggg gca ctc gga tat ctg ctc 403  
 Lys Thr Val Arg Arg Ala Met Arg Ala Gly Ala Leu Gly Tyr Leu Leu  
 90 95 100

aaa cca ttt ccc caa aaa cgt ctc gtg gaa cgc ctt gac cgt tac gtc 451  
 Lys Pro Phe Pro Gln Lys Arg Leu Val Glu Arg Leu Asp Arg Tyr Val  
 105 110 115

cgc tac cgc cat gtc tta tcc ggc acc caa gga ctt tcc caa gac aaa 499  
 Arg Tyr Arg His Val Leu Ser Gly Thr Gln Gly Leu Ser Gln Asp Lys  
 120 125 130

att gac cag gca acc gca atc ctc aac ggc acc caa gcg ccg gtc acc 547  
 Ile Asp Gln Ala Thr Ala Ile Leu Asn Gly Thr Gln Ala Pro Val Thr  
 135 140 145

gtc tct aga tcc gcc aca gag caa tta ctt ctc gac gcc ctg gaa ggc 595  
 Val Ser Arg Ser Ala Thr Glu Gln Leu Leu Leu Asp Ala Leu Glu Gly  
 150 155 160 165

caa gaa ctc tcc gca aca gaa gct tcc gaa gct gcc gga gtt tca cgt 643  
 Gln Glu Leu Ser Ala Thr Glu Ala Ser Glu Ala Ala Gly Val Ser Arg  
 170 175 180

gcc aca gca cag cgc agg ctg gca gcg atg gct agc caa ggt gtg atc 691  
 Ala Thr Ala Gln Arg Arg Leu Ala Ala Met Ala Ser Gln Gly Val Ile

185 190 195  
 cag gtt cgc ctt cgg tac gga cag tcc ggg cga cca gaa cat cta tat 739  
 Gln Val Arg Leu Arg Tyr Gly Gln Ser Gly Arg Pro Glu His Leu Tyr  
 200 205 210

tca aag cca ctg ctc tagtaacctt tgtggatgac cac 777  
 Ser Lys Pro Leu Leu  
 215

<210> 112  
 <211> 218  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 112  
 Met Asp Gln Thr Leu Lys Val Leu Val Ile Asp Asp Asp Phe Arg Val  
 1 5 10 15  
 Ala Gly Ile His Ala Ser Ile Val Asp Ala Ser Pro Gly Phe Ser Val  
 20 25 30  
 Val Gly Thr Ala Arg Thr Leu Ala Glu Ala Lys Thr Leu Ile Ala Thr  
 35 40 45  
 Phe Ser Pro Asp Leu Leu Leu Val Asp Val Tyr Leu Pro Asp Gly Asp  
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Met Thr Ser His Leu																5
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Leu	Val	Glu	Glu	Pro	Pro	Ala	Glu	Ser	Asp	Tyr	Glu	Asp	Pro	Met	Asp		
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Ser	Val	Trp	Pro	Val	Arg	Leu	Met	Val	Arg	Thr	Gly	Val	Asp	Ala	Pro		
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Gln	Ala	Ile	Gln	Lys	Gly	Ser	Ile	Asp	Ser	Gly	Gly	Met	Glu	Gln	Leu		
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Arg	Ser	Gln	Tyr	Glu	Thr	Ala	Lys	Thr	Thr	Ser	Met	Leu	Leu	Asp	Pro		
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Ala	Arg	Glu	Asp	Ala	Met	Leu	Gly	His	Met	Val	Asp	Ile	Ala	Gln	Asn		
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Gly	Asp	Trp	Asp	Ile	Phe	Leu	Thr	Thr	Glu	Glu	Ile	Val	Asn	Phe	Ile		
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Ser	His	Asp	Val	Ala	Lys	Leu	Arg	Lys	Ala	Gly	Ile	Pro	Val	Met	Leu		
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Pro	Lys	Ala	Trp	Ser	Thr	Tyr	Glu	Thr	Arg	Ala	Gln	Val	Glu	Ala	Arg		
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Thr	Pro	Asn	Asp	Ala	Ala	Asp	Ser	Ser	Thr	Lys	Ala	Ile	Ile	Gly	Leu		
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Leu	Ser	Asp	Glu	Glu	Met	Arg	Glu	Leu	Ile	Asp	Ser	Lys	Thr	Gly	Leu		
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Ile	Arg	Leu	Arg	Gly	Asp	Trp	Val	Met	Ala	Asp	Gln	Asp	Ala	Leu	Arg		



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Leu Arg Lys Glu Phe Asn Glu Lys Phe Ser Gly Asp Gly Gln Gly Glu																		
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Val Thr Leu Ala Glu Leu Arg Glu Ile Ala Leu Lys Ala Ala Glu Asn																		
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Gly Thr Glu Thr Pro Ala Pro Val Arg Val Asp Ile Pro Asp Thr Val																		
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Val Ile Thr Arg Asp Phe Lys Leu Met Gly Gln Val Gly Phe Glu Arg																		
665	670	675																

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Pro	Asn	Ile	Ile	Asp	Asp	Leu	Pro	Glu	Lys	Thr	Glu	Gln	Ile	Ile	Arg	
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 Ala Lys Leu Ala Glu Ala Asn Gly Glu Glu Gly Trp Gln Leu Leu Ala  
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 Ala Lys Ala Glu Thr Leu Arg Lys Glu Phe Asn Glu Lys Phe Ser Gly  
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 Asp Gly Gln Gly Glu Val Thr Leu Ala Glu Leu Arg Glu Ile Ala Leu  
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 Ser Ser Thr Arg Val Ser Lys Ala Val Arg Ser Leu Pro Ser Arg His  
 690 695 700  
 Arg Val Ala Leu Thr Gly Thr Pro Val Glu Asn Arg Leu Ser Glu Met  
 705 710 715 720  
 Arg Ser Ile Leu Asp Phe Cys Asn Pro Gly Val Leu Gly Ser Ala Ser  
 725 730 735  
 Phe Phe Arg Asn His Phe Ala Lys Ala Ile Glu Arg Glu Gln Asp Asp  
 740 745 750  
 Thr Met Thr Glu Arg Leu Arg Gln Leu Thr Ala Pro Phe Ile Leu Arg  
 755 760 765

Arg Leu Lys Thr Asp Pro Asn Ile Ile Asp Asp Leu Pro Glu Lys Thr  
 770 775 780  
 Glu Gln Ile Ile Arg Val Asp Met Thr Thr Glu Gln Ala Ser Leu Tyr  
 785 790 795 800  
 Lys Ala Leu Val Glu Asp Val Gln Lys Gln Leu Asp Glu Arg Gln Gly  
 805 810 815  
 Met Ser Arg Lys Gly Leu Val Leu Ala Thr Ile Thr Arg Ile Lys Gln  
 820 825 830  
 Ile Cys Asn His Pro Ala His Phe Leu Gly Asp Gly Ser Glu Val Thr  
 835 840 845  
 Leu Lys Gly Lys His Arg Ser Gly Lys Val Glu Ala Leu Met Glu Leu  
 850 855 860  
 Ile Asp Thr Ala Val Lys Glu Glu Arg Arg Met Leu Ile Phe Thr Gln  
 865 870 875 880  
 Tyr Ala Ala Phe Gly Arg Ile Leu Ala Pro Tyr Leu Ser Asp Arg Leu  
 885 890 895  
 Gly Thr Asn Ile Pro Phe Leu His Gly Gly Val Thr Lys Pro Gly Arg  
 900 905 910  
 Asp Arg Met Val Ala Glu Phe Gln Ser Glu Asp Gly Pro Pro Ala Met  
 915 920 925  
 Ile Leu Ser Leu Lys Ala Gly Gly Thr Gly Leu Asn Leu Thr Ala Ala  
 930 935 940  
 Ser Ile Val Val His Met Asp Arg Trp Trp Asn Pro Ala Val Glu Asn  
 945 950 955 960  
 Gln Ala Thr Asp Arg Ala Phe Arg Ile Gly Gln Arg Lys Asn Val Asp  
 965 970 975  
 Val Tyr Lys Met Ile Thr Val Gly Thr Met Glu Glu Ser Ile Gln Asp  
 980 985 990  
 Ile Leu Asp Gly Lys Thr His Leu Ala Ser Ala Ile Val Gly Glu Gly  
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 Ser Tyr Arg Glu Lys Glu Gly Ala Asp Asp  
 1025 1030

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 <212> DNA  
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 <223> RXA02760

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gggttttagg gtcgatagat aggttgggag aacacgcatt atg agc gat gag aac 115  
 Met Ser Asp Glu Asn  
 1 5

att aac gag ttt gag cag gac gag gat ctg aac ttc ggc gcg agc ttt 163  
 Ile Asn Glu Phe Glu Gln Asp Glu Asp Leu Asn Phe Gly Ala Ser Phe  
 10 15 20

agt gat gaa ttc gca gat gac gat ttc gat gca gaa gca gac gta gaa 211  
 Ser Asp Glu Phe Ala Asp Asp Asp Phe Asp Ala Glu Ala Asp Val Glu  
 25 30 35

gca gat gct gct gca gag gcc tct gcc ctg gaa gct gag cag gat ctg 259  
 Ala Asp Ala Ala Ala Glu Ala Ser Ala Leu Glu Ala Glu Gln Asp Leu  
 40 45 50

gaa gaa gag acc cta gat gct cca gaa gaa gcc gca gaa gaa gct cct 307  
 Glu Glu Glu Thr Leu Asp Ala Pro Glu Glu Ala Ala Glu Glu Ala Pro  
 55 60 65

gct gct gca gag tcc gaa gct cca gta gaa gag gac gaa gag gct gac 355  
 Ala Ala Ala Glu Ser Glu Ala Pro Val Glu Glu Asp Glu Glu Ala Asp  
 70 75 80 85

agc ctt gct cag gcg gct gct gca ctt ggt gac acc gat gag cag gac 403  
 Ser Leu Ala Gln Ala Ala Ala Ala Leu Gly Asp Thr Asp Glu Gln Asp  
 90 95 100

gcg gat gca gag tac aag gct cgt ctg cgt aag ttc act cgt gag ctg 451  
 Ala Asp Ala Glu Tyr Lys Ala Arg Leu Arg Lys Phe Thr Arg Glu Leu  
 105 110 115

aag aag cag cct ggt gtt tgg tac atc att cag tgc tac tcc ggc tac 499  
 Lys Lys Gln Pro Gly Val Trp Tyr Ile Ile Gln Cys Tyr Ser Gly Tyr  
 120 125 130

gag aac aag gtg aag gcg aac ctt gac atg cgt gct cag acc ctt gag 547  
 Glu Asn Lys Val Lys Ala Asn Leu Asp Met Arg Ala Gln Thr Leu Glu  
 135 140 145

gtt gag gat gac atc ttt gag gtt gtt gtt cct atc gag cag gtc act 595  
 Val Glu Asp Asp Ile Phe Glu Val Val Val Pro Ile Glu Gln Val Thr  
 150 155 160 165

gag atc cgt gat ggt aag cgc aag ctg gtt aag cgt aag ttg ctg ccg 643  
 Glu Ile Arg Asp Gly Lys Arg Lys Leu Val Lys Arg Lys Leu Leu Pro  
 170 175 180

ggc tac gtt ttg gtc cgc atg gac atg aat gac cgc gtg tgg tct gtt 691  
 Gly Tyr Val Leu Val Arg Met Asp Met Asn Asp Arg Val Trp Ser Val  
 185 190 195

gtt cgc gat aca cct ggt gtg acc agc ttt gtg ggt aac gag ggc aat 739  
 Val Arg Asp Thr Pro Gly Val Thr Ser Phe Val Gly Asn Glu Gly Asn  
 200 205 210

gca act cct gtg aag cac cgc gat gtt gcg aag ttc ttg atg cct cag 787

Ala Thr Pro Val Lys His Arg Asp Val Ala Lys Phe Leu Met Pro Gln  
 215 220 225

gag cag gct gtt gtc acc ggt gag gct gct gct gcg gct gcc gag ggt 835  
 Glu Gln Ala Val Val Thr Gly Glu Ala Ala Ala Ala Glu Gly  
 230 235 240 245

gag cag gtt gtg gct atg cct acc gat acc aag aag cct cag gtt gct 883  
 Glu Gln Val Val Ala Met Pro Thr Asp Thr Lys Lys Pro Gln Val Ala  
 250 255 260

gtg gac ttc act gtt ggt gag gct gtg acc att ctg act ggt gct ttc 931  
 Val Asp Phe Thr Val Gly Glu Ala Val Thr Ile Leu Thr Gly Ala Phe  
 265 270 275

gct tct gtt tct gca acg att tct tct atc gat cct gag ctg cag aag 979  
 Ala Ser Val Ser Ala Thr Ile Ser Ser Ile Asp Pro Glu Leu Gln Lys  
 280 285 290

ctg gaa gtt ttg gtg tcc atc ttt ggt cgt gaa act cct gtt gat ctc 1027  
 Leu Glu Val Leu Val Ser Ile Phe Gly Arg Glu Thr Pro Val Asp Leu  
 295 300 305

agc ttc gac cag gtt gag aag gtt agc tagtagctaa actgcaccac tta 1077  
 Ser Phe Asp Gln Val Glu Lys Val Ser  
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&lt;210&gt; 116

&lt;211&gt; 318

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 116

Met Ser Asp Glu Asn Ile Asn Glu Phe Glu Gln Asp Glu Asp Leu Asn  
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Phe Gly Ala Ser Phe Ser Asp Glu Phe Ala Asp Asp Asp Phe Asp Ala  
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Glu Ala Asp Val Glu Ala Asp Ala Ala Ala Glu Ala Ser Ala Leu Glu  
 35 40 45

Ala Glu Gln Asp Leu Glu Glu Glu Thr Leu Asp Ala Pro Glu Glu Ala  
 50 55 60

Ala Glu Glu Ala Pro Ala Ala Ala Glu Ser Glu Ala Pro Val Glu Glu  
 65 70 75 80

Asp Glu Glu Ala Asp Ser Leu Ala Gln Ala Ala Ala Ala Leu Gly Asp  
 85 90 95

Thr Asp Glu Gln Asp Ala Asp Ala Glu Tyr Lys Ala Arg Leu Arg Lys  
 100 105 110

Phe Thr Arg Glu Leu Lys Lys Gln Pro Gly Val Trp Tyr Ile Ile Gln  
 115 120 125

Cys Tyr Ser Gly Tyr Glu Asn Lys Val Lys Ala Asn Leu Asp Met Arg  
 130 135 140



Ala Gln Thr Leu Glu Val Glu Asp Asp Ile Phe Glu Val Val Val Pro  
 145 150 155 160

Ile Glu Gln Val Thr Glu Ile Arg Asp Gly Lys Arg Lys Leu Val Lys  
 165 170 175

Arg Lys Leu Leu Pro Gly Tyr Val Leu Val Arg Met Asp Met Asn Asp  
 180 185 190

Arg Val Trp Ser Val Val Arg Asp Thr Pro Gly Val Thr Ser Phe Val  
 195 200 205

Gly Asn Glu Gly Asn Ala Thr Pro Val Lys His Arg Asp Val Ala Lys  
 210 215 220

Phe Leu Met Pro Gln Glu Gln Ala Val Val Thr Gly Glu Ala Ala Ala  
 225 230 235 240

Ala Ala Ala Glu Gly Glu Gln Val Val Ala Met Pro Thr Asp Thr Lys  
 245 250 255

Lys Pro Gln Val Ala Val Asp Phe Thr Val Gly Glu Ala Val Thr Ile  
 260 265 270

Leu Thr Gly Ala Phe Ala Ser Val Ser Ala Thr Ile Ser Ser Ile Asp  
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Pro Glu Leu Gln Lys Leu Glu Val Leu Val Ser Ile Phe Gly Arg Glu  
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 Met Gln Pro Glu Glu  
 1 5

gtg cac atc aag gac gag acc atc aag tta ggt cag ttc atc aaa ttg 163  
 Val His Ile Lys Asp Glu Thr Ile Lys Leu Gly Gln Phe Ile Lys Leu  
 10 15 20

gcc aac ctt gtc gaa tca ggc gga gcg gcc aaa gat gcc atc gct aac 211  
 Ala Asn Leu Val Glu Ser Gly Gly Ala Ala Lys Asp Ala Ile Ala Asn  
 25 30 35

ggg gat gtc acc gtc aat ggt gaa gtg gat acc cga agg ggt aag aca 259

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<213> Corynebacterium glutamicum
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<210> 119
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<212> DNA
<213> Corynebacterium glutamicum
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gggtactata aactaatccc aattagcagg aaggattctc atg tca cag aaa att 115
Met Ser Gln Lys Ile
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ctc gtg gtt gat gat gat ccc gcc atc tcc gag atg ctc acc atc gtg			163
Leu Val Val Asp Asp Asp Pro Ala Ile Ser Glu Met Leu Thr Ile Val	10	20	
ctc agc gca gaa ggc ttt gac acc gta gct gtc acc gac ggc gca ctc			211
Leu Ser Ala Glu Gly Phe Asp Thr Val Ala Val Thr Asp Gly Ala Leu	25	30	35
gcc gtg gaa acc gcc tcc cgg gaa caa ccg gat ctg att ttg ctc gac			259
Ala Val Glu Thr Ala Ser Arg Glu Gln Pro Asp Leu Ile Leu Leu Asp	40	45	50
ttg atg ctt cca ggc atg aac ggc atc gac att tgt cgc ctc atc cgc			307
Leu Met Leu Pro Gly Met Asn Gly Ile Asp Ile Cys Arg Leu Ile Arg	55	60	65
caa gaa tcc tcc gta ccc atc atc atg ctc acc gcc aaa acc gac acc			355
Gln Glu Ser Ser Val Pro Ile Ile Met Leu Thr Ala Lys Thr Asp Thr	70	75	80
gtt gat gtg gtg ctc ggt ttg gaa tcc ggt gca gac gat tac gtg aac			403
Val Asp Val Val Leu Gly Leu Glu Ser Gly Ala Asp Asp Tyr Val Asn	90	95	100
aag cct ttc aaa gcg aaa gaa ctt gtc gcc cgc atc cgt gcc cgc ctc			451
Lys Pro Phe Lys Ala Lys Glu Leu Val Ala Arg Ile Arg Ala Arg Leu	105	110	115
cgc gca acc gtg gac gag ccc agc gaa atc atc gaa gtc ggc gat ctg			499
Arg Ala Thr Val Asp Glu Pro Ser Glu Ile Ile Glu Val Gly Asp Leu	120	125	130
tcc atc gac gtc cca gca cac acc gtc aaa cga aac ggc gct gag att			547
Ser Ile Asp Val Pro Ala His Thr Val Lys Arg Asn Gly Ala Glu Ile	135	140	145
tcc ttg acc cca ctc gaa ttc gac ctc ctg ctg gaa ctc gcc cgc aaa			595
Ser Leu Thr Pro Leu Glu Phe Asp Leu Leu Leu Glu Leu Ala Arg Lys	150	155	160
cca cag caa gta ttc acc cgt gaa gaa ttg ctg ggc aaa gtg tgg ggc			643
Pro Gln Gln Val Phe Thr Arg Glu Glu Leu Leu Gly Lys Val Trp Gly	170	175	180
tac cgc cac gca tcc gac act cga ctg gtc aac gtt cac gtt cag cgt			691
Tyr Arg His Ala Ser Asp Thr Arg Leu Val Asn Val His Val Gln Arg	185	190	195
ctg cgc gcc aag att gaa aaa gat cca gaa aat ccg cag atc gtc ctc			739
Leu Arg Ala Lys Ile Glu Lys Asp Pro Glu Asn Pro Gln Ile Val Leu	200	205	210
acc gtc cgc ggt gtt ggc tac aaa act ggc cac aac gat taagtttttc			788
Thr Val Arg Gly Val Gly Tyr Lys Thr Gly His Asn Asp	215	220	225
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                   20                  25                  30  
 Thr Asp Gly Ala Leu Ala Val Glu Thr Ala Ser Arg Glu Gln Pro Asp  
           35                  40                  45  
 Leu Ile Leu Leu Asp Leu Met Leu Pro Gly Met Asn Gly Ile Asp Ile  
   50                  55                  60  
 Cys Arg Leu Ile Arg Gln Glu Ser Ser Val Pro Ile Ile Met Leu Thr  
   65                  70                  75                  80  
 Ala Lys Thr Asp Thr Val Asp Val Val Leu Gly Leu Glu Ser Gly Ala  
                   85                  90                  95  
 Asp Asp Tyr Val Asn Lys Pro Phe Lys Ala Lys Glu Leu Val Ala Arg  
                   100                  105                  110  
 Ile Arg Ala Arg Leu Arg Ala Thr Val Asp Glu Pro Ser Glu Ile Ile  
           115                  120                  125  
 Glu Val Gly Asp Leu Ser Ile Asp Val Pro Ala His Thr Val Lys Arg  
   130                  135                  140  
 Asn Gly Ala Glu Ile Ser Leu Thr Pro Leu Glu Phe Asp Leu Leu Leu  
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 Glu Leu Ala Arg Lys Pro Gln Gln Val Phe Thr Arg Glu Glu Leu Leu  
                   165                  170                  175  
 Gly Lys Val Trp Gly Tyr Arg His Ala Ser Asp Thr Arg Leu Val Asn  
           180                  185                  190  
 Val His Val Gln Arg Leu Arg Ala Lys Ile Glu Lys Asp Pro Glu Asn  
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 Pro Gln Ile Val Leu Thr Val Arg Gly Val Gly Tyr Lys Thr Gly His  
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 Asn Asp  
 225

<210> 121  
 <211> 1149  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <223> RXA00885

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               Met Val Ser Ala Thr
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gag aaa cgt aga tac gaa gtg ttg cgg gcc atc gtc gct gat tac att 163
Glu Lys Arg Arg Tyr Glu Val Leu Arg Ala Ile Val Ala Asp Tyr Ile
               10 15 20

gcg tct cag gaa cct gtc gga tgc aag tca ctc ctc gag cgc cat aag 211
Ala Ser Gln Glu Pro Val Gly Ser Lys Ser Leu Leu Glu Arg His Lys
               25 30 35

ctc aac gtg agt tct gcg acg atc cgc aac gat atg tgc gtg ctg gaa 259
Leu Asn Val Ser Ser Ala Thr Ile Arg Asn Asp Met Ser Val Leu Glu
               40 45 50

tcc gat ggc ttt atc gtc cag gag cat gca agt tct ggc cgg gta cca 307
Ser Asp Gly Phe Ile Val Gln Glu His Ala Ser Ser Gly Arg Val Pro
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acc gaa agg ggt tac cgc ctt ttt gtt gat tcc atc cat gac atc aaa 355
Thr Glu Arg Gly Tyr Arg Leu Phe Val Asp Ser Ile His Asp Ile Lys
               70 75 80 85

ccg ctg tgc ctg gcg gaa cgg cgc gct att ttg ggc ttc ctt gaa ggg 403
Pro Leu Ser Leu Ala Glu Arg Arg Ala Ile Leu Gly Phe Leu Glu Gly
               90 95 100

gga gtg gac tta gag gac gtg ctg cgc aga tct gtg cag ctg ttg tct 451
Gly Val Asp Leu Glu Asp Val Leu Arg Arg Ser Val Gln Leu Leu Ser
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cag ctc acc cat cag gct gcc gtg gtg cag ctg ccc acc ctg aaa aca 499
Gln Leu Thr His Gln Ala Ala Val Val Gln Leu Pro Thr Leu Lys Thr
               120 125 130

gcg cgc gtg aag cac tgc gag gtg gtg ccg ctg tgc ccg atg cgc ttg 547
Ala Arg Val Lys His Cys Glu Val Val Pro Leu Ser Pro Met Arg Leu
               135 140 145

ctg ctg gtg ctc att acc gat act ggc cgt gta gat cag cgc aac gtg 595
Leu Leu Val Leu Ile Thr Asp Thr Gly Arg Val Asp Gln Arg Asn Val
               150 155 160 165

gaa ctt gag gaa ccg ctg gcg gcg gaa gaa gtt aat gtg ctg cgc gat 643
Glu Leu Glu Glu Pro Leu Ala Ala Glu Glu Val Asn Val Leu Arg Asp
               170 175 180

ctg ctc aac ggc gcg cta ggg gag aaa acg ctg acg gct gca tca gat 691
Leu Leu Asn Gly Ala Leu Gly Glu Lys Thr Leu Thr Ala Ala Ser Asp
               185 190 195

gcg ctg gaa gag ttg gct cag caa gcc cca acc gat att cgt gat gcc 739
Ala Leu Glu Glu Leu Ala Gln Gln Ala Pro Thr Asp Ile Arg Asp Ala
               200 205 210

atg cgc cgc tgc tgc gat gtg ctg gtg aac acg ctt gtc gat caa ccc 787

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Met	Arg	Arg	Cys	Cys	Asp	Val	Leu	Val	Asn	Thr	Leu	Val	Asp	Gln	Pro	
	215					220					225					
tct	gac	cgc	ctg	atc	ctc	gcc	ggc	acc	tca	aac	ctc	acc	cgc	tta	agc	835
Ser	Asp	Arg	Leu	Ile	Leu	Ala	Gly	Thr	Ser	Asn	Leu	Thr	Arg	Leu	Ser	
230					235					240					245	
cgg	gaa	acc	tcc	gcg	agc	ctg	ccc	atg	gtt	tta	gaa	gcc	ttg	gaa	gag	883
Arg	Glu	Thr	Ser	Ala	Ser	Leu	Pro	Met	Val	Leu	Glu	Ala	Leu	Glu	Glu	
				250					255					260		
cag	gtg	gtc	atg	ttg	aaa	ctg	ctg	tcc	aat	gtc	act	gat	ctt	gac	caa	931
Gln	Val	Val	Met	Leu	Lys	Leu	Leu	Ser	Asn	Val	Thr	Asp	Leu	Asp	Gln	
			265					270					275			
gtg	cgc	gtg	cat	att	ggc	ggc	gaa	aat	gaa	gac	att	gag	ctg	cgc	agc	979
Val	Arg	Val	His	Ile	Gly	Gly	Glu	Asn	Glu	Asp	Ile	Glu	Leu	Arg	Ser	
		280					285						290			
gca	acg	gtg	att	acc	acc	ggt	tac	ggc	tcc	cag	ggc	agc	gca	ctg	ggc	1027
Ala	Thr	Val	Ile	Thr	Thr	Gly	Tyr	Gly	Ser	Gln	Gly	Ser	Ala	Leu	Gly	
	295					300					305					
gga	ttg	ggg	gtg	gtt	ggc	ccc	acc	tat	atg	gac	tac	tcg	gga	aca	att	1075
Gly	Leu	Gly	Val	Val	Gly	Pro	Thr	Tyr	Met	Asp	Tyr	Ser	Gly	Thr	Ile	
310					315					320					325	
tct	aag	gtg	tcc	gcc	gtt	gct	aag	tat	gtt	ggc	cgt	gtg	ctc	gct	ggc	1123
Ser	Lys	Val	Ser	Ala	Val	Ala	Lys	Tyr	Val	Gly	Arg	Val	Leu	Ala	Gly	
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Glu																

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 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 122  
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 Leu Glu Arg His Lys Leu Asn Val Ser Ser Ala Thr Ile Arg Asn Asp  
 35 40 45  
 Met Ser Val Leu Glu Ser Asp Gly Phe Ile Val Gln Glu His Ala Ser  
 50 55 60  
 Ser Gly Arg Val Pro Thr Glu Arg Gly Tyr Arg Leu Phe Val Asp Ser  
 65 70 75 80  
 Ile His Asp Ile Lys Pro Leu Ser Leu Ala Glu Arg Arg Ala Ile Leu  
 85 90 95  
 Gly Phe Leu Glu Gly Gly Val Asp Leu Glu Asp Val Leu Arg Arg Ser

100					105					110					
Val	Gln	Leu	Leu	Ser	Gln	Leu	Thr	His	Gln	Ala	Ala	Val	Val	Gln	Leu
	115						120					125			
Pro	Thr	Leu	Lys	Thr	Ala	Arg	Val	Lys	His	Cys	Glu	Val	Val	Pro	Leu
	130					135					140				
Ser	Pro	Met	Arg	Leu	Leu	Leu	Val	Leu	Ile	Thr	Asp	Thr	Gly	Arg	Val
145					150					155					160
Asp	Gln	Arg	Asn	Val	Glu	Leu	Glu	Glu	Pro	Leu	Ala	Ala	Glu	Glu	Val
			165						170					175	
Asn	Val	Leu	Arg	Asp	Leu	Leu	Asn	Gly	Ala	Leu	Gly	Glu	Lys	Thr	Leu
			180					185					190		
Thr	Ala	Ala	Ser	Asp	Ala	Leu	Glu	Glu	Leu	Ala	Gln	Gln	Ala	Pro	Thr
	195						200					205			
Asp	Ile	Arg	Asp	Ala	Met	Arg	Arg	Cys	Cys	Asp	Val	Leu	Val	Asn	Thr
	210					215					220				
Leu	Val	Asp	Gln	Pro	Ser	Asp	Arg	Leu	Ile	Leu	Ala	Gly	Thr	Ser	Asn
225					230					235					240
Leu	Thr	Arg	Leu	Ser	Arg	Glu	Thr	Ser	Ala	Ser	Leu	Pro	Met	Val	Leu
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Glu	Ala	Leu	Glu	Glu	Gln	Val	Val	Met	Leu	Lys	Leu	Leu	Ser	Asn	Val
			260					265					270		
Thr	Asp	Leu	Asp	Gln	Val	Arg	Val	His	Ile	Gly	Gly	Glu	Asn	Glu	Asp
	275						280					285			
Ile	Glu	Leu	Arg	Ser	Ala	Thr	Val	Ile	Thr	Thr	Gly	Tyr	Gly	Ser	Gln
	290					295					300				
Gly	Ser	Ala	Leu	Gly	Gly	Leu	Gly	Val	Val	Gly	Pro	Thr	Tyr	Met	Asp
305					310					315					320
Tyr	Ser	Gly	Thr	Ile	Ser	Lys	Val	Ser	Ala	Val	Ala	Lys	Tyr	Val	Gly
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Arg	Val	Leu	Ala	Gly	Glu										
			340												

&lt;210&gt; 123

&lt;211&gt; 369

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(346)

&lt;223&gt; RXA01418

&lt;400&gt; 123

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Met Leu Gly Asp Arg  
1 5

acg cgc ctc cgc ctc ctc atc gcg ctg cat tat cac ggc ccc ggt gaa 163  
Thr Arg Leu Arg Leu Leu Ile Ala Leu His Tyr His Gly Pro Gly Glu  
10 15 20

gcc acc gtc tca gaa ctc gcg gac atc gtc ggc gtc acc ctg ccc acg 211  
Ala Thr Val Ser Glu Leu Ala Asp Ile Val Gly Val Thr Leu Pro Thr  
25 30 35

gcc tcc gca gcg ctc caa ctg ctc gca gat aac gga gtg gtc gag tcc 259  
Ala Ser Ala Ala Leu Gln Leu Leu Ala Asp Asn Gly Val Val Glu Ser  
40 45 50

ttc aag gag ggg cgg gtg aca aga tat aag ctt gtc gac gcc acg acc 307  
Phe Lys Glu Gly Arg Val Thr Arg Tyr Lys Leu Val Asp Ala Thr Thr  
55 60 65

cac acc ttg ctt cac cac ctc ggg ggc acc cac cga cat taaagggaac 356  
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<212> PRT  
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35 40 45

Gly Val Val Glu Ser Phe Lys Glu Gly Arg Val Thr Arg Tyr Lys Leu  
50 55 60

Val Asp Ala Thr Thr His Thr Leu Leu His His Leu Gly Gly Thr His  
65 70 75 80

Arg His

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<212> DNA  
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<220>  
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<222> (101)..(862)  
<223> RXA01759



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agc Ser	ctt Leu	gaa Glu	ggg Gly	ctc Leu	cgc Arg	tat Tyr	gcg Ala	cag Gln	gcc Ala	gtc Val	gca Ala	gaa Glu	act Thr	cac His	tca Ser	163
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ttc Phe	agc Ser	gca Ala	gca Ala	gcc Ala	cgc Arg	gaa Glu	tac Tyr	gga Gly	gtc Val	acc Thr	caa Gln	cct Pro	gcg Ala	cta Leu	tcc Ser	211
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cga Arg	tct Ser	act Thr	caa Gln	ggc Gly	gtc Val	acc Thr	ccg Pro	acg Thr	tcc Ser	ttt Phe	ggc Gly	ctc Leu	cac His	atc Ile	ctc Leu	307
	55					60					65					
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	70				75					80					85	
gcg Ala	cac His	cgt Arg	ttg Leu	att Ile	aac Asn	tca Ser	gaa Glu	gca Ala	cgc Arg	agc Ser	att Ile	cga Arg	gtt Val	gga Gly	atc Ile	403
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tcc Ser	cca Pro	ctt Leu	atc Ile	aac Asn	cct Pro	caa Gln	ctg Leu	gtt Val	gca Ala	cga Arg	aca Thr	tat Tyr	acc Thr	gcg Ala	gtt Val	451
			105					110					115			
cgt Arg	gag Glu	ctt Leu	ccc Pro	aca Thr	gca Ala	cac His	gac Asp	cta Leu	gta Val	ctc Leu	cgc Arg	gaa Glu	gca Ala	aac Asn	atg Met	499
		120					125					130				
aaa Lys	gaa Glu	cta Leu	cat His	gaa Glu	gga Gly	ctt Leu	ctt Leu	gca Ala	ggg Gly	gaa Glu	ctt Leu	aat Asn	gta Val	att Ile	ctc Leu	547
	135					140					145					
att Ile	ccc Pro	gca Ala	gtg Val	aaa Lys	cca Pro	cta Leu	ccc Pro	cat His	ttt Phe	gaa Glu	cac His	cgc Arg	atc Ile	att Ile	gac Asp	595
	150				155					160					165	
tcc Ser	gaa Glu	cca Pro	gtc Val	gtt Val	atc Ile	gtc Val	gaa Glu	tcc Ser	acc Thr	cag Gln	gac Asp	agc Ser	acc Thr	gac Asp	ccc Pro	643
				170					175					180		
ata Ile	gaa Glu	ctt Leu	cgc Arg	gag Glu	act Thr	cag Gln	cac His	gaa Glu	ccg Pro	ttc Phe	att Ile	ctg Leu	gta Val	ccc Pro	gac Asp	691
			185					190					195			
aca Thr	tgc Cys	ggg Gly	tta Leu	acc Thr	act Thr	ttc Phe	acc Thr	aat Asn	caa Gln	ctg Leu	ttt Phe	gaa Glu	aca Thr	aat Asn	gac Asp	739
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ctg	gca	tta	aac	gcc	tat	tcc	ggc	gaa	gca	gcc	agc	tac	caa	gta	ctc	787

Leu Ala Leu Asn Ala Tyr Ser Gly Glu Ala Ala Ser Tyr Gln Val Leu  
 215 220 225

gaa cag tgg gcc aca ctt gga ctc gga tct gca atg ctt cca ctt tct 835  
 Glu Gln Trp Ala Thr Leu Gly Leu Gly Ser Ala Met Leu Pro Leu Ser  
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aaa ctc agc tcc cct aca gca ccc cat tgaccactcc gcgaacaagg cct 885  
 Lys Leu Ser Ser Pro Thr Ala Pro His  
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<210> 126

<211> 254

<212> PRT

<213> Corynebacterium glutamicum

<400> 126

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 20 25 30

Gln Pro Ala Leu Ser Asn Gly Ile Ala Lys Leu Glu Asp Arg Leu Gly  
 35 40 45

Glu Gln Leu Phe Asp Arg Ser Thr Gln Gly Val Thr Pro Thr Ser Phe  
 50 55 60

Gly Leu His Ile Leu Pro Leu Ile Gln Arg Ala Leu Thr Glu Ile Asp  
 65 70 75 80

Ala Ile Thr Ala Glu Ala His Arg Leu Ile Asn Ser Glu Ala Arg Ser  
 85 90 95

Ile Arg Val Gly Ile Ser Pro Leu Ile Asn Pro Gln Leu Val Ala Arg  
 100 105 110

Thr Tyr Thr Ala Val Arg Glu Leu Pro Thr Ala His Asp Leu Val Leu  
 115 120 125

Arg Glu Ala Asn Met Lys Glu Leu His Glu Gly Leu Leu Ala Gly Glu  
 130 135 140

Leu Asn Val Ile Leu Ile Pro Ala Val Lys Pro Leu Pro His Phe Glu  
 145 150 155 160

His Arg Ile Ile Asp Ser Glu Pro Val Val Ile Val Glu Ser Thr Gln  
 165 170 175

Asp Ser Thr Asp Pro Ile Glu Leu Arg Glu Thr Gln His Glu Pro Phe  
 180 185 190

Ile Leu Val Pro Asp Thr Cys Gly Leu Thr Thr Phe Thr Asn Gln Leu  
 195 200 205

Phe Glu Thr Asn Asp Leu Ala Leu Asn Ala Tyr Ser Gly Glu Ala Ala  
 210 215 220

Ser Tyr Gln Val Leu Glu Gln Trp Ala Thr Leu Gly Leu Gly Ser Ala  
 225 230 235 240

Met Leu Pro Leu Ser Lys Leu Ser Ser Pro Thr Ala Pro His  
 245 250

<210> 127  
 <211> 843  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(820)  
 <223> RXN00363

<400> 127  
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 gagtaacatg ttaccgggta ctgtgggtgaa ttgtgcgata atg tca gac atg cca 115  
 Met Ser Asp Met Pro  
 1 5  
 aca aaa agg gtt gcc ccc gca cgc tca ctc acc gac caa gtc atg gat 163  
 Thr Lys Arg Val Ala Pro Ala Arg Ser Leu Thr Asp Gln Val Met Asp  
 10 15 20  
 ttc gtc cgc gaa tcc acc ctt gat aaa aca atg gtc acc gga gag tgg 211  
 Phe Val Arg Glu Ser Thr Leu Asp Lys Thr Met Val Thr Gly Glu Trp  
 25 30 35  
 tac agc gtt tac cag gtc agc gac caa tta ggc att tcc cgc tcc ccc 259  
 Tyr Ser Val Tyr Gln Val Ser Asp Gln Leu Gly Ile Ser Arg Ser Pro  
 40 45 50  
 gtc aga gac gcg ctg ctc cgc ctg gaa gaa gca ggg ctc atc cgc ttc 307  
 Val Arg Asp Ala Leu Leu Arg Leu Glu Glu Ala Gly Leu Ile Arg Phe  
 55 60 65  
 acc agg aac cgc gga ttc caa att gtc gaa acc aaa ccc tct gat gtc 355  
 Thr Arg Asn Arg Gly Phe Gln Ile Val Glu Thr Lys Pro Ser Asp Val  
 70 75 80 85  
 gcc gaa att ttt gcc ctt cgt cta ggc att gaa ccc gcc gca gca tac 403  
 Ala Glu Ile Phe Ala Leu Arg Leu Gly Ile Glu Pro Ala Ala Ala Tyr  
 90 95 100  
 cgg gca gca cag cta cgc acc gaa gaa cag ctc cac gaa gca gat gac 451  
 Arg Ala Ala Gln Leu Arg Thr Glu Glu Gln Leu His Glu Ala Asp Asp  
 105 110 115  
 atc att gca ctc atg gcg caa gcc gag gcc gac aat gac gaa gaa gca 499  
 Ile Ile Ala Leu Met Ala Gln Ala Glu Ala Asp Asn Asp Glu Glu Ala  
 120 125 130  
 ttt ttc acc cat gac cgg cag ttt cac cga caa att atg acc atg gga 547  
 Phe Phe Thr His Asp Arg Gln Phe His Arg Gln Ile Met Thr Met Gly  
 135 140 145  
 cac tcc caa cgc ggg gct gac ctg gta gaa aaa cta cgc gca cac acc 595

His Ser Gln Arg Gly Ala Asp Leu Val Glu Lys Leu Arg Ala His Thr  
 150 155 160 165  
 cgt atc ctc ggt gct tct act gcc ggg aac aaa cgc acc ctt ggc gat 643  
 Arg Ile Leu Gly Ala Ser Thr Ala Gly Asn Lys Arg Thr Leu Gly Asp  
 170 175 180  
 att ttg gaa gaa cac gaa cca atc ttg gat gcc atc aaa cga caa tca 691  
 Ile Leu Glu Glu His Glu Pro Ile Leu Asp Ala Ile Lys Arg Gln Ser  
 185 190 195  
 gca gaa atg gca cga gcc acc atg cgg gag cat atc caa gtc acc gga 739  
 Ala Glu Met Ala Arg Ala Thr Met Arg Glu His Ile Gln Val Thr Gly  
 200 205 210  
 aag cta cta cta gaa caa gca gtg gaa aaa tcc ggc gaa gga gct gct 787  
 Lys Leu Leu Leu Glu Gln Ala Val Glu Lys Ser Gly Glu Gly Ala Ala  
 215 220 225  
 cag aag att tgg gat cag tac acg gcg gga gtt taggcatatt tacctaataca 840  
 Gln Lys Ile Trp Asp Gln Tyr Thr Ala Gly Val  
 230 235 240  
 att 843  
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 <211> 240  
 <212> PRT  
 <213> Corynebacterium glutamicum  
 <400> 128  
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 Asp Gln Val Met Asp Phe Val Arg Glu Ser Thr Leu Asp Lys Thr Met  
 20 25 30  
 Val Thr Gly Glu Trp Tyr Ser Val Tyr Gln Val Ser Asp Gln Leu Gly  
 35 40 45  
 Ile Ser Arg Ser Pro Val Arg Asp Ala Leu Leu Arg Leu Glu Glu Ala  
 50 55 60  
 Gly Leu Ile Arg Phe Thr Arg Asn Arg Gly Phe Gln Ile Val Glu Thr  
 65 70 75 80  
 Lys Pro Ser Asp Val Ala Glu Ile Phe Ala Leu Arg Leu Gly Ile Glu  
 85 90 95  
 Pro Ala Ala Ala Tyr Arg Ala Ala Gln Leu Arg Thr Glu Glu Gln Leu  
 100 105 110  
 His Glu Ala Asp Asp Ile Ile Ala Leu Met Ala Gln Ala Glu Ala Asp  
 115 120 125  
 Asn Asp Glu Glu Ala Phe Phe Thr His Asp Arg Gln Phe His Arg Gln  
 130 135 140  
 Ile Met Thr Met Gly His Ser Gln Arg Gly Ala Asp Leu Val Glu Lys  
 145 150 155 160

Leu Arg Ala His Thr Arg Ile Leu Gly Ala Ser Thr Ala Gly Asn Lys  
 165 170 175  
 Arg Thr Leu Gly Asp Ile Leu Glu Glu His Glu Pro Ile Leu Asp Ala  
 180 185 190  
 Ile Lys Arg Gln Ser Ala Glu Met Ala Arg Ala Thr Met Arg Glu His  
 195 200 205  
 Ile Gln Val Thr Gly Lys Leu Leu Leu Glu Gln Ala Val Glu Lys Ser  
 210 215 220  
 Gly Glu Gly Ala Ala Gln Lys Ile Trp Asp Gln Tyr Thr Ala Gly Val  
 225 230 235 240

<210> 129  
 <211> 707  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(684)  
 <223> FRXA00363

<400> 129  
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 Arg Ser Leu Thr Asp Gln Val Met Asp Phe Val Arg Glu Ser Thr Leu  
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 gat aaa aca atg gtc acc gga gag tgg tac agc gtt tac cag gtc agc 96  
 Asp Lys Thr Met Val Thr Gly Glu Trp Tyr Ser Val Tyr Gln Val Ser  
 20 25 30  
 gac caa tta ggc att tcc cgc tcc ccc gtc aga gac gcg ctg ctc cgc 144  
 Asp Gln Leu Gly Ile Ser Arg Ser Pro Val Arg Asp Ala Leu Leu Arg  
 35 40 45  
 ctg gaa gaa gca ggg ctc atc cgc ttc acc agg aac cgc gga ttc caa 192  
 Leu Glu Glu Ala Gly Leu Ile Arg Phe Thr Arg Asn Arg Gly Phe Gln  
 50 55 60  
 att gtc gaa acc aaa ccc tct gat gtc gcc gaa att ttt gcc ctt cgt 240  
 Ile Val Glu Thr Lys Pro Ser Asp Val Ala Glu Ile Phe Ala Leu Arg  
 65 70 75 80  
 cta ggc att gaa ccc gcc gca gca tac cgg gca gca cag cta cgc acc 288  
 Leu Gly Ile Glu Pro Ala Ala Ala Tyr Arg Ala Ala Gln Leu Arg Thr  
 85 90 95  
 gaa gaa cag ctc cac gaa gca gat gac atc att gca ctc atg gcg caa 336  
 Glu Glu Gln Leu His Glu Ala Asp Asp Ile Ile Ala Leu Met Ala Gln  
 100 105 110  
 gcc gag gcc gac aat gac gaa gaa gca ttt ttc acc cat gac cgg cag 384  
 Ala Glu Ala Asp Asn Asp Glu Glu Ala Phe Phe Thr His Asp Arg Gln

115	120	125	
ttt cac cga caa att atg acc atg gga cac tcc caa cgc ggg gct gac			432
Phe His Arg Gln Ile Met Thr Met Gly His Ser Gln Arg Gly Ala Asp			
130	135	140	
ctg gta gaa aaa cta cgc gca cac acc cgt atc ctc ggt gct tct act			480
Leu Val Glu Lys Leu Arg Ala His Thr Arg Ile Leu Gly Ala Ser Thr			
145	150	155	160
gcc ggg aac aaa cgc acc ctt ggc gat att ttg gaa gaa cac gaa cca			528
Ala Gly Asn Lys Arg Thr Leu Gly Asp Ile Leu Glu Glu His Glu Pro			
	165	170	175
atc ttg gat gcc atc aaa cga caa tca gca gaa atg gca cga gcc acc			576
Ile Leu Asp Ala Ile Lys Arg Gln Ser Ala Glu Met Ala Arg Ala Thr			
	180	185	190
atg cgg gag cat atc caa gtc acc gga aag cta cta cta gaa caa gca			624
Met Arg Glu His Ile Gln Val Thr Gly Lys Leu Leu Leu Glu Gln Ala			
	195	200	205
gtg gaa aaa tcc ggc gaa gga gct gct cag aag att tgg gat cag tac			672
Val Glu Lys Ser Gly Glu Gly Ala Ala Gln Lys Ile Trp Asp Gln Tyr			
	210	215	220
acg gcg gga gtt taggcatatt tacctaataca att			707
Thr Ala Gly Val			
225			

&lt;210&gt; 130

&lt;211&gt; 228

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 130

Arg Ser Leu Thr Asp Gln Val Met Asp Phe Val Arg Glu Ser Thr Leu
1 5 10 15

Asp Lys Thr Met Val Thr Gly Glu Trp Tyr Ser Val Tyr Gln Val Ser
20 25 30

Asp Gln Leu Gly Ile Ser Arg Ser Pro Val Arg Asp Ala Leu Leu Arg
35 40 45

Leu Glu Glu Ala Gly Leu Ile Arg Phe Thr Arg Asn Arg Gly Phe Gln
50 55 60

Ile Val Glu Thr Lys Pro Ser Asp Val Ala Glu Ile Phe Ala Leu Arg
65 70 75 80

Leu Gly Ile Glu Pro Ala Ala Ala Tyr Arg Ala Ala Gln Leu Arg Thr
85 90 95

Glu Glu Gln Leu His Glu Ala Asp Asp Ile Ile Ala Leu Met Ala Gln
100 105 110

Ala Glu Ala Asp Asn Asp Glu Glu Ala Phe Phe Thr His Asp Arg Gln
115 120 125

Phe His Arg Gln Ile Met Thr Met Gly His Ser Gln Arg Gly Ala Asp  
 130 135 140  
 Leu Val Glu Lys Leu Arg Ala His Thr Arg Ile Leu Gly Ala Ser Thr  
 145 150 155 160  
 Ala Gly Asn Lys Arg Thr Leu Gly Asp Ile Leu Glu Glu His Glu Pro  
 165 170 175  
 Ile Leu Asp Ala Ile Lys Arg Gln Ser Ala Glu Met Ala Arg Ala Thr  
 180 185 190  
 Met Arg Glu His Ile Gln Val Thr Gly Lys Leu Leu Leu Glu Gln Ala  
 195 200 205  
 Val Glu Lys Ser Gly Glu Gly Ala Ala Gln Lys Ile Trp Asp Gln Tyr  
 210 215 220  
 Thr Ala Gly Val  
 225

<210> 131  
 <211> 843  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(820)  
 <223> RXA00516

<400> 131  
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 gtcacaaata gtctaaattt cgggtgtacta aggtgttgct atg gtc caa aaa gat 115  
 Met Val Gln Lys Asp  
 1 5  
 gcc cag gcc tcc cct gct acg aga aaa gca gat cag gta tac aca cag 163  
 Ala Gln Ala Ser Pro Ala Thr Arg Lys Ala Asp Gln Val Tyr Thr Gln  
 10 15 20  
 att cgt cgt gaa atc gaa gat gga acc tta aat cct ggg caa cga atg 211  
 Ile Arg Arg Glu Ile Glu Asp Gly Thr Leu Asn Pro Gly Gln Arg Met  
 25 30 35  
 tcg gaa gtg tgg ctg gtt gaa cac acc ggc gct tcg aga acc cca gtc 259  
 Ser Glu Val Trp Leu Val Glu His Thr Gly Ala Ser Arg Thr Pro Val  
 40 45 50  
 cgg gat gct ctc cgc cgg tta gcc gca gac gag ttg atc att ttg gag 307  
 Arg Asp Ala Leu Arg Arg Leu Ala Ala Asp Glu Leu Ile Ile Leu Glu  
 55 60 65  
 cca cgt cag gcg cct atg gtg tgc cca ctt tgc ctt cgc cac att aag 355  
 Pro Arg Gln Ala Pro Met Val Ser Pro Leu Ser Leu Arg His Ile Lys  
 70 75 80 85  
 gat ctg ttt gag ttc cgc agg atc gtc gag gtc gca gcg ctt gag gaa 403  
 Asp Leu Phe Glu Phe Arg Arg Ile Val Glu Val Ala Ala Leu Glu Glu

90										95					100					
atc	tct	gtt	gga	gcg	agt	aaa	tca	ccg	cgt	atc	ttt	ggt	gag	ttt	tct	451				
Ile	Ser	Val	Gly	Ala	Ser	Lys	Ser	Pro	Arg	Ile	Phe	Gly	Glu	Phe	Ser					
			105						110					115						
acg	ttg	gcg	gca	gat	ttt	cga	gag	ctg	gaa	aac	tct	gca	gac	gat	gca	499				
Thr	Leu	Ala	Ala	Asp	Phe	Arg	Glu	Leu	Glu	Asn	Ser	Ala	Asp	Asp	Ala					
		120						125					130							
gat	ttc	acc	gcc	gat	ttt	agg	cga	ttg	acc	agt	aag	ttt	gat	gat	ctt	547				
Asp	Phe	Thr	Ala	Asp	Phe	Arg	Arg	Leu	Thr	Ser	Lys	Phe	Asp	Asp	Leu					
		135					140					145								
gtt	gca	gca	aat	act	cac	aac	caa	ttc	ctt	gga	cgc	agc	atc	tta	agt	595				
Val	Ala	Ala	Asn	Thr	His	Asn	Gln	Phe	Leu	Gly	Arg	Ser	Ile	Leu	Ser					
					155					160					165					
tta	aaa	ccg	cac	acc	acg	agg	ctg	cgg	atc	att	gcg	cat	tcc	gat	cat	643				
Leu	Lys	Pro	His	Thr	Thr	Arg	Leu	Arg	Ile	Ile	Ala	His	Ser	Asp	His					
				170					175					180						
gcg	cgt	ctg	cgc	caa	tcg	gtt	cag	gaa	cat	att	gaa	atg	tgt	gaa	gct	691				
Ala	Arg	Leu	Arg	Gln	Ser	Val	Gln	Glu	His	Ile	Glu	Met	Cys	Glu	Ala					
				185				190					195							
gtg	gcc	tca	gga	gat	tta	agg	tcg	gca	ggc	gct	gcg	tgt	aga	cag	cac	739				
Val	Ala	Ser	Gly	Asp	Leu	Arg	Ser	Ala	Gly	Ala	Ala	Cys	Arg	Gln	His					
		200						205				210								
ctg	atc	cat	gta	gaa	aag	agc	att	ttg	acc	gca	ttg	att	aat	gct	gat	787				
Leu	Ile	His	Val	Glu	Lys	Ser	Ile	Leu	Thr	Ala	Leu	Ile	Asn	Ala	Asp					
		215					220				225									
tct	acg	ggc	tcg	cag	ggc	att	gat	att	agg	tct	tagaaccagc	gtgcactgat				840				
Ser	Thr	Gly	Ser	Gln	Gly	Ile	Asp	Ile	Arg	Ser										
		230				235				240										
ggc																843				

&lt;210&gt; 132

&lt;211&gt; 240

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 132

Met	Val	Gln	Lys	Asp	Ala	Gln	Ala	Ser	Pro	Ala	Thr	Arg	Lys	Ala	Asp
1				5					10					15	

Gln	Val	Tyr	Thr	Gln	Ile	Arg	Arg	Glu	Ile	Glu	Asp	Gly	Thr	Leu	Asn
			20					25					30		

Pro	Gly	Gln	Arg	Met	Ser	Glu	Val	Trp	Leu	Val	Glu	His	Thr	Gly	Ala
		35					40					45			

Ser	Arg	Thr	Pro	Val	Arg	Asp	Ala	Leu	Arg	Arg	Leu	Ala	Ala	Asp	Glu
	50					55					60				

Leu	Ile	Ile	Leu	Glu	Pro	Arg	Gln	Ala	Pro	Met	Val	Ser	Pro	Leu	Ser
65					70					75					80



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<210> 133
<211> 774
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(751)
<223> RXA01537
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aagtgcctag gtgtgtcccc agtcctttaa gatcagtcac atg acg cag gca ata 115
                                         Met Thr Gln Ala Ile
                                           1                               5

gca gca tcc ctt gat tta gcg gct cga atc acc gcc aaa att gat caa 163
Ala Ala Ser Leu Asp Leu Ala Ala Arg Ile Thr Ala Lys Ile Asp Gln
                        10                               15                               20

gga gtg ctc act cca ggt act cga cta ccc gag gtt gct ttg gca gaa 211
Gly Val Leu Thr Pro Gly Thr Arg Leu Pro Glu Val Ala Leu Ala Glu
                        25                               30                               35

gaa ctt ggc gtt tca cgg aac acg ctg cgt gaa gct ttt cgg gta ctc 259

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<400> 134  
Met Thr Gln Ala Ile Ala Ala Ser Leu Asp Leu Ala Ala Arg Ile Thr  
1 5 10 15  
Ala Lys Ile Asp Gln Gly Val Leu Thr Pro Gly Thr Arg Leu Pro Glu  
20 25 30  
Val Ala Leu Ala Glu Glu Leu Gly Val Ser Arg Asn Thr Leu Arg Glu

<210> 135  
<211> 819  
<212> DNA  
<213> *Corynebacterium glutamicum*

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<220>  
<221> CDS  
<222> (101)..(796)  
<223> RXA02494
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<400> 135																		
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cgact	gcgtc	caaag	catct	ggg	cgccgaa	agg	aaaaatc	atg	acg	aga	atc	ctg	115					
								Met	Thr	Arg	Ile	Leu						
								1				5						
atc	gtt	gaa	gat	gag	gaa	tcg	tta	gca	gat	cct	ttg	gcc	ttt	ctt	ctt	163		
Ile	Val	Glu	Asp	Glu	Glu	Ser	Leu	Ala	Asp	Pro	Leu	Ala	Phe	Leu	Leu			
				10					15					20				
cgc	aaa	gaa	ggt	ttt	gac	acc	atc	atc	gcc	ggt	gat	ggc	cca	acc	gca	211		
Arg	Lys	Glu	Gly	Phe	Asp	Thr	Ile	Ile	Ala	Gly	Asp	Gly	Pro	Thr	Ala			
			25					30					35					

ctt gtg gag ttc agt cgc aac gaa atc gac atc gtc ctc tta gac ctc 259  
 Leu Val Glu Phe Ser Arg Asn Glu Ile Asp Ile Val Leu Leu Asp Leu  
           40                                  45                                  50

atg ctc cca ggc atg tct ggc acc gac gta tgc aaa gaa ctc cgc agc 307  
 Met Leu Pro Gly Met Ser Gly Thr Asp Val Cys Lys Glu Leu Arg Ser  
           55                                  60                                  65

gta tcc act gtt ccc gtc atc atg gtc acc gcc cgc gac tcc gag atc 355  
 Val Ser Thr Val Pro Val Ile Met Val Thr Ala Arg Asp Ser Glu Ile  
           70                                  75                                  80                                  85

gac aaa gtt gtt ggc ctc gaa ctc ggc gcc gat gat tat gta acc aag 403  
 Asp Lys Val Val Gly Leu Glu Leu Gly Ala Asp Asp Tyr Val Thr Lys  
                                   90                                  95                                  100

cca tat tct tcc cgc gaa ctc atc gcc cgc atc cgc gct gtc ctg cgc 451  
 Pro Tyr Ser Ser Arg Glu Leu Ile Ala Arg Ile Arg Ala Val Leu Arg  
                                   105                                  110                                  115

cga cgc gga gtt act gaa acc gaa gcc gaa gaa tta cca ctt gac gat 499  
 Arg Arg Gly Val Thr Glu Thr Glu Ala Glu Glu Leu Pro Leu Asp Asp  
                                   120                                  125                                  130

caa atc ctc gaa ggc ggc cgc gtc cgc atg gac gtc gat tcc cac acc 547  
 Gln Ile Leu Glu Gly Gly Arg Val Arg Met Asp Val Asp Ser His Thr  
           135                                  140                                  145

gtc acc gtc ggt ggc gaa cca gtg agc atg cca ctg aag gaa ttc gac 595  
 Val Thr Val Gly Gly Glu Pro Val Ser Met Pro Leu Lys Glu Phe Asp  
           150                                  155                                  160                                  165

ctt ctg gag tac ctc ctc cga aac gcc ggc cga gtc ctc acc cgc gga 643  
 Leu Leu Glu Tyr Leu Leu Arg Asn Ala Gly Arg Val Leu Thr Arg Gly  
                                   170                                  175                                  180

cag ctc atc gac cga att tgg ggc gca gat tac gtc ggc gac acc aaa 691  
 Gln Leu Ile Asp Arg Ile Trp Gly Ala Asp Tyr Val Gly Asp Thr Lys  
                                   185                                  190                                  195

acc ctc gac gtt cat gtc aaa agg ttg cgt tcc aag atc gaa gaa gag 739  
 Thr Leu Asp Val His Val Lys Arg Leu Arg Ser Lys Ile Glu Glu Glu  
           200                                  205                                  210

cca tct cgc cct cgt tac ctc gtg acc gtg cgt gga ttg ggc tac aaa 787  
 Pro Ser Arg Pro Arg Tyr Leu Val Thr Val Arg Gly Leu Gly Tyr Lys  
           215                                  220                                  225

ttc gag ctg tagggctctg ttaggccctg ttg 819  
 Phe Glu Leu  
 230

&lt;210&gt; 136

&lt;211&gt; 232

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 136

Met Thr Arg Ile Leu Ile Val Glu Asp Glu Glu Ser Leu Ala Asp Pro  
   1                                  5                                  10                                  15

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<210> 137
<211> 660
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(637)  
<223> RXA00029
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<400> 137  
tctctgccccg caccacgggt ggagcgaaac gtgtgcccaa acgcggtact ccccaaccgt 60

ttgccgtgcg ccaggtgagg accgagaggc caaacgcatt ttg gcc cag gcc acc 115  
Leu Ala Gln Ala Thr  
1 5

gcc caa cta atc gct gat gat gaa gca gta att ttc gac aac ggc acc 163  
 Ala Gln Leu Ile Ala Asp Asp Glu Ala Val Ile Phe Asp Asn Gly Thr  
                   10                                  15                                  20

acc tgc cag gca gtg gcc caa gag ttg gcg ggg cgt ccc atc acg gca 211  
 Thr Cys Gln Ala Val Ala Gln Glu Leu Ala Gly Arg Pro Ile Thr Ala  
                   25                                  30                                  35

ttg tgt ctg tct cta cat tcg gcg gtc gcc ctg gga agc cga gct ggc 259  
 Leu Cys Leu Ser Leu His Ser Ala Val Ala Leu Gly Ser Arg Ala Gly  
                   40                                  45                                  50

acc aac gtt ttc atc ccc ggc ggc ccc gtg gaa aac gac tca ctc gcc 307  
 Thr Asn Val Phe Ile Pro Gly Gly Pro Val Glu Asn Asp Ser Leu Ala  
                   55                                  60                                  65

tta tct ggc ccg gct gtg atc acc gcg tta cga gat ttc tcc gcc gat 355  
 Leu Ser Gly Pro Ala Val Ile Thr Ala Leu Arg Asp Phe Ser Ala Asp  
                   70                                  75                                  80                                  85

gtc gtg atc ctc ggt tcc tgc tct aca tca ctg gag cac ggg ttg gcc 403  
 Val Val Ile Leu Gly Ser Cys Ser Thr Ser Leu Glu His Gly Leu Ala  
                                   90                                  95                                  100

acc act acc tac gac gat gcg gaa aac aag cgc gca gcc atc cat gct 451  
 Thr Thr Thr Tyr Asp Asp Ala Glu Asn Lys Arg Ala Ala Ile His Ala  
                   105                                  110                                  115

gcc acc cga cga atc ctt gtg gtg tcc gcc cgt aaa ctc aac cac gtt 499  
 Ala Thr Arg Arg Ile Leu Val Val Ser Ala Arg Lys Leu Asn His Val  
                   120                                  125                                  130

tcc act ttc cgt ttc gca gac gtc gcg gac tta cac cag ctg gtc aca 547  
 Ser Thr Phe Arg Phe Ala Asp Val Ala Asp Leu His Gln Leu Val Thr  
                   135                                  140                                  145

acc tcc gat gcg cca cgg gag att ctc gcc gag atc cgg gat ctc ggc 595  
 Thr Ser Asp Ala Pro Arg Glu Ile Leu Ala Glu Ile Arg Asp Leu Gly  
                   150                                  155                                  160                                  165

gtg cag gtt att act gtt ccc gcc cct gac gag caa cga agt 637  
 Val Gln Val Ile Thr Val Pro Ala Pro Asp Glu Gln Arg Ser  
                   170                                  175

taactcttca tgggtgctga gca 660

&lt;210&gt; 138

&lt;211&gt; 179

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 138

Leu Ala Gln Ala Thr Ala Gln Leu Ile Ala Asp Asp Glu Ala Val Ile  
   1                  5                                  10                                  15

Phe Asp Asn Gly Thr Thr Cys Gln Ala Val Ala Gln Glu Leu Ala Gly  
                   20                                  25                                  30

Arg Pro Ile Thr Ala Leu Cys Leu Ser Leu His Ser Ala Val Ala Leu  
                   35                                  40                                  45

Gly Ser Arg Ala Gly Thr Asn Val Phe Ile Pro Gly Gly Pro Val Glu  
 50 55 60  
 Asn Asp Ser Leu Ala Leu Ser Gly Pro Ala Val Ile Thr Ala Leu Arg  
 65 70 75 80  
 Asp Phe Ser Ala Asp Val Val Ile Leu Gly Ser Cys Ser Thr Ser Leu  
 85 90 95  
 Glu His Gly Leu Ala Thr Thr Thr Tyr Asp Asp Ala Glu Asn Lys Arg  
 100 105 110  
 Ala Ala Ile His Ala Ala Thr Arg Arg Ile Leu Val Val Ser Ala Arg  
 115 120 125  
 Lys Leu Asn His Val Ser Thr Phe Arg Phe Ala Asp Val Ala Asp Leu  
 130 135 140  
 His Gln Leu Val Thr Thr Ser Asp Ala Pro Arg Glu Ile Leu Ala Glu  
 145 150 155 160  
 Ile Arg Asp Leu Gly Val Gln Val Ile Thr Val Pro Ala Pro Asp Glu  
 165 170 175  
 Gln Arg Ser

<210> 139  
 <211> 762  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(739)  
 <223> RXA00655

<400> 139  
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 Val Ala Ala Ser Ala 5  
 1  
 tca ggc aag agt aaa aca agt gcc ggg gca aac cgt cgt cgc aat cga 163  
 Ser Gly Lys Ser Lys Thr Ser Ala Gly Ala Asn Arg Arg Arg Asn Arg 20  
 10 15  
 cca agc ccc cga cag cgt ctc ctc gat agc gca acc aac ctt ttc acc 211  
 Pro Ser Pro Arg Gln Arg Leu Leu Asp Ser Ala Thr Asn Leu Phe Thr 35  
 25 30  
 aca gaa ggt att cgc gtc atc ggt att gat cgt atc ctc cgt gaa gct 259  
 Thr Glu Gly Ile Arg Val Ile Gly Ile Asp Arg Ile Leu Arg Glu Ala 50  
 40 45  
 gac gtg gcg aag gcg agc ctc tat tcc ctt ttc gga tcg aag gac gcc 307  
 Asp Val Ala Lys Ala Ser Leu Tyr Ser Leu Phe Gly Ser Lys Asp Ala 65  
 55 60

ttg gtt att gca tac ctg gag aac ctc gat cag ctg tgg cgt gaa gcg 355  
 Leu Val Ile Ala Tyr Leu Glu Asn Leu Asp Gln Leu Trp Arg Glu Ala  
 70 75 80 85  
 tgg cgt gag cgc acc gtc ggt atg aag gat ccg gaa gat aaa atc atc 403  
 Trp Arg Glu Arg Thr Val Gly Met Lys Asp Pro Glu Asp Lys Ile Ile  
 90 95 100  
 gcg ttc ttt gat cag tgc att gag gaa gaa cca gaa aaa gat ttc cgc 451  
 Ala Phe Phe Asp Gln Cys Ile Glu Glu Glu Pro Glu Lys Asp Phe Arg  
 105 110 115  
 ggc tcg cac ttt cag aat gcg gct agt gag tac cct cgc ccc gaa act 499  
 Gly Ser His Phe Gln Asn Ala Ala Ser Glu Tyr Pro Arg Pro Glu Thr  
 120 125 130  
 gat agc gaa aag ggc att gtt gca gca gtg tta gag cac cgc gag tgg 547  
 Asp Ser Glu Lys Gly Ile Val Ala Ala Val Leu Glu His Arg Glu Trp  
 135 140 145  
 tgt cat aag act ctg act gat ttg ctc act gag aag aac ggc tac cca 595  
 Cys His Lys Thr Leu Thr Asp Leu Leu Thr Glu Lys Asn Gly Tyr Pro  
 150 155 160 165  
 ggc acc acc cag gcg aat cag ctg ttg gtg ttc ctt gat ggt gga ctt 643  
 Gly Thr Thr Gln Ala Asn Gln Leu Leu Val Phe Leu Asp Gly Gly Leu  
 170 175 180  
 gct gga tct cga ttg gtc cac aac atc agt cct ctt gag acg gct cgc 691  
 Ala Gly Ser Arg Leu Val His Asn Ile Ser Pro Leu Glu Thr Ala Arg  
 185 190 195  
 gat ttg gct cgg cag ttg ttg tcg gct cca cct gcg gac tac tca att 739  
 Asp Leu Ala Arg Gln Leu Leu Ser Ala Pro Pro Ala Asp Tyr Ser Ile  
 200 205 210  
 tagtttcttc attttccgaa ggg 762

&lt;210&gt; 140

&lt;211&gt; 213

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 140

Val Ala Ala Ser Ala Ser Gly Lys Ser Lys Thr Ser Ala Gly Ala Asn  
 1 5 10 15

Arg Arg Arg Asn Arg Pro Ser Pro Arg Gln Arg Leu Leu Asp Ser Ala  
 20 25 30

Thr Asn Leu Phe Thr Thr Glu Gly Ile Arg Val Ile Gly Ile Asp Arg  
 35 40 45

Ile Leu Arg Glu Ala Asp Val Ala Lys Ala Ser Leu Tyr Ser Leu Phe  
 50 55 60

Gly Ser Lys Asp Ala Leu Val Ile Ala Tyr Leu Glu Asn Leu Asp Gln  
 65 70 75 80



<400> 141																	
cttatcgacg agctccaagg ctggaccgtg gtacgtgccca cttccctgtc gtggctgaaa																	60
taaaaaatccc cgaaacctcc ttggacacat cgcccacaaa																	
											ttg	ggt	gcg	cac	tcc		115
											Leu	Gly	Ala	His	Ser		
											1				5		
gcc aac tcc atc cgt ggt gtg atc gac cgt ctc gat gcc tcc acc gtg																	163
Ala	Asn	Ser	Ile	Arg	Gly	Val	Ile	Asp	Arg	Leu	Asp	Ala	Ser	Thr	Val		
				10					15					20			
gtg atc gtt gcc gat gtc cac tgg gcc gac gtg gaa tcc atg caa aaa																	211
Val	Ile	Val	Ala	Asp	Val	His	Trp	Ala	Asp	Val	Glu	Ser	Met	Gln	Lys		
			25					30					35				
ctc atc gaa tat tcc atg cgc atg gtt tct ggc cgt ttc gca ctc atc																	259
Leu	Ile	Glu	Tyr	Ser	Met	Arg	Met	Val	Ser	Gly	Arg	Phe	Ala	Leu	Ile		
		40					45					50					
atg att ggc ctt gat gaa gag aac tta gtg ttc cac gat gag gtg gtc																	307
Met	Ile	Gly	Leu	Asp	Glu	Glu	Asn	Leu	Val	Phe	His	Asp	Glu	Val	Val		
	55					60					65						

tcg ctc ccc tcc atc gca gac tcc acc tac gta ttg ccg ccg atg agt	355
Ser Leu Pro Ser Ile Ala Asp Ser Thr Tyr Val Leu Pro Pro Met Ser	
70 75 80 85	
att gaa gaa atc cgc cag ctt gcg ctt acc gat gtc cgc ggc cgc atc	403
Ile Glu Glu Ile Arg Gln Leu Ala Leu Thr Asp Val Arg Gly Arg Ile	
90 95 100	
agc acc acc acc gcc aca gac atc cag cgc atc acc ggc ggc atc tac	451
Ser Thr Thr Thr Ala Thr Asp Ile Gln Arg Ile Thr Gly Gly Ile Tyr	
105 110 115	
ggg cga gtc aaa gaa gtc ctc cac tcg gaa tcc ccc gat cac tgg cga	499
Gly Arg Val Lys Glu Val Leu His Ser Glu Ser Pro Asp His Trp Arg	
120 125 130	
atg ccc aac cca aat att ccc atc cca caa agc tgg cat gcc aac ctg	547
Met Pro Asn Pro Asn Ile Pro Ile Pro Gln Ser Trp His Ala Asn Leu	
135 140 145	
ttg aga cgc atc acc aac gaa gaa gtc tgg cat gta cta ctc gcc gtc	595
Leu Arg Arg Ile Thr Asn Glu Glu Val Trp His Val Leu Leu Ala Val	
150 155 160 165	
gct gtc ctt ccc tcc gga ggc ccc att gac ctg gta aaa ctc ata ggc	643
Ala Val Leu Pro Ser Gly Gly Pro Ile Asp Leu Val Lys Leu Ile Gly	
170 175 180	
aac gac ccc acg ggc atg ctt tgc gac gac gcc gtc cgc tca ggc ctg	691
Asn Asp Pro Thr Gly Met Leu Cys Asp Asp Ala Val Arg Ser Gly Leu	
185 190 195	
ctc cgc gtg ctg ccg tct gac ggc caa cca caa gtg gat ttg gtc ctg	739
Leu Arg Val Leu Pro Ser Asp Gly Gln Pro Gln Val Asp Leu Val Leu	
200 205 210	
ccg atc gac cgc gcc gta ctg caa tca cgc act ccg ctc aac att ctg	787
Pro Ile Asp Arg Ala Val Leu Gln Ser Arg Thr Pro Leu Asn Ile Leu	
215 220 225	
gcg cag ttg cac cac aag gca gcc gaa tat tac ggc aag tgg aat caa	835
Ala Gln Leu His His Lys Ala Ala Glu Tyr Tyr Gly Lys Trp Asn Gln	
230 235 240 245	
aaa gat gcc caa ctg gag cac gaa gca ttt gct gca att gat cca aat	883
Lys Asp Ala Gln Leu Glu His Glu Ala Phe Ala Ala Ile Asp Pro Asn	
250 255 260	
gat cca gca gtg cga gcc cta gcg cag cgc gga tat gcg ttg ggt agg	931
Asp Pro Ala Val Arg Ala Leu Ala Gln Arg Gly Tyr Ala Leu Gly Arg	
265 270 275	
act ggc cac tgg atg gaa tcg gca cac gcc cta tct ctt gcc gcg aac	979
Thr Gly His Trp Met Glu Ser Ala His Ala Leu Ser Leu Ala Ala Asn	
280 285 290	
cgc act gca cac caa gaa gaa tca aat aag tac ttg ctg gag tcc atc	1027
Arg Thr Ala His Gln Glu Glu Ser Asn Lys Tyr Leu Leu Glu Ser Ile	
295 300 305	
gat tca ctg atc gcc gcc gcc gat ctc ccc caa gct cga tcc aga gca	1075

Asp 310	Ser	Leu	Ile	Ala	Ala 315	Ala	Asp	Leu	Pro	Gln 320	Ala	Arg	Ser	Arg	Ala 325	
tcc	acc	ctt	gat	ctt	gga	gaa	acc	ggc	att	caa	caa	gac	tca	atg	ctg	1123
Ser	Thr	Leu	Asp	Leu 330	Gly	Glu	Thr	Gly	Ile 335	Gln	Gln	Asp	Ser	Met	Leu 340	
ggc	tac	ctg	gca	atc	cac	gaa	ggc	cgg	cgc	ctc	gaa	gca	cgc	aat	ctc	1171
Gly	Tyr	Leu	Ala 345	Ile	His	Glu	Gly	Arg 350	Arg	Leu	Glu	Ala	Arg	Asn 355	Leu	
ctt	cat	cgt	gct	tct	gaa	gaa	ttg	ctg	gcg	cag	cac	ccg	att	gat	ccg	1219
Leu	His	Arg 360	Ala	Ser	Glu	Glu	Leu 365	Leu	Ala	Gln	His	Pro 370	Ile	Asp	Pro	
atc	cac	ggc	ccc	cgc	atg	gct	cag	cgc	aaa	gta	ctg	tta	aac	tta	gtg	1267
Ile	His 375	Gly	Pro	Arg	Met	Ala 380	Gln	Arg	Lys	Val	Leu 385	Leu	Asn	Leu	Val	
gac	tgg	aat	cca	gaa	gaa	ctc	ctg	gtg	tgg	gct	gat	aga	gca	gtc	gca	1315
Asp	Trp	Asn	Pro	Glu	Glu 395	Leu	Leu	Val	Trp	Ala 400	Asp	Arg	Ala	Val	Ala 405	
tgg	act	gaa	gag	gat	gct	ggc	gaa	aag	gtt	gag	gcc	caa	gct	att	tcc	1363
Trp	Thr	Glu	Glu	Asp 410	Ala	Gly	Glu	Lys	Val 415	Glu	Ala	Gln	Ala	Ile 420	Ser	
ctc	att	gga	caa	tcc	atc	ctc	gat	ggc	tgc	ctc	ccc	gaa	gat	aaa	ccc	1411
Leu	Ile	Gly 425	Gln	Ser	Ile	Leu	Asp	Gly 430	Cys	Leu	Pro	Glu	Asp 435	Lys	Pro	
atc	ccc	ggt	gaa	acc	acc	ctt	cac	gca	caa	cgc	cgc	cac	atg	gca	atg	1459
Ile	Pro 440	Gly	Glu	Thr	Thr	Leu	His 445	Ala	Gln	Arg	Arg	His 450	Met	Ala	Met	
ggc	tgg	ctt	tcc	atg	gtt	cac	gat	gat	cca	gta	act	gca	cgt	caa	aag	1507
Gly	Trp	Leu	Ser	Met	Val	His 460	Asp	Asp	Pro	Val	Thr 465	Ala	Arg	Gln	Lys	
ctt	gaa	cgt	cgc	aca	tcc	atc	aat	ggt	tca	gaa	cgc	atc	agt	ttg	tgg	1555
Leu	Glu	Arg	Arg	Thr	Ser 475	Ile	Asn	Gly	Ser	Glu 480	Arg	Ile	Ser	Leu 485	Trp	
caa	gac	gga	tgg	ctg	gct	cgg	tcc	cta	ctg	ctg	ctc	ggc	gaa	tgg	gag	1603
Gln	Asp	Gly	Trp	Leu 490	Ala	Arg	Ser	Leu	Leu 495	Leu	Leu	Gly	Glu	Trp 500	Glu	
tcc	gca	gca	cgc	acc	gta	gaa	atc	ggt	ctg	gcc	cgc	gcc	gaa	cag	ttt	1651
Ser	Ala	Ala	Arg	Thr 505	Val	Glu	Ile	Gly 510	Leu	Ala	Arg	Ala	Glu 515	Gln	Phe	
ggc	atc	cgc	ttc	ctc	gaa	cca	ctg	tta	ctg	tgg	tcg	ggc	gcc	aca	att	1699
Gly	Ile	Arg	Phe	Leu	Glu	Pro	Leu 525	Leu	Leu	Trp	Ser	Gly 530	Ala	Thr	Ile	
gca	aca	gcc	cgc	gga	aac	tct	gac	ttg	gca	cga	aat	tac	atg	agc	aga	1747
Ala	Thr 535	Ala	Arg	Gly	Asn	Ser 540	Asp	Leu	Ala	Arg	Asn 545	Tyr	Met	Ser	Arg	
ctg	tcc	acc	gat	caa	gac	tcc	ttc	atc	gtc	caa	tct	atg	cca	tct	gcg	1795
Leu	Ser	Thr	Asp	Gln	Asp	Ser	Phe	Ile	Val	Gln	Ser	Met	Pro	Ser	Ala	

550		555		560		565	
atg tgt cgc atg tgg gtc cac cgc cat aga aat gaa atc ccc ggt gcg	1843						
Met Cys Arg Met Trp Val His Arg His Arg Asn Glu Ile Pro Gly Ala							
		570		575		580	
atc gtg gcc gga gaa caa ttg gaa aaa atc gcc gca cac aaa cac gtc	1891						
Ile Val Ala Gly Glu Gln Leu Glu Lys Ile Ala Ala His Lys His Val		585		590		595	
aac gca cct gga ttc tgg cca tgg caa gac gtc cac gca acg cat ctc	1939						
Asn Ala Pro Gly Phe Trp Pro Trp Gln Asp Val His Ala Thr His Leu		600		605		610	
atc cgc atc ggc gaa act gag cgc gcc cag gag tta gtg aac tcc acg	1987						
Ile Arg Ile Gly Glu Thr Glu Arg Ala Gln Glu Leu Val Asn Ser Thr		615		620		625	
ctt gag gag ctc aga ggc tcc gat atc atg tct gcc cac gca aaa att	2035						
Leu Glu Glu Leu Arg Gly Ser Asp Ile Met Ser Ala His Ala Lys Ile		630		635		640	645
gcc gtt ccc gac gcc atg ttg atg atc cac cac gga gat gtg aaa aag	2083						
Ala Val Pro Asp Ala Met Leu Met Ile His His Gly Asp Val Lys Lys		650		655		660	
gga ttt aag cgt ttc gac gac gcc ctc gat atg atc gat ccc ctc acc	2131						
Gly Phe Lys Arg Phe Asp Asp Ala Leu Asp Met Ile Asp Pro Leu Thr		665		670		675	
ctc ccc tac tat cgg gca cgc atc tgc ttt gaa tac ggc cag gcc ctg	2179						
Leu Pro Tyr Tyr Arg Ala Arg Ile Cys Phe Glu Tyr Gly Gln Ala Leu		680		685		690	
aga cgc cag ggg caa cgt cga cgt gct gat gaa caa ttt gcc cgt gca	2227						
Arg Arg Gln Gly Gln Arg Arg Arg Ala Asp Glu Gln Phe Ala Arg Ala		695		700		705	
gct tcc cta ttc caa gac atg ggc gcc gac gcg atg gtc acc cta gcc	2275						
Ala Ser Leu Phe Gln Asp Met Gly Ala Asp Ala Met Val Thr Leu Ala		710		715		720	725
aac cga gaa cgc cgg gtg ggt ggc ctt ggt caa cga tcc gag caa gcc	2323						
Asn Arg Glu Arg Arg Val Gly Gly Leu Gly Gln Arg Ser Glu Gln Ala		730		735		740	
ggt ggg ctc acc cct cag gaa tat gaa att gcc cga tta gtg tca tct	2371						
Gly Gly Leu Thr Pro Gln Glu Tyr Glu Ile Ala Arg Leu Val Ser Ser		745		750		755	
ggg cat gcc aac cga gag gtc gca cag gag ctt ttc ctc tcg cct aag	2419						
Gly His Ala Asn Arg Glu Val Ala Gln Glu Leu Phe Leu Ser Pro Lys		760		765		770	
acc gtg gaa tac cat ctc acc cgg gtg tac aaa aag ctc gga ata cgc	2467						
Thr Val Glu Tyr His Leu Thr Arg Val Tyr Lys Lys Leu Gly Ile Arg		775		780		785	
aat cgg atg gaa ctt gcc gag gct ttg aag aag tac tca cac gac gcc	2515						
Asn Arg Met Glu Leu Ala Glu Ala Leu Lys Lys Tyr Ser His Asp Ala		790		795		800	805

tagcagcgga tatgtttgcg gac

2538

&lt;210&gt; 142

&lt;211&gt; 805

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 142

Leu Gly Ala His Ser Ala Asn Ser Ile Arg Gly Val Ile Asp Arg Leu  
 1 5 10 15

Asp Ala Ser Thr Val Val Ile Val Ala Asp Val His Trp Ala Asp Val  
 20 25 30

Glu Ser Met Gln Lys Leu Ile Glu Tyr Ser Met Arg Met Val Ser Gly  
 35 40 45

Arg Phe Ala Leu Ile Met Ile Gly Leu Asp Glu Glu Asn Leu Val Phe  
 50 55 60

His Asp Glu Val Val Ser Leu Pro Ser Ile Ala Asp Ser Thr Tyr Val  
 65 70 75 80

Leu Pro Pro Met Ser Ile Glu Glu Ile Arg Gln Leu Ala Leu Thr Asp  
 85 90 95

Val Arg Gly Arg Ile Ser Thr Thr Thr Ala Thr Asp Ile Gln Arg Ile  
 100 105 110

Thr Gly Gly Ile Tyr Gly Arg Val Lys Glu Val Leu His Ser Glu Ser  
 115 120 125

Pro Asp His Trp Arg Met Pro Asn Pro Asn Ile Pro Ile Pro Gln Ser  
 130 135 140

Trp His Ala Asn Leu Leu Arg Arg Ile Thr Asn Glu Glu Val Trp His  
 145 150 155 160

Val Leu Leu Ala Val Ala Val Leu Pro Ser Gly Gly Pro Ile Asp Leu  
 165 170 175

Val Lys Leu Ile Gly Asn Asp Pro Thr Gly Met Leu Cys Asp Asp Ala  
 180 185 190

Val Arg Ser Gly Leu Leu Arg Val Leu Pro Ser Asp Gly Gln Pro Gln  
 195 200 205

Val Asp Leu Val Leu Pro Ile Asp Arg Ala Val Leu Gln Ser Arg Thr  
 210 215 220

Pro Leu Asn Ile Leu Ala Gln Leu His His Lys Ala Ala Glu Tyr Tyr  
 225 230 235 240

Gly Lys Trp Asn Gln Lys Asp Ala Gln Leu Glu His Glu Ala Phe Ala  
 245 250 255

Ala Ile Asp Pro Asn Asp Pro Ala Val Arg Ala Leu Ala Gln Arg Gly  
 260 265 270

Tyr Ala Leu Gly Arg Thr Gly His Trp Met Glu Ser Ala His Ala Leu  
 275 280 285  
 Ser Leu Ala Ala Asn Arg Thr Ala His Gln Glu Glu Ser Asn Lys Tyr  
 290 295 300  
 Leu Leu Glu Ser Ile Asp Ser Leu Ile Ala Ala Ala Asp Leu Pro Gln  
 305 310 315 320  
 Ala Arg Ser Arg Ala Ser Thr Leu Asp Leu Gly Glu Thr Gly Ile Gln  
 325 330 335  
 Gln Asp Ser Met Leu Gly Tyr Leu Ala Ile His Glu Gly Arg Arg Leu  
 340 345 350  
 Glu Ala Arg Asn Leu Leu His Arg Ala Ser Glu Glu Leu Leu Ala Gln  
 355 360 365  
 His Pro Ile Asp Pro Ile His Gly Pro Arg Met Ala Gln Arg Lys Val  
 370 375 380  
 Leu Leu Asn Leu Val Asp Trp Asn Pro Glu Glu Leu Leu Val Trp Ala  
 385 390 395 400  
 Asp Arg Ala Val Ala Trp Thr Glu Glu Asp Ala Gly Glu Lys Val Glu  
 405 410 415  
 Ala Gln Ala Ile Ser Leu Ile Gly Gln Ser Ile Leu Asp Gly Cys Leu  
 420 425 430  
 Pro Glu Asp Lys Pro Ile Pro Gly Glu Thr Thr Leu His Ala Gln Arg  
 435 440 445  
 Arg His Met Ala Met Gly Trp Leu Ser Met Val His Asp Asp Pro Val  
 450 455 460  
 Thr Ala Arg Gln Lys Leu Glu Arg Arg Thr Ser Ile Asn Gly Ser Glu  
 465 470 475 480  
 Arg Ile Ser Leu Trp Gln Asp Gly Trp Leu Ala Arg Ser Leu Leu Leu  
 485 490 495  
 Leu Gly Glu Trp Glu Ser Ala Ala Arg Thr Val Glu Ile Gly Leu Ala  
 500 505 510  
 Arg Ala Glu Gln Phe Gly Ile Arg Phe Leu Glu Pro Leu Leu Leu Trp  
 515 520 525  
 Ser Gly Ala Thr Ile Ala Thr Ala Arg Gly Asn Ser Asp Leu Ala Arg  
 530 535 540  
 Asn Tyr Met Ser Arg Leu Ser Thr Asp Gln Asp Ser Phe Ile Val Gln  
 545 550 555 560  
 Ser Met Pro Ser Ala Met Cys Arg Met Trp Val His Arg His Arg Asn  
 565 570 575  
 Glu Ile Pro Gly Ala Ile Val Ala Gly Glu Gln Leu Glu Lys Ile Ala  
 580 585 590  
 Ala His Lys His Val Asn Ala Pro Gly Phe Trp Pro Trp Gln Asp Val

595					600					605					
His	Ala	Thr	His	Leu	Ile	Arg	Ile	Gly	Glu	Thr	Glu	Arg	Ala	Gln	Glu
610					615					620					
Leu	Val	Asn	Ser	Thr	Leu	Glu	Glu	Leu	Arg	Gly	Ser	Asp	Ile	Met	Ser
625					630					635					640
Ala	His	Ala	Lys	Ile	Ala	Val	Pro	Asp	Ala	Met	Leu	Met	Ile	His	His
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Gly	Asp	Val	Lys	Lys	Gly	Phe	Lys	Arg	Phe	Asp	Asp	Ala	Leu	Asp	Met
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Ile	Asp	Pro	Leu	Thr	Leu	Pro	Tyr	Tyr	Arg	Ala	Arg	Ile	Cys	Phe	Glu
		675					680					685			
Tyr	Gly	Gln	Ala	Leu	Arg	Arg	Gln	Gly	Gln	Arg	Arg	Arg	Ala	Asp	Glu
	690					695					700				
Gln	Phe	Ala	Arg	Ala	Ala	Ser	Leu	Phe	Gln	Asp	Met	Gly	Ala	Asp	Ala
705				710						715					720
Met	Val	Thr	Leu	Ala	Asn	Arg	Glu	Arg	Arg	Val	Gly	Gly	Leu	Gly	Gln
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Arg	Ser	Glu	Gln	Ala	Gly	Gly	Leu	Thr	Pro	Gln	Glu	Tyr	Glu	Ile	Ala
			740					745					750		
Arg	Leu	Val	Ser	Ser	Gly	His	Ala	Asn	Arg	Glu	Val	Ala	Gln	Glu	Leu
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Phe	Leu	Ser	Pro	Lys	Thr	Val	Glu	Tyr	His	Leu	Thr	Arg	Val	Tyr	Lys
	770					775					780				
Lys	Leu	Gly	Ile	Arg	Asn	Arg	Met	Glu	Leu	Ala	Glu	Ala	Leu	Lys	Lys
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Tyr	Ser	His	Asp	Ala											
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 <223> FRXA00645

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 Leu Gly Ala His Ser  
 1 5  
 gcc aac tcc atc cgt ggt gtg atc gac cgt ctc gat gcc tcc acc gtg 163  
 Ala Asn Ser Ile Arg Gly Val Ile Asp Arg Leu Asp Ala Ser Thr Val

10										15										20									
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Val	Ile	Val	Ala	Asp	Val	His	Trp	Ala	Asp	Val	Glu	Ser	Met	Gln	Lys														
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ctc	atc	gaa	tat	tcc	atg	cgc	atg	gtt	tct	ggc	cgt	ttc	gca	ctc	atc					259									
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Ile	Glu	Glu	Ile	Arg	Gln	Leu	Ala	Leu	Thr	Asp	Val	Arg	Gly	Arg	Ile														
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agc	acc	acc	acc	gcc	aca	gac	atc	cag	cgc	atc	acc	ggc	ggc	atc	tac					451									
Ser	Thr	Thr	Thr	Ala	Thr	Asp	Ile	Gln	Arg	Ile	Thr	Gly	Gly	Ile	Tyr														
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Gly	Arg	Val	Lys	Glu	Val	Leu	His	Ser	Glu	Ser	Pro	Asp	His	Trp	Arg														
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Met	Pro	Asn	Pro	Asn	Ile	Pro	Ile	Pro	Gln	Ser	Trp	His	Ala	Asn	Leu														
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Ala	Val	Leu	Pro	Ser	Gly	Gly	Pro	Ile	Asp	Leu	Val	Lys	Leu	Ile	Gly														
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aac	gac	ccc	acg	ggc	atg	ctt	tgc	gac	gac	gcc	gtc	cgc	tca	ggc	ctg					691									
Asn	Asp	Pro	Thr	Gly	Met	Leu	Cys	Asp	Asp	Ala	Val	Arg	Ser	Gly	Leu														
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ctc	cgc	gtg	ctg	ccg	tct	gac	ggc	caa	cca	caa	gtg	gat	ttg	gtc	ctg					739									
Leu	Arg	Val	Leu	Pro	Ser	Asp	Gly	Gln	Pro	Gln	Val	Asp	Leu	Val	Leu														
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ccg	atc	gac	cgc	gcc	gta	ctg	caa	tca	cgc	act	ccg	ctc	aac	att	ctg					787									
Pro	Ile	Asp	Arg	Ala	Val	Leu	Gln	Ser	Arg	Thr	Pro	Leu	Asn	Ile	Leu														
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gcg	cag	ttg	cac	cac	aag	gca	gcc	gaa	tat	tac	ggc	aag	tgg	aat	caa					835									
Ala	Gln	Leu	His	His	Lys	Ala	Ala	Glu	Tyr	Tyr	Gly	Lys	Trp	Asn	Gln														
230					235				240					245															
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Lys	Asp	Ala	Gln	Leu	Glu	His	Glu	Ala	Phe	Ala	Ala	Ile	Asp	Pro	Asn														
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gat	cca	gca	gtg	cga	gcc	cta	gcg	cag	cgc	gga	tat	gcg	ttg	ggg	agg	931
Asp	Pro	Ala	Val	Arg	Ala	Leu	Ala	Gln	Arg	Gly	Tyr	Ala	Leu	Gly	Arg	
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act	ggc	cac	tgg	atg	gaa	tcg	gca	cac	gcc	cta	tct	ctt	gcc	gcg	aac	979
Thr	Gly	His	Trp	Met	Glu	Ser	Ala	His	Ala	Leu	Ser	Leu	Ala	Ala	Asn	
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Arg	Thr	Ala	His	Gln	Glu	Glu	Ser	Asn	Lys	Tyr	Leu	Leu	Glu	Ser	Ile	
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Asp	Ser	Leu	Ile	Ala	Ala	Ala	Asp	Leu	Pro	Gln	Ala	Arg	Ser	Arg	Ala	
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Ser	Thr	Leu	Asp	Leu	Gly	Glu	Thr	Gly	Ile	Gln	Gln	Asp	Ser	Met	Leu	
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ggc	tac	ctg	gca	atc	cac	gaa	ggc	cgg	cgc	ctc	gaa	gca	cgc	aat	ctc	1171
Gly	Tyr	Leu	Ala	Ile	His	Glu	Gly	Arg	Arg	Leu	Glu	Ala	Arg	Asn	Leu	
			345					350					355			
ctt	cat	cgt	gct	tct	gaa	gaa	ttg	ctg	gcg	cag	cac	ccg	att	gat	ccg	1219
Leu	His	Arg	Ala	Ser	Glu	Glu	Leu	Leu	Ala	Gln	His	Pro	Ile	Asp	Pro	
		360					365					370				
atc	cac	ggc	ccc	cgc	atg	gct	cag	cgc	aaa	gta	ctg	tta	aac	tta	gtg	1267
Ile	His	Gly	Pro	Arg	Met	Ala	Gln	Arg	Lys	Val	Leu	Leu	Asn	Leu	Val	
	375					380					385					
gac	tgg	aat	cca	gaa	gaa	ctc	ctg	gtg	tgg	gct	gat	aga	gca	gtc	gca	1315
Asp	Trp	Asn	Pro	Glu	Glu	Leu	Leu	Val	Trp	Ala	Asp	Arg	Ala	Val	Ala	
390					395					400					405	
tgg	act	gaa	gag	gat	gct	ggc	gaa	aag	ggt	gag	gcc	caa	gct	att	tcc	1363
Trp	Thr	Glu	Glu	Asp	Ala	Gly	Glu	Lys	Val	Glu	Ala	Gln	Ala	Ile	Ser	
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ctc	att	gga	caa	tcc	atc	ctc	gat	ggc	tgc	ctc	ccc	gaa	gat	aaa	ccc	1411
Leu	Ile	Gly	Gln	Ser	Ile	Leu	Asp	Gly	Cys	Leu	Pro	Glu	Asp	Lys	Pro	
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Ile	Pro	Gly	Glu	Thr	Thr	Leu	His	Ala	Gln	Arg	Arg	His	Met	Ala	Met	
		440					445					450				
ggc	tgg	ctt	tcc	atg	ggt	cac	gat	gat	cca	gta	act	gca	cgt	caa	aag	1507
Gly	Trp	Leu	Ser	Met	Val	His	Asp	Asp	Pro	Val	Thr	Ala	Arg	Gln	Lys	
	455					460					465					
ctt	gaa	cgt	cgc	aca	tcc	atc	aat	ggt	tca	gaa	cgc	atc	agt	ttg	tgg	1555
Leu	Glu	Arg	Arg	Thr	Ser	Ile	Asn	Gly	Ser	Glu	Arg	Ile	Ser	Leu	Trp	
470					475					480					485	
caa	gac	gga	tgg	ctg	gct	cgg	tcc	cta	ctg	ctg	ctc	ggc	gaa	tgg	gag	1603
Gln	Asp	Gly	Trp	Leu	Ala	Arg	Ser	Leu	Leu	Leu	Leu	Gly	Glu	Trp	Glu	
				490					495					500		

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Ser Ala Ala Arg Thr Val Glu Ile Gly Leu Ala Arg Ala Glu Gln Phe	
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ggc atc cgc ttc ctc gaa cca ctg tta ctg tgg tcg ggc gcc aca att	1699
Gly Ile Arg Phe Leu Glu Pro Leu Leu Trp Ser Gly Ala Thr Ile	
520 525 530	
gca aca gcc cgc gga aac tct gac ttg gca cga aat tac atg agc aga	1747
Ala Thr Ala Arg Gly Asn Ser Asp Leu Ala Arg Asn Tyr Met Ser Arg	
535 540 545	
ctg tcc acc gat caa gac tcc ttc atc gtc caa tct atg cca tct gcg	1795
Leu Ser Thr Asp Gln Asp Ser Phe Ile Val Gln Ser Met Pro Ser Ala	
550 555 560 565	
atg tgt cgc atg tgg gtc cac cgc cat aga aat gaa atc ccc ggt gcg	1843
Met Cys Arg Met Trp Val His Arg His Arg Asn Glu Ile Pro Gly Ala	
570 575 580	
atc gtg gcc gga gaa caa ttg gaa aaa atc gcc gca cac aaa cac gtc	1891
Ile Val Ala Gly Glu Gln Leu Glu Lys Ile Ala Ala His Lys His Val	
585 590 595	
aac gca cct gga ttc tgg cca tgg caa gac gtc cac gca acg cat ctc	1939
Asn Ala Pro Gly Phe Trp Pro Trp Gln Asp Val His Ala Thr His Leu	
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Ile Arg Ile Gly Glu Thr Glu Arg Ala Gln Glu Leu Val Asn Ser Thr	
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ctt gag gag ctc aga ggc tcc gat atc atg tct gcc cac gca aaa att	2035
Leu Glu Glu Leu Arg Gly Ser Asp Ile Met Ser Ala His Ala Lys Ile	
630 635 640 645	
gcc gtt ccc gac gcc atg ttg atg atc cac cac gga gat gtg aaa aag	2083
Ala Val Pro Asp Ala Met Leu Met Ile His His Gly Asp Val Lys Lys	
650 655 660	
gga ttt aag cgt ttc gac gac gcc ctc gat atg atc gat ccc ctc acc	2131
Gly Phe Lys Arg Phe Asp Asp Ala Leu Asp Met Ile Asp Pro Leu Thr	
665 670 675	
ctc ccc tac tat cgg gca cgc atc tgc ttt gaa tac ggc cag gcc ctg	2179
Leu Pro Tyr Tyr Arg Ala Arg Ile Cys Phe Glu Tyr Gly Gln Ala Leu	
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aga cgc cag ggg caa cgt cga cgt gct gat gaa caa ttt gcc cgt gca	2227
Arg Arg Gln Gly Gln Arg Arg Arg Ala Asp Glu Gln Phe Ala Arg Ala	
695 700 705	
gct tcc cta ttc caa gac atg ggc gcc gac gcg atg gtc acc cta gcc	2275
Ala Ser Leu Phe Gln Asp Met Gly Ala Asp Ala Met Val Thr Leu Ala	
710 715 720 725	
aac cga gaa cgc cgg gtg ggt ggc ctt ggt caa cga tcc gag caa gcc	2323
Asn Arg Glu Arg Arg Val Gly Gly Leu Gly Gln Arg Ser Glu Gln Ala	
730 735 740	
ggc ggg ctc acc cct cag gaa tat gaa att gcc cga tta gtg tca tct	2371

Gly Gly Leu Thr Pro Gln Glu Tyr Glu Ile Ala Arg Leu Val Ser Ser  
 745 750 755

ggg cat gcc aac cga gag gtc gca cag gag ctt ttc ctc tcg cct aag 2419  
 Gly His Ala Asn Arg Glu Val Ala Gln Glu Leu Phe Leu Ser Pro Lys  
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acc gtg gaa tac 2431  
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<211> 777

<212> PRT

<213> Corynebacterium glutamicum

<400> 144

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Glu Ser Met Gln Lys Leu Ile Glu Tyr Ser Met Arg Met Val Ser Gly  
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Arg Phe Ala Leu Ile Met Ile Gly Leu Asp Glu Glu Asn Leu Val Phe  
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His Asp Glu Val Val Ser Leu Pro Ser Ile Ala Asp Ser Thr Tyr Val  
 65 70 75 80

Leu Pro Pro Met Ser Ile Glu Glu Ile Arg Gln Leu Ala Leu Thr Asp  
 85 90 95

Val Arg Gly Arg Ile Ser Thr Thr Thr Ala Thr Asp Ile Gln Arg Ile  
 100 105 110

Thr Gly Gly Ile Tyr Gly Arg Val Lys Glu Val Leu His Ser Glu Ser  
 115 120 125

Pro Asp His Trp Arg Met Pro Asn Pro Asn Ile Pro Ile Pro Gln Ser  
 130 135 140

Trp His Ala Asn Leu Leu Arg Arg Ile Thr Asn Glu Glu Val Trp His  
 145 150 155 160

Val Leu Leu Ala Val Ala Val Leu Pro Ser Gly Gly Pro Ile Asp Leu  
 165 170 175

Val Lys Leu Ile Gly Asn Asp Pro Thr Gly Met Leu Cys Asp Asp Ala  
 180 185 190

Val Arg Ser Gly Leu Leu Arg Val Leu Pro Ser Asp Gly Gln Pro Gln  
 195 200 205

Val Asp Leu Val Leu Pro Ile Asp Arg Ala Val Leu Gln Ser Arg Thr  
 210 215 220

Pro Leu Asn Ile Leu Ala Gln Leu His His Lys Ala Ala Glu Tyr Tyr

225		230		235		240
Gly Lys Trp Asn Gln Lys Asp Ala Gln Leu Glu His Glu Ala Phe Ala						
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Ala Ile Asp Pro Asn Asp Pro Ala Val Arg Ala Leu Ala Gln Arg Gly						
	260			265		270
Tyr Ala Leu Gly Arg Thr Gly His Trp Met Glu Ser Ala His Ala Leu						
	275			280		285
Ser Leu Ala Ala Asn Arg Thr Ala His Gln Glu Glu Ser Asn Lys Tyr						
	290			295		300
Leu Leu Glu Ser Ile Asp Ser Leu Ile Ala Ala Ala Asp Leu Pro Gln						
	305			310		315
Ala Arg Ser Arg Ala Ser Thr Leu Asp Leu Gly Glu Thr Gly Ile Gln						
	325			330		335
Gln Asp Ser Met Leu Gly Tyr Leu Ala Ile His Glu Gly Arg Arg Leu						
	340			345		350
Glu Ala Arg Asn Leu Leu His Arg Ala Ser Glu Glu Leu Leu Ala Gln						
	355			360		365
His Pro Ile Asp Pro Ile His Gly Pro Arg Met Ala Gln Arg Lys Val						
	370			375		380
Leu Leu Asn Leu Val Asp Trp Asn Pro Glu Glu Leu Leu Val Trp Ala						
	385			390		395
Asp Arg Ala Val Ala Trp Thr Glu Glu Asp Ala Gly Glu Lys Val Glu						
	405			410		415
Ala Gln Ala Ile Ser Leu Ile Gly Gln Ser Ile Leu Asp Gly Cys Leu						
	420			425		430
Pro Glu Asp Lys Pro Ile Pro Gly Glu Thr Thr Leu His Ala Gln Arg						
	435			440		445
Arg His Met Ala Met Gly Trp Leu Ser Met Val His Asp Asp Pro Val						
	450			455		460
Thr Ala Arg Gln Lys Leu Glu Arg Arg Thr Ser Ile Asn Gly Ser Glu						
	465			470		475
Arg Ile Ser Leu Trp Gln Asp Gly Trp Leu Ala Arg Ser Leu Leu Leu						
	485			490		495
Leu Gly Glu Trp Glu Ser Ala Ala Arg Thr Val Glu Ile Gly Leu Ala						
	500			505		510
Arg Ala Glu Gln Phe Gly Ile Arg Phe Leu Glu Pro Leu Leu Leu Trp						
	515			520		525
Ser Gly Ala Thr Ile Ala Thr Ala Arg Gly Asn Ser Asp Leu Ala Arg						
	530			535		540
Asn Tyr Met Ser Arg Leu Ser Thr Asp Gln Asp Ser Phe Ile Val Gln						
	545			550		555
						560

Ser Met Pro Ser Ala Met Cys Arg Met Trp Val His Arg His Arg Asn  
 565 570 575  
 Glu Ile Pro Gly Ala Ile Val Ala Gly Glu Gln Leu Glu Lys Ile Ala  
 580 585 590  
 Ala His Lys His Val Asn Ala Pro Gly Phe Trp Pro Trp Gln Asp Val  
 595 600 605  
 His Ala Thr His Leu Ile Arg Ile Gly Glu Thr Glu Arg Ala Gln Glu  
 610 615 620  
 Leu Val Asn Ser Thr Leu Glu Glu Leu Arg Gly Ser Asp Ile Met Ser  
 625 630 635 640  
 Ala His Ala Lys Ile Ala Val Pro Asp Ala Met Leu Met Ile His His  
 645 650 655  
 Gly Asp Val Lys Lys Gly Phe Lys Arg Phe Asp Asp Ala Leu Asp Met  
 660 665 670  
 Ile Asp Pro Leu Thr Leu Pro Tyr Tyr Arg Ala Arg Ile Cys Phe Glu  
 675 680 685  
 Tyr Gly Gln Ala Leu Arg Arg Gln Gly Gln Arg Arg Arg Ala Asp Glu  
 690 695 700  
 Gln Phe Ala Arg Ala Ala Ser Leu Phe Gln Asp Met Gly Ala Asp Ala  
 705 710 715 720  
 Met Val Thr Leu Ala Asn Arg Glu Arg Arg Val Gly Gly Leu Gly Gln  
 725 730 735  
 Arg Ser Glu Gln Ala Gly Gly Leu Thr Pro Gln Glu Tyr Glu Ile Ala  
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 Phe Leu Ser Pro Lys Thr Val Glu Tyr  
 770 775

&lt;210&gt; 145

&lt;211&gt; 471

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(448)

&lt;223&gt; RXA00593

&lt;400&gt; 145

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Met Thr Ser Val Ile

1

5

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      25              30              35

cga aat ggc gac cca gat gca ttg ttt gtt cgt ggt gca gcg caa cgc 259
Arg Asn Gly Asp Pro Asp Ala Leu Phe Val Arg Gly Ala Ala Gln Arg
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cga gca gca gca att tgc cgc cac tgc cct gta gcc atg cag tgc tgc 307
Arg Ala Ala Ala Ile Cys Arg His Cys Pro Val Ala Met Gln Cys Cys
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gcc gat gcc tta gat aac aag gtg gaa ttc gga gtc tgg gga ggc ctg 355
Ala Asp Ala Leu Asp Asn Lys Val Glu Phe Gly Val Trp Gly Gly Leu
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acc gag cgc cag cgc cgt gca ttg ctt cga aag aag ccg cac att act 403
Thr Glu Arg Gln Arg Arg Ala Leu Leu Arg Lys Lys Pro His Ile Thr
      90              95              100

aac tgg gct gaa tat ttg gct cag ggg ggc gag atc gcc ggg gtt 448
Asn Trp Ala Glu Tyr Leu Ala Gln Gly Gly Glu Ile Ala Gly Val
      105              110              115

taattaattt caagggctgg cca 471

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&lt;210&gt; 146

&lt;211&gt; 116

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 146

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Met Thr Ser Val Ile Pro Glu Gln Arg Asn Asn Pro Phe Tyr Arg Asp
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Ser Ala Thr Ile Ala Ser Ser Asp His Thr Glu Arg Gly Glu Trp Val
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Thr Gln Ala Lys Cys Arg Asn Gly Asp Pro Asp Ala Leu Phe Val Arg
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Gly Ala Ala Gln Arg Arg Ala Ala Ala Ile Cys Arg His Cys Pro Val
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Ala Met Gln Cys Cys Ala Asp Ala Leu Asp Asn Lys Val Glu Phe Gly
      65              70              75              80

Val Trp Gly Gly Leu Thr Glu Arg Gln Arg Arg Ala Leu Leu Arg Lys
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Lys Pro His Ile Thr Asn Trp Ala Glu Tyr Leu Ala Gln Gly Gly Glu
      100              105              110

Ile Ala Gly Val
      115

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Met Leu Ile Gly Glu 5															
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gtg tcc aag ctc agt ggg gtg agt gcg cgc atg ttg cgg cac tac gaa 163															
Val Ser Lys Leu Ser Gly Val Ser Ala Arg Met Leu Arg His Tyr Glu 20															
10 15															
aag ctg ggt ttg gtc gag ccg aag cag tcg acg gcg ggg tat cgg gaa 211															
Lys Leu Gly Leu Val Glu Pro Lys Gln Ser Thr Ala Gly Tyr Arg Glu 35															
25 30															
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Tyr Ser Glu Gly Asp Val Arg Arg Ile Phe His Ile Glu Gly Leu Arg 50															
40 45															
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Ser Leu Gly Leu Ser Leu Lys Gln Val Gly Asp Ala Leu Glu Asp Pro 65															
55 60															
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Asp Phe Asp Pro Gln Ala Val Ile Ser Glu Met Ile Ala Glu Thr Ser 85															
70 75															
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Ala Arg Ile Ser Met Glu Arg Glu Leu Leu Ala Arg Leu Lys Ala Val 100															
90 95															
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Arg His Ala Gln Ala Ser Asp Trp Glu Ser Ala Leu Asp Ala Val Gln 115															
105 110															
att tta cgt cgc ctg cga tcg ggg gat ccg gcg caa cgt caa gcc gtg 499															
Ile Leu Arg Arg Leu Arg Ser Gly Asp Pro Ala Gln Arg Gln Ala Val 130															
120 125															
gcc tat gac tct gtc tct ggt aaa gaa gca gtt gcg cta gaa acc ttg 547															
Ala Tyr Asp Ser Val Ser Gly Lys Glu Ala Val Ala Leu Glu Thr Leu 145															
135 140															
gtg gaa tcg gcg ctc ggt gag tcg cat ttg aac gcg gag ggg gcg ctg 595															
Val Glu Ser Ala Leu Gly Glu Ser His Leu Asn Ala Glu Gly Ala Leu 165															
150 155 160															
tcg tgg gcg gtt gtg cag cgt ggt gag gaa gct gtt gca ttg gcg gca 643															
Ser Trp Ala Val Val Gln Arg Gly Glu Glu Ala Val Ala Leu Ala Ala 180															
170 175 180															

cga ggt ttg cgc tca agg gat gcg gcg gtg cgg ctg cgg gct gta agg 691  
 Arg Gly Leu Arg Ser Arg Asp Ala Ala Val Arg Leu Arg Ala Val Arg  
 185 190 195

att gtg gcg agc gcg ccg agt gct gtt gcg gat cga gta gag tgg cta 739  
 Ile Val Ala Ser Ala Pro Ser Ala Val Ala Asp Arg Val Glu Trp Leu  
 200 205 210

cgg cca atg att cgc gat ccc gat gct ctc gtg cgt gct gaa act gcg 787  
 Arg Pro Met Ile Arg Asp Pro Asp Ala Leu Val Arg Ala Glu Thr Ala  
 215 220 225

ttg gcg ttg gga aaa tca ggc gat gag agt gca gtt gag cag ctc gtg 835  
 Leu Ala Leu Gly Lys Ser Gly Asp Glu Ser Ala Val Glu Gln Leu Val  
 230 235 240 245

tcc atg gtt ctc acc ggt ctt cgg gac gtg gag gca gcc gaa ttg ctt 883  
 Ser Met Val Leu Thr Gly Leu Arg Asp Val Glu Ala Ala Glu Leu Leu  
 250 255 260

gcc gga ttt ggg gag ccc gtg cag tta gat gtg ttc aag aaa ttt gcg 931  
 Ala Gly Phe Gly Glu Pro Val Gln Leu Asp Val Phe Lys Lys Phe Ala  
 265 270 275

cgg acg ctg gat gat gag gaa aca atg tcc ccg acg 967  
 Arg Thr Leu Asp Asp Glu Glu Thr Met Ser Pro Thr  
 280 285

&lt;210&gt; 148

&lt;211&gt; 289

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 148

Met Leu Ile Gly Glu Val Ser Lys Leu Ser Gly Val Ser Ala Arg Met  
 1 5 10 15

Leu Arg His Tyr Glu Lys Leu Gly Leu Val Glu Pro Lys Gln Ser Thr  
 20 25 30

Ala Gly Tyr Arg Glu Tyr Ser Glu Gly Asp Val Arg Arg Ile Phe His  
 35 40 45

Ile Glu Gly Leu Arg Ser Leu Gly Leu Ser Leu Lys Gln Val Gly Asp  
 50 55 60

Ala Leu Glu Asp Pro Asp Phe Asp Pro Gln Ala Val Ile Ser Glu Met  
 65 70 75 80

Ile Ala Glu Thr Ser Ala Arg Ile Ser Met Glu Arg Glu Leu Leu Ala  
 85 90 95

Arg Leu Lys Ala Val Arg His Ala Gln Ala Ser Asp Trp Glu Ser Ala  
 100 105 110

Leu Asp Ala Val Gln Ile Leu Arg Arg Leu Arg Ser Gly Asp Pro Ala  
 115 120 125

Gln Arg Gln Ala Val Ala Tyr Asp Ser Val Ser Gly Lys Glu Ala Val



130	135	140
Ala Leu Glu Thr Leu Val Glu Ser Ala Leu Gly Glu Ser His Leu Asn 145 150 155 160		
Ala Glu Gly Ala Leu Ser Trp Ala Val Val Gln Arg Gly Glu Glu Ala 165 170 175		
Val Ala Leu Ala Ala Arg Gly Leu Arg Ser Arg Asp Ala Ala Val Arg 180 185 190		
Leu Arg Ala Val Arg Ile Val Ala Ser Ala Pro Ser Ala Val Ala Asp 195 200 205		
Arg Val Glu Trp Leu Arg Pro Met Ile Arg Asp Pro Asp Ala Leu Val 210 215 220		
Arg Ala Glu Thr Ala Leu Ala Leu Gly Lys Ser Gly Asp Glu Ser Ala 225 230 235 240		
Val Glu Gln Leu Val Ser Met Val Leu Thr Gly Leu Arg Asp Val Glu 245 250 255		
Ala Ala Glu Leu Leu Ala Gly Phe Gly Glu Pro Val Gln Leu Asp Val 260 265 270		
Phe Lys Lys Phe Ala Arg Thr Leu Asp Asp Glu Glu Thr Met Ser Pro 275 280 285		

Thr

<210> 149  
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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(397)  
 <223> RXA00494

<400> 149  
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 aaagctataa aaagtagctg acaataggga gtatttgaag atg aca ttg cct cac 115  
 Met Thr Leu Pro His  
 1 5  
 cag ctt ccc ggg cca aat gca gac ttc tgg gac tgg cag ttg cac gga 163  
 Gln Leu Pro Gly Pro Asn Ala Asp Phe Trp Asp Trp Gln Leu His Gly  
 10 15 20  
 acg tgc cgc ggc gag acc tcc gac gtg ttc tat cac ccg gac ggc gag 211  
 Thr Cys Arg Gly Glu Thr Ser Asp Val Phe Tyr His Pro Asp Gly Glu  
 25 30 35  
 cgc ggt cgt gct cgc cag cgt cgg gag ctg cgc gca aag gcc atc tgt 259  
 Arg Gly Arg Ala Arg Gln Arg Arg Glu Leu Arg Ala Lys Ala Ile Cys  
 40 45 50

gca gca tgc cca gta ttg gaa tcc tgc cgc aag cat gca cta gct gta 307  
 Ala Ala Cys Pro Val Leu Glu Ser Cys Arg Lys His Ala Leu Ala Val  
 55 60 65

gca gag cct tat gga gta tgg ggc gga ctt tca gag tcc gaa cga ctg 355  
 Ala Glu Pro Tyr Gly Val Trp Gly Gly Leu Ser Glu Ser Glu Arg Leu  
 70 75 80 85

gtt atc ctt cgc aac aac gag cgc aag caa cca gta gca gtt 397  
 Val Ile Leu Arg Asn Asn Glu Arg Lys Gln Pro Val Ala Val  
 90 95

taaaagagca gacccggtca cca 420

<210> 150

<211> 99

<212> PRT

<213> Corynebacterium glutamicum

<400> 150

Met Thr Leu Pro His Gln Leu Pro Gly Pro Asn Ala Asp Phe Trp Asp  
 1 5 10 15

Trp Gln Leu His Gly Thr Cys Arg Gly Glu Thr Ser Asp Val Phe Tyr  
 20 25 30

His Pro Asp Gly Glu Arg Gly Arg Ala Arg Gln Arg Arg Glu Leu Arg  
 35 40 45

Ala Lys Ala Ile Cys Ala Ala Cys Pro Val Leu Glu Ser Cys Arg Lys  
 50 55 60

His Ala Leu Ala Val Ala Glu Pro Tyr Gly Val Trp Gly Gly Leu Ser  
 65 70 75 80

Glu Ser Glu Arg Leu Val Ile Leu Arg Asn Asn Glu Arg Lys Gln Pro  
 85 90 95

Val Ala Val

<210> 151

<211> 435

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(412)

<223> RXN01368

<400> 151

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cagacttaaa gtagctttga aagtgaagagg ggggagagta atg gaa gat tca gct 115  
 Met Glu Asp Ser Ala  
 1 5

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ggg gac gta tct gca aag ttg aaa gca ggc cag act cgc acc gca ctg 163
Gly Asp Val Ser Ala Lys Leu Lys Ala Gly Gln Thr Arg Thr Ala Leu
      10                      15                      20

gag atg act ttg gat gat ctg ttc gga gcg gtt gag caa gaa tgg cag 211
Glu Met Thr Leu Asp Asp Leu Phe Gly Ala Val Glu Gln Glu Trp Gln
      25                      30                      35

gag cag gcg ctg tgt gcg caa act gat cct gaa gca ttc ttt cca gaa 259
Glu Gln Ala Leu Cys Ala Gln Thr Asp Pro Glu Ala Phe Phe Pro Glu
      40                      45                      50

aaa ggt ggc tca act cgc gaa gcc aag cgg atc tgc cag ggc tgc ccg 307
Lys Gly Gly Ser Thr Arg Glu Ala Lys Arg Ile Cys Gln Gly Cys Pro
      55                      60                      65

gtt cgg gat gaa tgc cta gag ttt gct ctt gag cat gat gaa cgc ttt 355
Val Arg Asp Glu Cys Leu Glu Phe Ala Leu Glu His Asp Glu Arg Phe
      70                      75                      80                      85

gga att tgg ggt ggt ctc tct gaa cgt gag cgc cgc cgc ctg aaa cgc 403
Gly Ile Trp Gly Gly Leu Ser Glu Arg Glu Arg Arg Arg Leu Lys Arg
      90                      95                      100

gaa att tcg taaaacttca agaccagtaa gcg 435
Glu Ile Ser

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<210> 152
<211> 104
<212> PRT
<213> Corynebacterium glutamicum

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<400> 152
Met Glu Asp Ser Ala Gly Asp Val Ser Ala Lys Leu Lys Ala Gly Gln
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Thr Arg Thr Ala Leu Glu Met Thr Leu Asp Asp Leu Phe Gly Ala Val
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Glu Gln Glu Trp Gln Glu Gln Ala Leu Cys Ala Gln Thr Asp Pro Glu
      35                      40                      45

Ala Phe Phe Pro Glu Lys Gly Gly Ser Thr Arg Glu Ala Lys Arg Ile
      50                      55                      60

Cys Gln Gly Cys Pro Val Arg Asp Glu Cys Leu Glu Phe Ala Leu Glu
      65                      70                      75                      80

His Asp Glu Arg Phe Gly Ile Trp Gly Gly Leu Ser Glu Arg Glu Arg
      85                      90                      95

Arg Arg Leu Lys Arg Glu Ile Ser
      100

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<210> 153
<211> 152
<212> DNA
<213> Corynebacterium glutamicum

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<220>  
 <221> CDS  
 <222> (1)..(129)  
 <223> FRXA01368

<400> 153  
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 Lys Arg Ile Cys Gln Gly Cys Pro Val Arg Asp Glu Cys Leu Glu Phe  
 1 5 10 15  
 gct ctt gag cat gat gaa cgc ttt gga att tgg ggt ggt ctc tct gaa 96  
 Ala Leu Glu His Asp Glu Arg Phe Gly Ile Trp Gly Gly Leu Ser Glu  
 20 25 30  
 cgt gag cgc cgc cgc ctg aaa cgc gaa att tcg taaaacttca agaccagtaa 149  
 Arg Glu Arg Arg Arg Leu Lys Arg Glu Ile Ser  
 35 40  
 gcg 152

<210> 154  
 <211> 43  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 154  
 Lys Arg Ile Cys Gln Gly Cys Pro Val Arg Asp Glu Cys Leu Glu Phe  
 1 5 10 15  
 Ala Leu Glu His Asp Glu Arg Phe Gly Ile Trp Gly Gly Leu Ser Glu  
 20 25 30  
 Arg Glu Arg Arg Arg Leu Lys Arg Glu Ile Ser  
 35 40

<210> 155  
 <211> 897  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(874)  
 <223> RXN00464

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 aattctgccca tttcgcctca aatcgggcta gttttgaagc atg agc gaa cgt cag 115  
 Met Ser Glu Arg Gln  
 1 5  
 ctg gaa aag tca att gag cac gcc gtc gag tta gcc cgc gaa gcc cga 163  
 Leu Glu Lys Ser Ile Glu His Ala Val Glu Leu Ala Arg Glu Ala Arg  
 10 15 20  
 aac atc gaa gtt ttt acc gga gcc gga atg agc gcc gac tcc ggg ttg 211  
 Asn Ile Glu Val Phe Thr Gly Ala Gly Met Ser Ala Asp Ser Gly Leu

				25				30				35							
gaa	acg	tat	cgt	gat	gat	aaa	acc	ggg	ctg	tgg	agc	aac	gta	gat	cca	259			
Glu	Thr	Tyr	Arg	Asp	Asp	Lys	Thr	Gly	Leu	Trp	Ser	Asn	Val	Asp	Pro				
40				45				50											
caa	gcg	atg	gca	agt	atc	gat	gca	tgg	cgc	aaa	gat	cca	gag	cca	atg	307			
Gln	Ala	Met	Ala	Ser	Ile	Asp	Ala	Trp	Arg	Lys	Asp	Pro	Glu	Pro	Met				
55				60				65											
tgg	gcg	tgg	tat	cgc	tgg	cgc	gcc	ggg	gtg	gca	gct	agg	gca	gaa	ccc	355			
Trp	Ala	Trp	Tyr	Arg	Trp	Arg	Ala	Gly	Val	Ala	Ala	Arg	Ala	Glu	Pro				
70				75				80				85							
aac	gcg	ggg	cat	caa	gct	att	tcc	tac	tgg	gag	ggg	agt	gac	acc	gtc	403			
Asn	Ala	Gly	His	Gln	Ala	Ile	Ser	Tyr	Trp	Glu	Gly	Ser	Asp	Thr	Val				
90				95				100											
gaa	cac	gtt	cac	atc	acc	acc	cag	aac	att	gac	aac	ctg	cac	gag	cga	451			
Glu	His	Val	His	Ile	Thr	Thr	Gln	Asn	Ile	Asp	Asn	Leu	His	Glu	Arg				
105				110				115											
gct	ggc	tct	agc	gat	gtg	aca	cat	ctt	cat	ggc	agc	ttg	ttt	gaa	tac	499			
Ala	Gly	Ser	Ser	Asp	Val	Thr	His	Leu	His	Gly	Ser	Leu	Phe	Glu	Tyr				
120				125				130											
agg	tgc	tct	gat	tgt	gcg	act	cca	tgg	gaa	gac	gat	aaa	aac	tat	ccg	547			
Arg	Cys	Ser	Asp	Cys	Ala	Thr	Pro	Trp	Glu	Asp	Asp	Lys	Asn	Tyr	Pro				
135				140				145											
caa	gaa	ccc	att	gca	cgc	ctt	gct	cct	cca	caa	tgt	gaa	aag	tgc	gga	595			
Gln	Glu	Pro	Ile	Ala	Arg	Leu	Ala	Pro	Pro	Gln	Cys	Glu	Lys	Cys	Gly				
150				155				160				165							
ggg	ctg	att	aga	cca	ggt	gtg	gtg	tgg	ttt	ggt	gag	aac	ctg	ccc	gta	643			
Gly	Leu	Ile	Arg	Pro	Gly	Val	Val	Trp	Phe	Gly	Glu	Asn	Leu	Pro	Val				
170				175				180											
gaa	gag	tgg	gat	att	gca	gag	caa	cgc	atc	gca	gaa	gcc	gat	ctc	atg	691			
Glu	Glu	Trp	Asp	Ile	Ala	Glu	Gln	Arg	Ile	Ala	Glu	Ala	Asp	Leu	Met				
185				190				195											
atc	att	gtg	ggt	acc	tcc	ggg	att	gtt	cat	cct	gca	gca	gca	ctc	ccg	739			
Ile	Ile	Val	Gly	Thr	Ser	Gly	Ile	Val	His	Pro	Ala	Ala	Ala	Leu	Pro				
200				205				210											
caa	tta	gcc	caa	caa	cgc	ggc	gtt	ccc	atc	gtg	gag	atc	tcc	cca	acg	787			
Gln	Leu	Ala	Gln	Gln	Arg	Gly	Val	Pro	Ile	Val	Glu	Ile	Ser	Pro	Thr				
215				220				225											
cgc	acc	gaa	ctt	agc	cgg	atc	gca	gac	ttc	acc	tgg	atg	tcc	acc	gca	835			
Arg	Thr	Glu	Leu	Ser	Arg	Ile	Ala	Asp	Phe	Thr	Trp	Met	Ser	Thr	Ala				
230				235				240				245							
gcc	caa	gcg	cta	cca	gcg	ttg	atg	cga	ggt	ttg	agc	gcc	taac	atg	gact	884			
Ala	Gln	Ala	Leu	Pro	Ala	Leu	Met	Arg	Gly	Leu	Ser	Ala							
250				255															
gaagatgacttag																897			

<210> 156  
 <211> 258  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 156  
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 Ala Arg Glu Ala Arg Asn Ile Glu Val Phe Thr Gly Ala Gly Met Ser  
           20                  25                  30  
 Ala Asp Ser Gly Leu Glu Thr Tyr Arg Asp Asp Lys Thr Gly Leu Trp  
           35                  40                  45  
 Ser Asn Val Asp Pro Gln Ala Met Ala Ser Ile Asp Ala Trp Arg Lys  
           50                  55                  60  
 Asp Pro Glu Pro Met Trp Ala Trp Tyr Arg Trp Arg Ala Gly Val Ala  
   65                  70                  75                  80  
 Ala Arg Ala Glu Pro Asn Ala Gly His Gln Ala Ile Ser Tyr Trp Glu  
                   85                  90                  95  
 Gly Ser Asp Thr Val Glu His Val His Ile Thr Thr Gln Asn Ile Asp  
           100                  105                  110  
 Asn Leu His Glu Arg Ala Gly Ser Ser Asp Val Thr His Leu His Gly  
           115                  120                  125  
 Ser Leu Phe Glu Tyr Arg Cys Ser Asp Cys Ala Thr Pro Trp Glu Asp  
   130                  135                  140  
 Asp Lys Asn Tyr Pro Gln Glu Pro Ile Ala Arg Leu Ala Pro Pro Gln  
  145                  150                  155                  160  
 Cys Glu Lys Cys Gly Gly Leu Ile Arg Pro Gly Val Val Trp Phe Gly  
           165                  170                  175  
 Glu Asn Leu Pro Val Glu Glu Trp Asp Ile Ala Glu Gln Arg Ile Ala  
           180                  185                  190  
 Glu Ala Asp Leu Met Ile Ile Val Gly Thr Ser Gly Ile Val His Pro  
           195                  200                  205  
 Ala Ala Ala Leu Pro Gln Leu Ala Gln Gln Arg Gly Val Pro Ile Val  
   210                  215                  220  
 Glu Ile Ser Pro Thr Arg Thr Glu Leu Ser Arg Ile Ala Asp Phe Thr  
  225                  230                  235                  240  
 Trp Met Ser Thr Ala Ala Gln Ala Leu Pro Ala Leu Met Arg Gly Leu  
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 Ser Ala

<210> 157  
 <211> 355  
 <212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (75)..(332)

<223> FRXA00464

<400> 157

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ttagaccagg tgtg gtg tgg ttt ggt gag aac ctg ccc gta gaa gag tgg 110
      Val Trp Phe Gly Glu Asn Leu Pro Val Glu Glu Trp
      1              5              10

gat att gca gag caa cgc atc gca gaa gcc gat ctc atg atc att gtg 158
Asp Ile Ala Glu Gln Arg Ile Ala Glu Ala Asp Leu Met Ile Ile Val
      15              20              25

ggt acc tcc ggg att gtt cat cct gca gca gca ctc ccg caa tta gcc 206
Gly Thr Ser Gly Ile Val His Pro Ala Ala Ala Leu Pro Gln Leu Ala
      30              35              40

caa caa cgc ggc gtt ccc atc gtg gag atc tcc cca acg cgc acc gaa 254
Gln Gln Arg Gly Val Pro Ile Val Glu Ile Ser Pro Thr Arg Thr Glu
      45              50              55              60

ctt agc cgg atc gca gac ttc acc tgg atg tcc acc gca gcc caa gcg 302
Leu Ser Arg Ile Ala Asp Phe Thr Trp Met Ser Thr Ala Ala Gln Ala
      65              70              75

cta cca gcg ttg atg cga ggt ttg agc gcc taacatgact gaagatgact tag 355
Leu Pro Ala Leu Met Arg Gly Leu Ser Ala
      80              85

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<210> 158

<211> 86

<212> PRT

<213> Corynebacterium glutamicum

<400> 158

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Val Trp Phe Gly Glu Asn Leu Pro Val Glu Glu Trp Asp Ile Ala Glu
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Gln Arg Ile Ala Glu Ala Asp Leu Met Ile Ile Val Gly Thr Ser Gly
      20              25              30

Ile Val His Pro Ala Ala Ala Leu Pro Gln Leu Ala Gln Gln Arg Gly
      35              40              45

Val Pro Ile Val Glu Ile Ser Pro Thr Arg Thr Glu Leu Ser Arg Ile
      50              55              60

Ala Asp Phe Thr Trp Met Ser Thr Ala Ala Gln Ala Leu Pro Ala Leu
      65              70              75              80

Met Arg Gly Leu Ser Ala
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<222> (101) .. (1459)
<223> RXA01655
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				Met	Leu	Ala	Asp	Leu	5							
				1												
ccc	atc	gcc	tta	aac	cca	cac	gaa	cca	aca	tcc	atc	ccc	acg	cag	ctc	163
Pro	Ile	Ala	Leu	Asn	Pro	His	Glu	Pro	Thr	Ser	Ile	Pro	Thr	Gln	Leu	
				10					15					20		
aca	gaa	cag	atc	cgt	cgt	ctc	gtg	gcg	agg	gga	att	ctc	acc	cca	gga	211
Thr	Glu	Gln	Ile	Arg	Arg	Leu	Val	Ala	Arg	Gly	Ile	Leu	Thr	Pro	Gly	
			25					30					35			
gac	ccg	ctt	ccc	agc	agt	cgc	tca	cta	tcc	acc	caa	ttg	ggg	gta	tcc	259
Asp	Pro	Leu	Pro	Ser	Ser	Arg	Ser	Leu	Ser	Thr	Gln	Leu	Gly	Val	Ser	
		40					45					50				
cgc	ggc	agt	gtg	gtg	acc	gct	tat	gac	caa	ttg	gcc	ggg	gaa	ggc	tac	307
Arg	Gly	Ser	Val	Val	Thr	Ala	Tyr	Asp	Gln	Leu	Ala	Gly	Glu	Gly	Tyr	
	55					60					65					
ctc	agc	acc	gcc	cgc	ggg	tcc	ggg	aca	acg	atc	aac	cca	gat	ctg	cat	355
Leu	Ser	Thr	Ala	Arg	Gly	Ser	Gly	Thr	Thr	Ile	Asn	Pro	Asp	Leu	His	
	70				75					80					85	
ttg	ttg	aag	cct	gtg	gaa	att	gag	aag	aag	gag	acg	tcg	aga	agc	gtc	403
Leu	Leu	Lys	Pro	Val	Glu	Ile	Glu	Lys	Lys	Glu	Thr	Ser	Arg	Ser	Val	
				90					95					100		
ccg	ccc	ccg	ctg	ctc	aac	ctg	agc	ccc	ggc	gtg	ccc	gat	acc	gcg	acg	451
Pro	Pro	Pro	Leu	Leu	Asn	Leu	Ser	Pro	Gly	Val	Pro	Asp	Thr	Ala	Thr	
			105					110					115			
ctc	gcc	gat	tcc	gca	tgg	cgc	gct	gcg	tgg	cgc	gaa	gcc	tgc	gcc	aag	499
Leu	Ala	Asp	Ser	Ala	Trp	Arg	Ala	Ala	Trp	Arg	Glu	Ala	Cys	Ala	Lys	
		120					125					130				
cca	ccc	acg	cac	tcc	cct	gag	cag	gga	ctt	ttg	agg	ctg	cgg	atc	gag	547
Pro	Pro	Thr	His	Ser	Pro	Glu	Gln	Gly	Leu	Leu	Arg	Leu	Arg	Ile	Glu	
	135					140					145					
atc	gcc	gac	cac	ctg	cgc	cag	atg	cgt	ggc	ctc	atg	gtc	gag	ccg	gag	595
Ile	Ala	Asp	His	Leu	Arg	Gln	Met	Arg	Gly	Leu	Met	Val	Glu	Pro	Glu	
	150				155					160					165	
cag	atc	atc	gtc	acc	gcc	ggc	gcg	cgc	gag	ggg	ctg	agt	ctg	ctg	ctg	643
Gln	Ile	Ile	Val	Thr	Ala	Gly	Ala	Arg	Glu	Gly	Leu	Ser	Leu	Leu	Leu	
			170					175						180		



cgc acc atg gat gcg cct gcc cgc atc ggc gtc gaa tcg ccc ggc tac	691
Arg Thr Met Asp Ala Pro Ala Arg Ile Gly Val Glu Ser Pro Gly Tyr	
185 190 195	
ccc agc ctg cgc cgc atc ccg cag gtg ctt ggc cat gag acg atc gat	739
Pro Ser Leu Arg Arg Ile Pro Gln Val Leu Gly His Glu Thr Ile Asp	
200 205 210	
gtg ccg acc gac gaa tcc ggc ctc gta ccc cgc gcg ctg ccc cac gac	787
Val Pro Thr Asp Glu Ser Gly Leu Val Pro Arg Ala Leu Pro His Asp	
215 220 225	
ctt aac gcg cta ctg gta acc cct agc cat caa tat ccc tac ggc ggc	835
Leu Asn Ala Leu Leu Val Thr Pro Ser His Gln Tyr Pro Tyr Gly Gly	
230 235 240 245	
tcg ctg ccc gcc gat cgc cgc acc gcg cta gtc gcg tgg gct gag gca	883
Ser Leu Pro Ala Asp Arg Arg Thr Ala Leu Val Ala Trp Ala Glu Ala	
250 255 260	
aac gat gcg ttg ctt att gaa gac gac ttc gat tct gag ctg cgc tac	931
Asn Asp Ala Leu Leu Ile Glu Asp Asp Phe Asp Ser Glu Leu Arg Tyr	
265 270 275	
gtc ggt atg ccg ctt ccg ccg ctg cgt gcg ctg gcg ccc gat cgc acg	979
Val Gly Met Pro Leu Pro Pro Leu Arg Ala Leu Ala Pro Asp Arg Thr	
280 285 290	
att ctg ctc ggc acg ttt tcc tcc gtg atc aca cca caa gtc gcc tgc	1027
Ile Leu Leu Gly Thr Phe Ser Ser Val Ile Thr Pro Gln Val Ala Cys	
295 300 305	
gga tac ctc atc gcg ccg acg ccc cag gcg cgc gtg ctc gcc acg ctt	1075
Gly Tyr Leu Ile Ala Pro Thr Pro Gln Ala Arg Val Leu Ala Thr Leu	
310 315 320 325	
cgc ggg att ctc ggc cag cca gtc ggc gcc atc acc caa cac gcg ctc	1123
Arg Gly Ile Leu Gly Gln Pro Val Gly Ala Ile Thr Gln His Ala Leu	
330 335 340	
gcg tcc tac ctc gcc tca ggc gct tta cga cgc cgc acc caa cgt ttg	1171
Ala Ser Tyr Leu Ala Ser Gly Ala Leu Arg Arg Arg Thr Gln Arg Leu	
345 350 355	
cgg cgc ctt tac cga cac cgc cgc tcc atc gtc caa gac acc ctc ggt	1219
Arg Arg Leu Tyr Arg His Arg Arg Ser Ile Val Gln Asp Thr Leu Gly	
360 365 370	
gac ctc ccg aat acg cag ctt cgc ccc atc aac ggt ggc ctc cac gca	1267
Asp Leu Pro Asn Thr Gln Leu Arg Pro Ile Asn Gly Gly Leu His Ala	
375 380 385	
gtt ctc ctt tgc gac aaa ccc caa gac ctc gtt gtc acc aca ctc gcc	1315
Val Leu Leu Cys Asp Lys Pro Gln Asp Leu Val Val Thr Thr Leu Ala	
390 395 400 405	
tcc cga ggc ctt aac gtc acc gcg ctt tcc cac tac tgg ggc ggc acc	1363
Ser Arg Gly Leu Asn Val Thr Ala Leu Ser His Tyr Trp Gly Gly Thr	
410 415 420	
ggc gca gac aac ggc atc gtc ttc ggc ttc ggc tcc cac gac gaa gac	1411

Gly Ala Asp Asn Gly Ile Val Phe Gly Phe Gly Ser His Asp Glu Asp  
 425 430 435

acc ctc aga tgg gtg ctt gct gag atc agc gat gcg gtg tct cta ggc 1459  
 Thr Leu Arg Trp Val Leu Ala Glu Ile Ser Asp Ala Val Ser Leu Gly  
 440 445 450

taaagaaaaa acagcccgag agg 1482

<210> 160

<211> 453

<212> PRT

<213> Corynebacterium glutamicum

<400> 160

Met Leu Ala Asp Leu Pro Ile Ala Leu Asn Pro His Glu Pro Thr Ser  
 1 5 10 15

Ile Pro Thr Gln Leu Thr Glu Gln Ile Arg Arg Leu Val Ala Arg Gly  
 20 25 30

Ile Leu Thr Pro Gly Asp Pro Leu Pro Ser Ser Arg Ser Leu Ser Thr  
 35 40 45

Gln Leu Gly Val Ser Arg Gly Ser Val Val Thr Ala Tyr Asp Gln Leu  
 50 55 60

Ala Gly Glu Gly Tyr Leu Ser Thr Ala Arg Gly Ser Gly Thr Thr Ile  
 65 70 75 80

Asn Pro Asp Leu His Leu Leu Lys Pro Val Glu Ile Glu Lys Lys Glu  
 85 90 95

Thr Ser Arg Ser Val Pro Pro Pro Leu Leu Asn Leu Ser Pro Gly Val  
 100 105 110

Pro Asp Thr Ala Thr Leu Ala Asp Ser Ala Trp Arg Ala Ala Trp Arg  
 115 120 125

Glu Ala Cys Ala Lys Pro Pro Thr His Ser Pro Glu Gln Gly Leu Leu  
 130 135 140

Arg Leu Arg Ile Glu Ile Ala Asp His Leu Arg Gln Met Arg Gly Leu  
 145 150 155 160

Met Val Glu Pro Glu Gln Ile Ile Val Thr Ala Gly Ala Arg Glu Gly  
 165 170 175

Leu Ser Leu Leu Leu Arg Thr Met Asp Ala Pro Ala Arg Ile Gly Val  
 180 185 190

Glu Ser Pro Gly Tyr Pro Ser Leu Arg Arg Ile Pro Gln Val Leu Gly  
 195 200 205

His Glu Thr Ile Asp Val Pro Thr Asp Glu Ser Gly Leu Val Pro Arg  
 210 215 220

Ala Leu Pro His Asp Leu Asn Ala Leu Leu Val Thr Pro Ser His Gln  
 225 230 235 240

Tyr Pro Tyr Gly Gly Ser Leu Pro Ala Asp Arg Arg Thr Ala Leu Val  
 245 250 255  
 Ala Trp Ala Glu Ala Asn Asp Ala Leu Leu Ile Glu Asp Asp Phe Asp  
 260 265 270  
 Ser Glu Leu Arg Tyr Val Gly Met Pro Leu Pro Pro Leu Arg Ala Leu  
 275 280 285  
 Ala Pro Asp Arg Thr Ile Leu Leu Gly Thr Phe Ser Ser Val Ile Thr  
 290 295 300  
 Pro Gln Val Ala Cys Gly Tyr Leu Ile Ala Pro Thr Pro Gln Ala Arg  
 305 310 315 320  
 Val Leu Ala Thr Leu Arg Gly Ile Leu Gly Gln Pro Val Gly Ala Ile  
 325 330 335  
 Thr Gln His Ala Leu Ala Ser Tyr Leu Ala Ser Gly Ala Leu Arg Arg  
 340 345 350  
 Arg Thr Gln Arg Leu Arg Arg Leu Tyr Arg His Arg Arg Ser Ile Val  
 355 360 365  
 Gln Asp Thr Leu Gly Asp Leu Pro Asn Thr Gln Leu Arg Pro Ile Asn  
 370 375 380  
 Gly Gly Leu His Ala Val Leu Leu Cys Asp Lys Pro Gln Asp Leu Val  
 385 390 395 400  
 Val Thr Thr Leu Ala Ser Arg Gly Leu Asn Val Thr Ala Leu Ser His  
 405 410 415  
 Tyr Trp Gly Gly Thr Gly Ala Asp Asn Gly Ile Val Phe Gly Phe Gly  
 420 425 430  
 Ser His Asp Glu Asp Thr Leu Arg Trp Val Leu Ala Glu Ile Ser Asp  
 435 440 445  
 Ala Val Ser Leu Gly  
 450

<210> 161  
 <211> 786  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(763)  
 <223> RXA00126

<400> 161  
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 acatcaatgc ggtgaccaca attgggagga gaagtagcac gtg act aca cct gct 115  
 Val Thr Thr Pro Ala  
 1 5  
 gag aac aac acc ctt agc ccc gag acc aaa gta agc atc act ggt cga 163

Glu	Asn	Asn	Thr	Leu	Ser	Pro	Glu	Thr	Lys	Val	Ser	Ile	Thr	Gly	Arg	
				10					15					20		
aac	ggt	gag	ggt	cct	gat	cac	ttt	gca	gaa	cga	gta	aat	acc	aaa	ctc	211
Asn	Val	Glu	Val	Pro	Asp	His	Phe	Ala	Glu	Arg	Val	Asn	Thr	Lys	Leu	
			25					30					35			
gca	aag	att	gag	cgc	ctc	gac	cca	acg	ctg	acc	ttc	ttc	cac	ggt	gag	259
Ala	Lys	Ile	Glu	Arg	Leu	Asp	Pro	Thr	Leu	Thr	Phe	Phe	His	Val	Glu	
		40					45					50				
cta	cag	cac	gag	cca	aac	cca	cgt	cgt	gct	gac	gaa	agt	gat	cgc	att	307
Leu	Gln	His	Glu	Pro	Asn	Pro	Arg	Arg	Ala	Asp	Glu	Ser	Asp	Arg	Ile	
	55					60					65					
cag	atc	acc	gcc	acc	ggc	aag	gga	cac	atc	gcc	cga	gca	gaa	gca	aag	355
Gln	Ile	Thr	Ala	Thr	Gly	Lys	Gly	His	Ile	Ala	Arg	Ala	Glu	Ala	Lys	
70					75					80					85	
gaa	gac	agc	ttc	tac	gcg	gca	ctg	gaa	act	gca	cta	gcc	aag	atg	gag	403
Glu	Asp	Ser	Phe	Tyr	Ala	Ala	Leu	Glu	Thr	Ala	Leu	Ala	Lys	Met	Glu	
				90					95					100		
cgc	tcc	ctg	cgc	aaa	gtg	aag	gca	cgt	cgc	agc	att	tcc	cgc	tcc	ggt	451
Arg	Ser	Leu	Arg	Lys	Val	Lys	Ala	Arg	Arg	Ser	Ile	Ser	Arg	Ser	Gly	
			105					110					115			
cac	cgc	gca	cca	cta	ggc	act	ggt	gag	gtc	ggt	gca	cag	ttg	gta	gcc	499
His	Arg	Ala	Pro	Leu	Gly	Thr	Gly	Glu	Val	Gly	Ala	Gln	Leu	Val	Ala	
		120					125					130				
gag	tcc	caa	gag	gca	cgc	ggt	gcc	gat	gaa	ctg	ggc	aaa	tac	gat	ggt	547
Glu	Ser	Gln	Glu	Ala	Arg	Gly	Ala	Asp	Glu	Leu	Gly	Lys	Tyr	Asp	Val	
	135					140					145					
gat	cct	tat	gca	gat	aag	gtc	gat	gac	gtc	atg	cca	ggc	cag	ggt	ggt	595
Asp	Pro	Tyr	Ala	Asp	Lys	Val	Asp	Asp	Val	Met	Pro	Gly	Gln	Val	Val	
150					155					160					165	
cgt	acc	aag	gaa	cac	cca	gca	acc	cca	atg	agt	gtg	gat	gac	gca	cta	643
Arg	Thr	Lys	Glu	His	Pro	Ala	Thr	Pro	Met	Ser	Val	Asp	Asp	Ala	Leu	
				170					175					180		
tcc	gag	atg	gaa	ttg	ggt	gga	cac	gat	ttc	tac	ctc	ttc	gtc	aac	gaa	691
Ser	Glu	Met	Glu	Leu	Val	Gly	His	Asp	Phe	Tyr	Leu	Phe	Val	Asn	Glu	
			185					190					195			
gag	acc	aac	cag	cca	tcg	gtg	gtg	tac	cgc	cga	cac	gca	ttc	gac	tat	739
Glu	Thr	Asn	Gln	Pro	Ser	Val	Val	Tyr	Arg	Arg	His	Ala	Phe	Asp	Tyr	
		200					205					210				
gga	tta	att	tcc	ctg	tcc	gat	gca	tagcaattag	ttgctaagta	ccc						786
Gly	Leu	Ile	Ser	Leu	Ser	Asp	Ala									
	215					220										

&lt;210&gt; 162

&lt;211&gt; 221

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 162

Val Thr Thr Pro Ala Glu Asn Asn Thr Leu Ser Pro Glu Thr Lys Val  
 1 5 10 15

Ser Ile Thr Gly Arg Asn Val Glu Val Pro Asp His Phe Ala Glu Arg  
 20 25 30

Val Asn Thr Lys Leu Ala Lys Ile Glu Arg Leu Asp Pro Thr Leu Thr  
 35 40 45

Phe Phe His Val Glu Leu Gln His Glu Pro Asn Pro Arg Arg Ala Asp  
 50 55 60

Glu Ser Asp Arg Ile Gln Ile Thr Ala Thr Gly Lys Gly His Ile Ala  
 65 70 75 80

Arg Ala Glu Ala Lys Glu Asp Ser Phe Tyr Ala Ala Leu Glu Thr Ala  
 85 90 95

Leu Ala Lys Met Glu Arg Ser Leu Arg Lys Val Lys Ala Arg Arg Ser  
 100 105 110

Ile Ser Arg Ser Gly His Arg Ala Pro Leu Gly Thr Gly Glu Val Gly  
 115 120 125

Ala Gln Leu Val Ala Glu Ser Gln Glu Ala Arg Gly Ala Asp Glu Leu  
 130 135 140

Gly Lys Tyr Asp Val Asp Pro Tyr Ala Asp Lys Val Asp Asp Val Met  
 145 150 155 160

Pro Gly Gln Val Val Arg Thr Lys Glu His Pro Ala Thr Pro Met Ser  
 165 170 175

Val Asp Asp Ala Leu Ser Glu Met Glu Leu Val Gly His Asp Phe Tyr  
 180 185 190

Leu Phe Val Asn Glu Glu Thr Asn Gln Pro Ser Val Val Tyr Arg Arg  
 195 200 205

His Ala Phe Asp Tyr Gly Leu Ile Ser Leu Ser Asp Ala  
 210 215 220

&lt;210&gt; 163

&lt;211&gt; 678

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(655)

&lt;223&gt; RXN02450

&lt;400&gt; 163

ccagaccgat ctccatcaat tcacaggcga agcgaaccga aaacgattgc gttgttctac 60

actgatcaga gcccgtcct caacaagaag agcaacacca atg aat ctg aaa gat 115  
 Met Asn Leu Lys Asp  
 1 5

ctc aag gcc gca gag acc cgt caa agg ttt atc gat gta gcc cac gaa 163  
 Leu Lys Ala Ala Glu Thr Arg Gln Arg Phe Ile Asp Val Ala His Glu  
 10 15 20

ctc ttc ttg gag cac ggt tat ggt tcc acc tcc atg aat cag att gct 211  
 Leu Phe Leu Glu His Gly Tyr Gly Ser Thr Ser Met Asn Gln Ile Ala  
 25 30 35

cag gca gcg ggt ggt agc cgg gca aac ctt tac ctt cat ttc cgt aac 259  
 Gln Ala Ala Gly Gly Ser Arg Ala Asn Leu Tyr Leu His Phe Arg Asn  
 40 45 50

aag ccc gat ctc atg atg gct aaa atg cgg gaa ctt gaa ccc gcg gtc 307  
 Lys Pro Asp Leu Met Met Ala Lys Met Arg Glu Leu Glu Pro Ala Val  
 55 60 65

cgc acc cct gtc cta aaa gtt ttt gat ctc cct gaa cac act ttg gag 355  
 Arg Thr Pro Val Leu Lys Val Phe Asp Leu Pro Glu His Thr Leu Glu  
 70 75 80 85

tcc att ctt aga tgg ctg gac tcc atg acg gag gtg tgg aaa gcg aat 403  
 Ser Ile Leu Arg Trp Leu Asp Ser Met Thr Glu Val Trp Lys Ala Asn  
 90 95 100

gcc aaa gtg ttc ggg gcg atg gaa caa gcg atg gtc gaa gat gct gcg 451  
 Ala Lys Val Phe Gly Ala Met Glu Gln Ala Met Val Glu Asp Ala Ala  
 105 110 115

gtg gcc gat gag tgg ctt tca atg atg cag agg ttg agc caa tcg gtg 499  
 Val Ala Asp Glu Trp Leu Ser Met Met Gln Arg Leu Ser Gln Ser Val  
 120 125 130

ccc gaa ttg gtt gag aat gaa gag cgt cga gtt cag ttc ctg gct agc 547  
 Pro Glu Leu Val Glu Asn Glu Glu Arg Arg Val Gln Phe Leu Ala Ser  
 135 140 145

ttg atg ggc atg gat aga aac ttt tac ttc ctc tat gtc cga ggg caa 595  
 Leu Met Gly Met Asp Arg Asn Phe Tyr Phe Leu Tyr Val Arg Gly Gln  
 150 155 160 165

gat gtt gat gag gaa ttg cta aag ttg gct gtg gct cgc caa tgg ttg 643  
 Asp Val Asp Glu Leu Leu Lys Leu Ala Val Ala Arg Gln Trp Leu  
 170 175 180

gca gtt ttc caa taggcaatgc gccccaatcc cct 678  
 Ala Val Phe Gln  
 185

&lt;210&gt; 164

&lt;211&gt; 185

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 164

Met Asn Leu Lys Asp Leu Lys Ala Ala Glu Thr Arg Gln Arg Phe Ile  
 1 5 10 15

Asp Val Ala His Glu Leu Phe Leu Glu His Gly Tyr Gly Ser Thr Ser  
 20 25 30

Met Asn Gln Ile Ala Gln Ala Ala Gly Gly Ser Arg Ala Asn Leu Tyr  
 35 40 45

Leu His Phe Arg Asn Lys Pro Asp Leu Met Met Ala Lys Met Arg Glu  
 50 55 60

Leu Glu Pro Ala Val Arg Thr Pro Val Leu Lys Val Phe Asp Leu Pro  
 65 70 75 80

Glu His Thr Leu Glu Ser Ile Leu Arg Trp Leu Asp Ser Met Thr Glu  
 85 90 95

Val Trp Lys Ala Asn Ala Lys Val Phe Gly Ala Met Glu Gln Ala Met  
 100 105 110

Val Glu Asp Ala Ala Val Ala Asp Glu Trp Leu Ser Met Met Gln Arg  
 115 120 125

Leu Ser Gln Ser Val Pro Glu Leu Val Glu Asn Glu Glu Arg Arg Val  
 130 135 140

Gln Phe Leu Ala Ser Leu Met Gly Met Asp Arg Asn Phe Tyr Phe Leu  
 145 150 155 160

Tyr Val Arg Gly Gln Asp Val Asp Glu Glu Leu Leu Lys Leu Ala Val  
 165 170 175

Ala Arg Gln Trp Leu Ala Val Phe Gln  
 180 185

&lt;210&gt; 165

&lt;211&gt; 678

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(655)

&lt;223&gt; FRXA02450

&lt;400&gt; 165

ccagaccgat ctccatcaat tcacaggcga agcgaaccga aaacgattgc gttgttctac 60

actgatcaga gcccgtccct caacaagaag agcaacacca atg aat ctg aaa gat 115  
 Met Asn Leu Lys Asp  
 1 5

ctc aag gcc gca gag acc cgt caa agg ttt atc gat gta gcc cac gaa 163  
 Leu Lys Ala Ala Glu Thr Arg Gln Arg Phe Ile Asp Val Ala His Glu  
 10 15 20

ctc ttc ttg gag cac ggt tat ggt tcc acc tcc atg aat cag att gct 211  
 Leu Phe Leu Glu His Gly Tyr Gly Ser Thr Ser Met Asn Gln Ile Ala  
 25 30 35

cag gca gcg ggt ggt agc cgg gca aac ctt tac ctt cat ttc cgt aac 259  
 Gln Ala Ala Gly Gly Ser Arg Ala Asn Leu Tyr Leu His Phe Arg Asn  
 40 45 50

aag ccc gat ctc atg atg gct aaa atg cgg gaa ctt gaa ccc gcg gtc 307

Lys Pro Asp Leu Met Met Ala Lys Met Arg Glu Leu Glu Pro Ala Val  
 55 60 65  
 cgc acc cct gtc cta aaa gtt ttt gat ctc cct gaa cac act ttg gag 355  
 Arg Thr Pro Val Leu Lys Val Phe Asp Leu Pro Glu His Thr Leu Glu  
 70 75 80 85  
 tcc att ctt aga tgg ctg gac tcc atg acg gag gtg tgg aaa gcg aat 403  
 Ser Ile Leu Arg Trp Leu Asp Ser Met Thr Glu Val Trp Lys Ala Asn  
 90 95 100  
 gcc aaa gtg ttc ggg gcg atg gaa caa gcg atg gtc gaa gat gct gcg 451  
 Ala Lys Val Phe Gly Ala Met Glu Gln Ala Met Val Glu Asp Ala Ala  
 105 110 115  
 gtg gcc gat gag tgg ctt tca atg atg cag agg ttg agc caa tcg gtg 499  
 Val Ala Asp Glu Trp Leu Ser Met Met Gln Arg Leu Ser Gln Ser Val  
 120 125 130  
 ccc gaa ttg gtt gag aat gaa gag cgt cga gtt cag ttc ctg gct agc 547  
 Pro Glu Leu Val Glu Asn Glu Glu Arg Arg Val Gln Phe Leu Ala Ser  
 135 140 145  
 ttg atg ggc atg gat aga aac ttt tac ttc ctc tat gtc cga ggg caa 595  
 Leu Met Gly Met Asp Arg Asn Phe Tyr Phe Leu Tyr Val Arg Gly Gln  
 150 155 160 165  
 gat gtt gat gag gaa ttg cta aag ttg gct gtg gct cgc caa tgg ttg 643  
 Asp Val Asp Glu Glu Leu Leu Lys Leu Ala Val Ala Arg Gln Trp Leu  
 170 175 180  
 gca gtt ttc caa taggcaatgc gcccgaatcc cct 678  
 Ala Val Phe Gln  
 185

&lt;210&gt; 166

&lt;211&gt; 185

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 166

Met Asn Leu Lys Asp Leu Lys Ala Ala Glu Thr Arg Gln Arg Phe Ile  
 1 5 10 15  
 Asp Val Ala His Glu Leu Phe Leu Glu His Gly Tyr Gly Ser Thr Ser  
 20 25 30  
 Met Asn Gln Ile Ala Gln Ala Ala Gly Gly Ser Arg Ala Asn Leu Tyr  
 35 40 45  
 Leu His Phe Arg Asn Lys Pro Asp Leu Met Met Ala Lys Met Arg Glu  
 50 55 60  
 Leu Glu Pro Ala Val Arg Thr Pro Val Leu Lys Val Phe Asp Leu Pro  
 65 70 75 80  
 Glu His Thr Leu Glu Ser Ile Leu Arg Trp Leu Asp Ser Met Thr Glu  
 85 90 95  
 Val Trp Lys Ala Asn Ala Lys Val Phe Gly Ala Met Glu Gln Ala Met



100					105					110					
Val	Glu	Asp	Ala	Ala	Val	Ala	Asp	Glu	Trp	Leu	Ser	Met	Met	Gln	Arg
		115					120					125			
Leu	Ser	Gln	Ser	Val	Pro	Glu	Leu	Val	Glu	Asn	Glu	Glu	Arg	Arg	Val
		130					135					140			
Gln	Phe	Leu	Ala	Ser	Leu	Met	Gly	Met	Asp	Arg	Asn	Phe	Tyr	Phe	Leu
		145					150					155			160
Tyr	Val	Arg	Gly	Gln	Asp	Val	Asp	Glu	Glu	Leu	Leu	Lys	Leu	Ala	Val
				165					170					175	
Ala	Arg	Gln	Trp	Leu	Ala	Val	Phe	Gln							
			180					185							

&lt;210&gt; 167

&lt;211&gt; 816

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(793)

&lt;223&gt; RXA01898

&lt;400&gt; 167

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caacggcact tttgcgccca atgatcgacg ccccggtgaa ctaatccgcc tccttgatag 60
cctcctaacg gctgtccgcg attaaggctc tgaaatacta atg agt gtg aaa gca 115
                                         Met Ser Val Lys Ala
                                         1                               5

cat gaa tct gtc atg gat tgg gtc acc gag gag ctc cgc agc ggt cgc 163
His Glu Ser Val Met Asp Trp Val Thr Glu Glu Leu Arg Ser Gly Arg
                        10                        15                        20

cta aaa atc ggt gac cac ctc ccc agc gaa cgg gcg ctc tcc gaa acc 211
Leu Lys Ile Gly Asp His Leu Pro Ser Glu Arg Ala Leu Ser Glu Thr
                        25                        30                        35

ctc gga gtt tcc cga agc tcc ctg cgc gag gcg ctt cgt gtg ctc gaa 259
Leu Gly Val Ser Arg Ser Ser Leu Arg Glu Ala Leu Arg Val Leu Glu
                        40                        45                        50

gcc ctc ggc acc att tcc acc gcc acc gga tcc ggc ccg cgg tct ggc 307
Ala Leu Gly Thr Ile Ser Thr Ala Thr Gly Ser Gly Pro Arg Ser Gly
                        55                        60                        65

acc atc atc act gct gcc cct ggc cag gcg ctt tcc ctc tcc gtg acg 355
Thr Ile Ile Thr Ala Ala Pro Gly Gln Ala Leu Ser Leu Ser Val Thr
                        70                        75                        80                        85

ctg cag ttg gtc acc aac cag gtc ggc cac cac gat att tat gaa acc 403
Leu Gln Leu Val Thr Asn Gln Val Gly His His Asp Ile Tyr Glu Thr
                        90                        95                        100

cgc caa ctc ctt gaa ggc tgg gct gcc ctg cat tcc agc gcc gaa cgt 451
Arg Gln Leu Leu Glu Gly Trp Ala Ala Leu His Ser Ser Ala Glu Arg

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105	110	115	
ggc gac tgg gac gtg gca gaa gcg ttg ctg gaa aag atg gac gac ccc Gly Asp Trp Asp Val Ala Glu Ala Leu Leu Glu Lys Met Asp Asp Pro 120 125 130			499
tcg cta ccg ctc gag gat ttt ttg cgt ttc gac gcc gaa ttc cac gtt Ser Leu Pro Leu Glu Asp Phe Leu Arg Phe Asp Ala Glu Phe His Val 135 140 145			547
gtt atc tcc aaa ggc gcg gaa aac cct ctg atc agt acg ctc atg gaa Val Ile Ser Lys Gly Ala Glu Asn Pro Leu Ile Ser Thr Leu Met Glu 150 155 160 165			595
gcc ctc cgt ttg tcc gtg gca gat cac acc gtt gcc agg gcc cgg gcg Ala Leu Arg Leu Ser Val Ala Asp His Thr Val Ala Arg Ala Arg Ala 170 175 180			643
ctc ccc gat tgg cga gcc acc tcg gcg cgt ctg cag aaa gaa cac cgc Leu Pro Asp Trp Arg Ala Thr Ser Ala Arg Leu Gln Lys Glu His Arg 185 190 195			691
gca atc ctc gca gca ctt cgc gca ggc gaa tcc aca gtg gcc gca acc Ala Ile Leu Ala Ala Leu Arg Ala Gly Glu Ser Thr Val Ala Ala Thr 200 205 210			739
ttg atc aaa gaa cac atc gaa ggc tac tac gaa gaa acc gct gcc gcc Leu Ile Lys Glu His Ile Glu Gly Tyr Tyr Glu Glu Thr Ala Ala Ala 215 220 225			787
gag gcc taaatgtccc gcactctgtg ggc Glu Ala 230			816

&lt;210&gt; 168

&lt;211&gt; 231

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 168

Met	Ser	Val	Lys	Ala	His	Glu	Ser	Val	Met	Asp	Trp	Val	Thr	Glu	Glu
1				5					10					15	

Leu	Arg	Ser	Gly	Arg	Leu	Lys	Ile	Gly	Asp	His	Leu	Pro	Ser	Glu	Arg
			20					25					30		

Ala	Leu	Ser	Glu	Thr	Leu	Gly	Val	Ser	Arg	Ser	Ser	Leu	Arg	Glu	Ala
		35					40					45			

Leu	Arg	Val	Leu	Glu	Ala	Leu	Gly	Thr	Ile	Ser	Thr	Ala	Thr	Gly	Ser
	50					55					60				

Gly	Pro	Arg	Ser	Gly	Thr	Ile	Ile	Thr	Ala	Ala	Pro	Gly	Gln	Ala	Leu
65					70					75					80

Ser	Leu	Ser	Val	Thr	Leu	Gln	Leu	Val	Thr	Asn	Gln	Val	Gly	His	His
				85					90					95	

Asp	Ile	Tyr	Glu	Thr	Arg	Gln	Leu	Leu	Glu	Gly	Trp	Ala	Ala	Leu	His
			100					105					110		

Ser Ser Ala Glu Arg Gly Asp Trp Asp Val Ala Glu Ala Leu Leu Glu  
 115 120 125

Lys Met Asp Asp Pro Ser Leu Pro Leu Glu Asp Phe Leu Arg Phe Asp  
 130 135 140

Ala Glu Phe His Val Val Ile Ser Lys Gly Ala Glu Asn Pro Leu Ile  
 145 150 155 160

Ser Thr Leu Met Glu Ala Leu Arg Leu Ser Val Ala Asp His Thr Val  
 165 170 175

Ala Arg Ala Arg Ala Leu Pro Asp Trp Arg Ala Thr Ser Ala Arg Leu  
 180 185 190

Gln Lys Glu His Arg Ala Ile Leu Ala Ala Leu Arg Ala Gly Glu Ser  
 195 200 205

Thr Val Ala Ala Thr Leu Ile Lys Glu His Ile Glu Gly Tyr Tyr Glu  
 210 215 220

Glu Thr Ala Ala Ala Glu Ala  
 225 230

<210> 169  
 <211> 594  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(571)  
 <223> RXA00004

<400> 169  
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tgccttcccg aagtattttc caattcccga tgtaggggtca gtg ctg act caa ttg 115  
 Val Leu Thr Gln Leu  
 1 5

att gaa tca tcg att ttc gac aac gtt gcg agc agg gag tcc tct gaa 163  
 Ile Glu Ser Ser Ile Phe Asp Asn Val Ala Ser Arg Glu Ser Ser Glu  
 10 15 20

ttt ctc ggc cat gct gcc atc gat cta ctt gct ggc ctt gtc tat gaa 211  
 Phe Leu Gly His Ala Ala Ile Asp Leu Leu Ala Gly Leu Val Tyr Glu  
 25 30 35

aaa gcc act ccc tat gct cca gat gaa gca ctt aga gtg gca gtt tat 259  
 Lys Ala Thr Pro Tyr Ala Pro Asp Glu Ala Leu Arg Val Ala Val Tyr  
 40 45 50

ggc tat att cgg gag aac ctt gga tcc tca caa ctt acg gtc gca gct 307  
 Gly Tyr Ile Arg Glu Asn Leu Gly Ser Ser Gln Leu Thr Val Ala Ala  
 55 60 65

gta gcc ggg gcg cat aga atc gcg gtt cgt acg ttg cat cga tta ttt 355  
 Val Ala Gly Ala His Arg Ile Ala Val Arg Thr Leu His Arg Leu Phe

70	75	80	85	
gaa ggc gaa gca tac	gga gta gcg gaa tta atc cga cac ctc cga tta			403
Glu Gly Glu Ala Tyr	Gly Val Ala Glu Leu Ile Arg His Leu Arg Leu			
	90	95	100	
gag gca gta tat gaa gac ctt cgg gat cct cgc ctc cag aac ctg acc				451
Glu Ala Val Tyr Glu Asp Leu Arg Asp Pro Arg Leu Gln Asn Leu Thr				
	105	110	115	
att ttg gct atc ggc atg cgc cac ggc att tcc agc caa gct cat tta				499
Ile Leu Ala Ile Gly Met Arg His Gly Ile Ser Ser Gln Ala His Leu				
	120	125	130	
aca aga ctg ttt cgc gct aaa tat ggg gta ccg ccg gca gag ttt cgc				547
Thr Arg Leu Phe Arg Ala Lys Tyr Gly Val Pro Pro Ala Glu Phe Arg				
	135	140	145	
cga ggg tat att aat agc gct gct tgagggcacc gcaagcgtgg cgc				594
Arg Gly Tyr Ile Asn Ser Ala Ala				
150	155			

&lt;210&gt; 170

&lt;211&gt; 157

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 170

Val Leu Thr Gln Leu Ile Glu Ser Ser Ile Phe Asp Asn Val Ala Ser				
1	5	10		15
Arg Glu Ser Ser Glu Phe Leu Gly His Ala Ala Ile Asp Leu Leu Ala				
	20	25		30
Gly Leu Val Tyr Glu Lys Ala Thr Pro Tyr Ala Pro Asp Glu Ala Leu				
	35	40		45
Arg Val Ala Val Tyr Gly Tyr Ile Arg Glu Asn Leu Gly Ser Ser Gln				
	50	55		60
Leu Thr Val Ala Ala Val Ala Gly Ala His Arg Ile Ala Val Arg Thr				
	65	70		75
Leu His Arg Leu Phe Glu Gly Glu Ala Tyr Gly Val Ala Glu Leu Ile				
	85	90		95
Arg His Leu Arg Leu Glu Ala Val Tyr Glu Asp Leu Arg Asp Pro Arg				
	100	105		110
Leu Gln Asn Leu Thr Ile Leu Ala Ile Gly Met Arg His Gly Ile Ser				
	115	120		125
Ser Gln Ala His Leu Thr Arg Leu Phe Arg Ala Lys Tyr Gly Val Pro				
	130	135		140
Pro Ala Glu Phe Arg Arg Gly Tyr Ile Asn Ser Ala Ala				
145	150	155		

&lt;210&gt; 171

<211> 418  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(418)  
 <223> RXA01001

<400> 171  
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 atctccggca ccatccgccg ccgcatcatg aagggggcta gtg acc gtg tcg tgg 115  
 Val Thr Val Ser Trp  
 1 5  
 cac caa gca act gac gct cca cca agc atc cgc atc acc acg ctt gcg 163  
 His Gln Ala Thr Asp Ala Pro Pro Ser Ile Arg Ile Thr Thr Leu Ala  
 10 15 20  
 cca tcg ctg cag cct aat cag cgc aaa gtc gcc gaa gtc atg ctt gtc 211  
 Pro Ser Leu Gln Pro Asn Gln Arg Lys Val Ala Glu Val Met Leu Val  
 25 30 35  
 gac gcc ccc agc atc gtc gaa ctg acc gct cag ggc ctt gca gat cgc 259  
 Asp Ala Pro Ser Ile Val Glu Leu Thr Ala Gln Gly Leu Ala Asp Arg  
 40 45 50  
 gtg ggg gtt ggg cgt gcc acc gtc atc cgc acc gcc cag tcc tta ggc 307  
 Val Gly Val Gly Arg Ala Thr Val Ile Arg Thr Ala Gln Ser Leu Gly  
 55 60 65  
 tac gac gga ttc ccg cag ctg cgc gtc gcc ctg gcg cag gaa ctg gca 355  
 Tyr Asp Gly Phe Pro Gln Leu Arg Val Ala Leu Ala Gln Glu Leu Ala  
 70 75 80 85  
 ctg gcg cag ggc gcg tcg aga agc atg gtt gaa gga gcg tta agc tcc 403  
 Leu Ala Gln Gly Ala Ser Arg Ser Met Val Glu Gly Ala Leu Ser Ser  
 90 95 100  
 tcg ttg ctt ggt cat 418  
 Ser Leu Leu Gly His  
 105

<210> 172  
 <211> 106  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 172  
 Val Thr Val Ser Trp His Gln Ala Thr Asp Ala Pro Pro Ser Ile Arg  
 1 5 10 15  
 Ile Thr Thr Leu Ala Pro Ser Leu Gln Pro Asn Gln Arg Lys Val Ala  
 20 25 30  
 Glu Val Met Leu Val Asp Ala Pro Ser Ile Val Glu Leu Thr Ala Gln  
 35 40 45  
 Gly Leu Ala Asp Arg Val Gly Val Gly Arg Ala Thr Val Ile Arg Thr

50	55	60
Ala Gln Ser Leu Gly Tyr Asp Gly Phe Pro Gln Leu Arg Val Ala Leu		
65	70	75 80
Ala Gln Glu Leu Ala Leu Ala Gln Gly Ala Ser Arg Ser Met Val Glu		
	85	90 95
Gly Ala Leu Ser Ser Ser Leu Leu Gly His		
	100	105

<210> 173  
 <211> 1578  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1555)  
 <223> RXA01375

<400> 173  
 caagcagcca atggccgcgt atgaaaaccc ccgctccata aatacagaac acatacagaa 60  
 cttgaccgac aatctaatta ccgcgaaggg ttagcagcac gtg act gaa aag tat 115  
 Val Thr Glu Lys Tyr  
 1 5  
 cgt ccc gtc cgt gac att aag cct gct ccg gca gca atg caa tca act 163  
 Arg Pro Val Arg Asp Ile Lys Pro Ala Pro Ala Ala Met Gln Ser Thr  
 10 15 20  
 aaa caa gcg ggc cat cct gtg ttc cga agc gtt gtc gct ttt gtt tca 211  
 Lys Gln Ala Gly His Pro Val Phe Arg Ser Val Val Ala Phe Val Ser  
 25 30 35  
 gtg ctg gtg ttg gtg gta tcg ggt ttg ggg tat ctt gct gtc gga aaa 259  
 Val Leu Val Leu Val Val Ser Gly Leu Gly Tyr Leu Ala Val Gly Lys  
 40 45 50  
 gtg gat ggt gtc gct tct ggc aac ttg aac ctt ggt ggc ggt cgc ggc 307  
 Val Asp Gly Val Ala Ser Gly Asn Leu Asn Leu Gly Gly Gly Arg Gly  
 55 60 65  
 atc cag gac ggc aat gct gct gac ggt gct acc gat att ttg ttg gtg 355  
 Ile Gln Asp Gly Asn Ala Ala Asp Gly Ala Thr Asp Ile Leu Leu Val  
 70 75 80 85  
 ggt tct gat tcc cgt tcc gat gct cag ggc aac acg ctg act gag gag 403  
 Gly Ser Asp Ser Arg Ser Asp Ala Gln Gly Asn Thr Leu Thr Glu Glu  
 90 95 100  
 gag ctg gcg atg ctc cgc gca ggc gac gag gag aac gac aac acc gat 451  
 Glu Leu Ala Met Leu Arg Ala Gly Asp Glu Glu Asn Asp Asn Thr Asp  
 105 110 115  
 acg atc atg gtg att cgt gtt cct aac gat ggt tcc tct gcc acc gct 499  
 Thr Ile Met Val Ile Arg Val Pro Asn Asp Gly Ser Ser Ala Thr Ala  
 120 125 130

gtc gcg att cct cgc gat acc tat att cat gat gac gat tac ggc aac	547
Val Ala Ile Pro Arg Asp Thr Tyr Ile His Asp Asp Asp Tyr Gly Asn	
135 140 145	
atg aag atc aac ggc gtt tac ggt gcg tac aag gat gcc cgt cgc gct	595
Met Lys Ile Asn Gly Val Tyr Gly Ala Tyr Lys Asp Ala Arg Arg Ala	
150 155 160 165	
gag ctc atg gaa cag ggt ttc acc aat gag tca gag ctg gaa acc cgg	643
Glu Leu Met Glu Gln Gly Phe Thr Asn Glu Ser Glu Leu Glu Thr Arg	
170 175 180	
gcg aag gat gct ggc cga gaa ggt ttg atc gat gct gtg tca gat ctc	691
Ala Lys Asp Ala Gly Arg Glu Gly Leu Ile Asp Ala Val Ser Asp Leu	
185 190 195	
acc ggc atc acc gtc gat cac tac gcc gaa gtt ggc ctt ttg gga ttc	739
Thr Gly Ile Thr Val Asp His Tyr Ala Glu Val Gly Leu Leu Gly Phe	
200 205 210	
gtc ctg ctc acc gat gct gtc ggt ggt gtc gaa gtc tgc ctc aac aac	787
Val Leu Leu Thr Asp Ala Val Gly Gly Val Glu Val Cys Leu Asn Asn	
215 220 225	
gcc gtc gat gag cct tta tcc ggc gcc aac ttc cct gca ggc cgt caa	835
Ala Val Asp Glu Pro Leu Ser Gly Ala Asn Phe Pro Ala Gly Arg Gln	
230 235 240 245	
acc ctc ggt ggc tcc gat gcg ttg tct tat gtg cgc cag cgc cac gat	883
Thr Leu Gly Gly Ser Asp Ala Leu Ser Tyr Val Arg Gln Arg His Asp	
250 255 260	
ctc ccc cgc ggc gac ctc gac cgc atc gtc cgc cag cag tcg tat atg	931
Leu Pro Arg Gly Asp Leu Asp Arg Ile Val Arg Gln Gln Ser Tyr Met	
265 270 275	
gca tcg ctt gtt aat cag gtg ctg tct tct gga aca ctc acc aac cct	979
Ala Ser Leu Val Asn Gln Val Leu Ser Ser Gly Thr Leu Thr Asn Pro	
280 285 290	
gca aag ctt tcc gca ctt gct gat gcc gtc acc cgc tcc gtc gtc atc	1027
Ala Lys Leu Ser Ala Leu Ala Asp Ala Val Thr Arg Ser Val Val Ile	
295 300 305	
gac gaa ggc tgg gag atc atg agc ttt gcc act cag ctg cag aac ctc	1075
Asp Glu Gly Trp Glu Ile Met Ser Phe Ala Thr Gln Leu Gln Asn Leu	
310 315 320 325	
gcg ggc ggc aac gtc aca ttt gcc acc atc ccg gtt acc tct atc gac	1123
Ala Gly Gly Asn Val Thr Phe Ala Thr Ile Pro Val Thr Ser Ile Asp	
330 335 340	
ggc acc ggc gat tac ggc gag tcc gtt gtc acc atc gat gtc aac cag	1171
Gly Thr Gly Asp Tyr Gly Glu Ser Val Val Thr Ile Asp Val Asn Gln	
345 350 355	
gtg cat gca ttc ttc caa gaa gca ctc ggc gaa gca gag cca gct cca	1219
Val His Ala Phe Phe Gln Glu Ala Leu Gly Glu Ala Glu Pro Ala Pro	
360 365 370	
gaa gac ggc tcc gac gat caa tct gct gat cag gcc cct gac cta agc	1267

Glu Asp Gly Ser Asp Asp Gln Ser Ala Asp Gln Ala Pro Asp Leu Ser  
 375 380 385  
 gaa gtc gag gtc cac gtc ctc aac gct tcc tac gtc gaa ggc ctc gcc 1315  
 Glu Val Glu Val His Val Leu Asn Ala Ser Tyr Val Glu Gly Leu Ala  
 390 395 400 405  
 aac ggt atc gcc gcg caa ctg cag gaa ttg ggt tac tcc atc gca gag 1363  
 Asn Gly Ile Ala Ala Gln Leu Gln Glu Leu Gly Tyr Ser Ile Ala Glu  
 410 415 420  
 acc ggc aac gca gcg gaa ggc ctc tac tac gag tcc cag atc ctc gcc 1411  
 Thr Gly Asn Ala Ala Glu Gly Leu Tyr Tyr Glu Ser Gln Ile Leu Ala  
 425 430 435  
 gcc gaa gaa gac agc gcc aag gcc ctc gcg att tcc gaa gcc ctc ggt 1459  
 Ala Glu Glu Asp Ser Ala Lys Ala Leu Ala Ile Ser Glu Ala Leu Gly  
 440 445 450  
 ggt ctc cca tcg tgg cca act ctt ccc tcg acg aca aca ccg tca tcg 1507  
 Gly Leu Pro Ser Trp Pro Thr Leu Pro Ser Thr Thr Thr Pro Ser Ser  
 455 460 465  
 tcg tat ccg ccg gcg att acg ctg gcc cta ccg cgg aag caa acg ccg 1555  
 Ser Tyr Pro Pro Ala Ile Thr Leu Ala Leu Pro Arg Lys Gln Thr Pro  
 470 475 480 485  
 tgacatccag caccgtcggc cag 1578

&lt;210&gt; 174

&lt;211&gt; 485

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 174

Val Thr Glu Lys Tyr Arg Pro Val Arg Asp Ile Lys Pro Ala Pro Ala  
 1 5 10 15  
 Ala Met Gln Ser Thr Lys Gln Ala Gly His Pro Val Phe Arg Ser Val  
 20 25 30  
 Val Ala Phe Val Ser Val Leu Val Leu Val Val Ser Gly Leu Gly Tyr  
 35 40 45  
 Leu Ala Val Gly Lys Val Asp Gly Val Ala Ser Gly Asn Leu Asn Leu  
 50 55 60  
 Gly Gly Gly Arg Gly Ile Gln Asp Gly Asn Ala Ala Asp Gly Ala Thr  
 65 70 75 80  
 Asp Ile Leu Leu Val Gly Ser Asp Ser Arg Ser Asp Ala Gln Gly Asn  
 85 90 95  
 Thr Leu Thr Glu Glu Glu Leu Ala Met Leu Arg Ala Gly Asp Glu Glu  
 100 105 110  
 Asn Asp Asn Thr Asp Thr Ile Met Val Ile Arg Val Pro Asn Asp Gly  
 115 120 125  
 Ser Ser Ala Thr Ala Val Ala Ile Pro Arg Asp Thr Tyr Ile His Asp



130					135					140					
Asp	Asp	Tyr	Gly	Asn	Met	Lys	Ile	Asn	Gly	Val	Tyr	Gly	Ala	Tyr	Lys
145					150					155					160
Asp	Ala	Arg	Arg	Ala	Glu	Leu	Met	Glu	Gln	Gly	Phe	Thr	Asn	Glu	Ser
				165					170					175	
Glu	Leu	Glu	Thr	Arg	Ala	Lys	Asp	Ala	Gly	Arg	Glu	Gly	Leu	Ile	Asp
			180					185					190		
Ala	Val	Ser	Asp	Leu	Thr	Gly	Ile	Thr	Val	Asp	His	Tyr	Ala	Glu	Val
		195					200					205			
Gly	Leu	Leu	Gly	Phe	Val	Leu	Leu	Thr	Asp	Ala	Val	Gly	Gly	Val	Glu
	210					215					220				
Val	Cys	Leu	Asn	Asn	Ala	Val	Asp	Glu	Pro	Leu	Ser	Gly	Ala	Asn	Phe
225					230					235					240
Pro	Ala	Gly	Arg	Gln	Thr	Leu	Gly	Gly	Ser	Asp	Ala	Leu	Ser	Tyr	Val
				245					250					255	
Arg	Gln	Arg	His	Asp	Leu	Pro	Arg	Gly	Asp	Leu	Asp	Arg	Ile	Val	Arg
			260					265					270		
Gln	Gln	Ser	Tyr	Met	Ala	Ser	Leu	Val	Asn	Gln	Val	Leu	Ser	Ser	Gly
		275					280					285			
Thr	Leu	Thr	Asn	Pro	Ala	Lys	Leu	Ser	Ala	Leu	Ala	Asp	Ala	Val	Thr
	290					295					300				
Arg	Ser	Val	Val	Ile	Asp	Glu	Gly	Trp	Glu	Ile	Met	Ser	Phe	Ala	Thr
305					310					315					320
Gln	Leu	Gln	Asn	Leu	Ala	Gly	Gly	Asn	Val	Thr	Phe	Ala	Thr	Ile	Pro
			325						330					335	
Val	Thr	Ser	Ile	Asp	Gly	Thr	Gly	Asp	Tyr	Gly	Glu	Ser	Val	Val	Thr
			340					345					350		
Ile	Asp	Val	Asn	Gln	Val	His	Ala	Phe	Phe	Gln	Glu	Ala	Leu	Gly	Glu
		355					360					365			
Ala	Glu	Pro	Ala	Pro	Glu	Asp	Gly	Ser	Asp	Asp	Gln	Ser	Ala	Asp	Gln
	370					375					380				
Ala	Pro	Asp	Leu	Ser	Glu	Val	Glu	Val	His	Val	Leu	Asn	Ala	Ser	Tyr
385					390					395					400
Val	Glu	Gly	Leu	Ala	Asn	Gly	Ile	Ala	Ala	Gln	Leu	Gln	Glu	Leu	Gly
			405						410					415	
Tyr	Ser	Ile	Ala	Glu	Thr	Gly	Asn	Ala	Ala	Glu	Gly	Leu	Tyr	Tyr	Glu
			420				425						430		
Ser	Gln	Ile	Leu	Ala	Ala	Glu	Glu	Asp	Ser	Ala	Lys	Ala	Leu	Ala	Ile
		435					440					445			
Ser	Glu	Ala	Leu	Gly	Gly	Leu	Pro	Ser	Trp	Pro	Thr	Leu	Pro	Ser	Thr
	450					455					460				

Thr Thr Pro Ser Ser Ser Tyr Pro Pro Ala Ile Thr Leu Ala Leu Pro  
 465 470 475 480

Arg Lys Gln Thr Pro  
 485

<210> 175  
 <211> 508  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(508)  
 <223> RXA02831

<400> 175  
 cgaactggcg cgtgtcttgt ccgacgcagc ctagcccgcc tttattgacc cctccggcac 60

gcttcgatag ggctaggaaa accctgtcgg aggagcgccc atg aca cat cgg atc 115  
 Met Thr His Arg Ile  
 1 5

aca ccc gaa ctc tcg gcc gaa ttg cgg ggg gtg gcc cac agc ctt gca 163  
 Thr Pro Glu Leu Ser Ala Glu Leu Arg Gly Val Ala His Ser Leu Ala  
 10 15 20

gat gcg gcg cgg ccc gtc acc ttg caa tac ttc cgc aca gca gtc gcg 211  
 Asp Ala Ala Arg Pro Val Thr Leu Gln Tyr Phe Arg Thr Ala Val Ala  
 25 30 35

gca gat aac aaa ggc gcg ctg cgc ggg atg gct tac gac ccc gtc acc 259  
 Ala Asp Asn Lys Gly Ala Leu Arg Gly Met Ala Tyr Asp Pro Val Thr  
 40 45 50

att gcc gac cgt gca agc gaa cag gcc atg cgt gac att ctg gcc cgt 307  
 Ile Ala Asp Arg Ala Ser Glu Gln Ala Met Arg Asp Ile Leu Ala Arg  
 55 60 65

cta cgc ccc gat gat gcg atc ttg ggt gaa gaa ttc ggc ccc aaa gcg 355  
 Leu Arg Pro Asp Asp Ala Ile Leu Gly Glu Glu Phe Gly Pro Lys Ala  
 70 75 80 85

ggc aca acg ggc ctc aca tgg gtg ctg gac ccg att gac ggc act cgc 403  
 Gly Thr Thr Gly Leu Thr Trp Val Leu Asp Pro Ile Asp Gly Thr Arg  
 90 95 100

gca tat atc gcg ggc gcg ccc act tgg ggc gtg ctg atc gca gta tcg 451  
 Ala Tyr Ile Ala Gly Ala Pro Thr Trp Gly Val Leu Ile Ala Val Ser  
 105 110 115

gat gat cag ggc ccg ctg ttc ggt atc gtc gac caa ccc tat att ggc 499  
 Asp Asp Gln Gly Pro Leu Phe Gly Ile Val Asp Gln Pro Tyr Ile Gly  
 120 125 130

gag cgt ttt 508  
 Glu Arg Phe  
 135

<210> 176  
 <211> 136  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 176  
 Met Thr His Arg Ile Thr Pro Glu Leu Ser Ala Glu Leu Arg Gly Val  
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 Ala His Ser Leu Ala Asp Ala Ala Arg Pro Val Thr Leu Gln Tyr Phe  
                   20                  25                  30  
 Arg Thr Ala Val Ala Ala Asp Asn Lys Gly Ala Leu Arg Gly Met Ala  
           35                  40                  45  
 Tyr Asp Pro Val Thr Ile Ala Asp Arg Ala Ser Glu Gln Ala Met Arg  
       50                  55                  60  
 Asp Ile Leu Ala Arg Leu Arg Pro Asp Asp Ala Ile Leu Gly Glu Glu  
   65                  70                  75                  80  
 Phe Gly Pro Lys Ala Gly Thr Thr Gly Leu Thr Trp Val Leu Asp Pro  
                   85                  90                  95  
 Ile Asp Gly Thr Arg Ala Tyr Ile Ala Gly Ala Pro Thr Trp Gly Val  
       100                  105                  110  
 Leu Ile Ala Val Ser Asp Asp Gln Gly Pro Leu Phe Gly Ile Val Asp  
       115                  120                  125  
 Gln Pro Tyr Ile Gly Glu Arg Phe  
       130                  135

<210> 177  
 <211> 696  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(673)  
 <223> RXA01110

<400> 177  
 atcatcgaca tgctccggaa aacttaaaaa ttcccggacg gttcacgcag attaccctag 60  
 caaagcaatc tagctgacga cccaatatag tcctgtcatt atg ctg gca att gtg 115  
   Met Leu Ala Ile Val  
   1                  5  
 cag cta tca aaa gaa tct att att ggc gca gcc gtt tcg atc ttg agc 163  
 Gln Leu Ser Lys Glu Ser Ile Ile Gly Ala Ala Val Ser Ile Leu Ser  
                   10                  15                  20  
 gaa ttc ggt ttg tcg gat atg acc atg cgc cgc gtc gca aag cag tta 211  
 Glu Phe Gly Leu Ser Asp Met Thr Met Arg Arg Val Ala Lys Gln Leu  
       25                  30                  35  
 aat gtc gcg ccg ggc gcg ctg tat tgg cat ttt aaa aat aag cag gag 259

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<210> 178
<211> 191
<212> PRT
<213> Corynebacterium glutamicum
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Met Leu Ala Ile Val Gln Leu Ser Lys Glu Ser Ile Ile Gly Ala Ala  
1 5 10 15

Val Ser Ile Leu Ser Glu Phe Gly Leu Ser Asp Met Thr Met Arg Arg  
20 25 30

Val Ala Lys Gln Leu Asn Val Ala Pro Gly Ala Leu Tyr Trp His Phe  
35 40 45

Lys Asn Lys Gln Glu Leu Ile Asp Ala Thr Ser Arg Tyr Leu Leu Ala  
50 55 60

Pro Val Leu Gly Arg Asn Asp Glu Gln Arg Ala Ser Ile Ser Ala Gln  
65 70 75 80

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<210> 179
<211> 861
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(838)  
<223> RXA00253
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<400> 179															
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cgctggttgt cttgtagaaa aaggcgtaac gtcataataac															
Met Pro Ser Glu Thr															115
1 5															
atg aaa cca gcc gta gcg tca act ctg gcg gcc act tcc acg gga cgt															163
Met Lys Pro Ala Val Ala Ser Thr Leu Ala Ala Thr Ser Thr Gly Arg															
10 15 20															
cgt cct gga cgc ccc acc caa cgt atc ctt tcc gtc gaa tcc ata gtg															211
Arg Pro Gly Arg Pro Thr Gln Arg Ile Leu Ser Val Glu Ser Ile Val															
25 30 35															
gag cgc act tta aac att gcc ggc cgc gaa gga ttc gct gcc gtg acc															259
Glu Arg Thr Leu Asn Ile Ala Gly Arg Glu Gly Phe Ala Ala Val Thr															
40 45 50															
atg aac cgc ctc gcc cga gac atg ggt gtc acc cct cgc gca ctg tat															307
Met Asn Arg Leu Ala Arg Asp Met Gly Val Thr Pro Arg Ala Leu Tyr															
55 60 65															
aac cat gtg cta aat cgt caa gaa atc att gat cgc gtc tgg gtg cgc															355
Asn His Val Leu Asn Arg Gln Glu Ile Ile Asp Arg Val Trp Val Arg															
70 75 80 85															
atc atc gat gat atc aaq qtg ccc gat ctt gat ccg qac aat tqg cgg															403

<400> 180  
Met Pro Ser Glu Thr Met Lys Pro Ala Val Ala Ser Thr Leu Ala Ala  
1 5 10 15  
Thr Ser Thr Gly Arg Arg Pro Gly Arg Pro Thr Gln Arg Ile Leu Ser  
20 25 30  
Val Glu Ser Ile Val Glu Arg Thr Leu Asn Ile Ala Gly Arg Glu Gly  
35 40 45  
Phe Ala Ala Val Thr Met Asn Arg Leu Ala Arg Asp Met Gly Val Thr  
50 55 60

Pro Arg Ala Leu Tyr Asn His Val Leu Asn Arg Gln Glu Ile Ile Asp  
 65 70 75 80  
 Arg Val Trp Val Arg Ile Ile Asp Asp Ile Lys Val Pro Asp Leu Asp  
 85 90 95  
 Pro Asp Asn Trp Arg Gln Ser Ile His Thr Leu Trp Ser Ser Leu Arg  
 100 105 110  
 Asp Gln Phe Arg Glu Thr Pro Arg Val Leu Leu Val Ala Leu Asp Glu  
 115 120 125  
 Gln Ile Ser Thr Gln Gly Thr Ser Pro Leu Arg Ile Ala Gly Ala Glu  
 130 135 140  
 Glu Ser Leu Lys Phe Leu Thr Asp Ile Gly Leu Ser Leu Lys Glu Ala  
 145 150 155 160  
 Thr Ile Ile Arg Glu Met Met Met Ala Asp Val Phe Ser Phe Thr Leu  
 165 170 175  
 Thr Ser Asp Tyr Thr Phe Asp Asn Arg Pro Glu Gly Glu Lys Pro Asp  
 180 185 190  
 Val Phe Ala Pro Val Pro Lys Pro Trp Leu Asp Glu Asn Pro Asp Val  
 195 200 205  
 Glu Ala Pro Leu Thr Arg Lys Ala Val Glu Glu Ser Val Ser Thr Ser  
 210 215 220  
 Asp Glu Leu Phe Gly Tyr Met Val Glu Ala Arg Ile Ala Tyr Ile Glu  
 225 230 235 240  
 Lys Leu Leu Ala Ala Lys  
 245

<210> 181  
 <211> 888  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(865)  
 <223> RXA01118

<400> 181  
 agtggagaa atgctcttgt taatcatgtg agacatgcta acgtaatgtt catcatatgc 60  
 acaagggttc gcaatgcgaa caaaaagagg agttgatggg atg gtc gaa caa tcg 115  
 Met Val Glu Gln Ser  
 1 5  
 cca gat ttc gta caa tca ttt gcc cgc ggc tta tct gtg atc cga agt 163  
 Pro Asp Phe Val Gln Ser Phe Ala Arg Gly Leu Ser Val Ile Arg Ser  
 10 15 20  
 ttc agc gca gat aat cca tcg caa aca ctg tcc gaa gtc gcc agc caa 211  
 Phe Ser Ala Asp Asn Pro Ser Gln Thr Leu Ser Glu Val Ala Ser Gln

25										30										35										
act	gga	ctc	tca	agg	gcc	acc	gct	agg	cgc	ttt	ctc	cac	acc	ttg	acc	259														
Thr	Gly	Leu	Ser	Arg	Ala	Thr	Ala	Arg	Arg	Phe	Leu	His	Thr	Leu	Thr															
	40						45				50																			
gac	ctt	gga	tat	gcg	gta	aac	aac	gat	tcc	cgg	ttc	cag	ctc	aca	cca	307														
Asp	Leu	Gly	Tyr	Ala	Val	Asn	Asn	Asp	Ser	Arg	Phe	Gln	Leu	Thr	Pro															
	55					60					65																			
cgt	gtt	ttg	gag	ctt	gga	gca	agc	tac	ctt	tcc	gca	ttg	tcc	ctg	cct	355														
Arg	Val	Leu	Glu	Leu	Gly	Ala	Ser	Tyr	Leu	Ser	Ala	Leu	Ser	Leu	Pro															
	70				75					80					85															
gcg	atc	gcg	cag	ccc	cgc	ctg	gag	gta	ctc	tcc	cgc	cag	gtc	ggc	gaa	403														
Ala	Ile	Ala	Gln	Pro	Arg	Leu	Glu	Val	Leu	Ser	Arg	Gln	Val	Gly	Glu															
				90					95					100																
tca	agc	tcc	atg	tcc	gta	ctc	gac	ggc	act	gac	atc	atc	tac	gtt	tgc	451														
Ser	Ser	Ser	Met	Ser	Val	Leu	Asp	Gly	Thr	Asp	Ile	Ile	Tyr	Val	Cys															
			105					110					115																	
cgc	gtt	ccg	gtg	cgc	cgc	atc	atg	acg	gtg	aac	atc	acc	atc	ggc	acc	499														
Arg	Val	Pro	Val	Arg	Arg	Ile	Met	Thr	Val	Asn	Ile	Thr	Ile	Gly	Thr															
		120				125						130																		
cgt	ttc	cct	gcg	tac	gcc	acc	tcc	atg	gga	cgc	atc	atg	ctg	gcc	aac	547														
Arg	Phe	Pro	Ala	Tyr	Ala	Thr	Ser	Met	Gly	Arg	Ile	Met	Leu	Ala	Asn															
	135					140					145																			
ctt	ccc	gaa	gaa	gaa	tta	gat	gaa	atg	ctg	gcg	gcg	gca	ccc	cct	gaa	595														
Leu	Pro	Glu	Glu	Glu	Leu	Asp	Glu	Met	Leu	Ala	Ala	Ala	Pro	Pro	Glu															
	150				155					160					165															
cag	ttg	acc	acc	cgg	tca	ctg	acc	tcc	atc	gcc	tca	atc	cgg	gaa	gag	643														
Gln	Leu	Thr	Thr	Arg	Ser	Leu	Thr	Ser	Ile	Ala	Ser	Ile	Arg	Glu	Glu															
				170					175					180																
atc	att	gct	acc	cgc	gaa	agg	ggg	tgg	tca	ttg	gtg	gat	cag	gag	ctc	691														
Ile	Ile	Ala	Thr	Arg	Glu	Arg	Gly	Trp	Ser	Leu	Val	Asp	Gln	Glu	Leu															
			185				190						195																	
gag	ccg	ggc	ctg	cgt	tcg	ctc	gcg	gcg	ccg	atc	acc	aat	gcc	cag	ggc	739														
Glu	Pro	Gly	Leu	Arg	Ser	Leu	Ala	Ala	Pro	Ile	Thr	Asn	Ala	Gln	Gly															
		200					205					210																		
gaa	gtg	gtt	gct	tcc	atc	aat	gtg	tcg	acc	caa	tcg	gca	tca	cat	tcg	787														
Glu	Val	Val	Ala	Ser	Ile	Asn	Val	Ser	Thr	Gln	Ser	Ala	Ser	His	Ser															
		215				220					225																			
gtg	gaa	gat	atc	cgc	aag	ctg	gtg	ctg	ccg	cag	ctt	tta	gaa	acg	gct	835														
Val	Glu	Asp	Ile	Arg	Lys	Leu	Val	Leu	Pro	Gln	Leu	Leu	Glu	Thr	Ala															
	230				235					240					245															
caa	gca	att	tcg	aca	gat	ctc	tct	gca	ctc	taaattaagg atcaaaaaat gaa					888															
Gln	Ala	Ile	Ser	Thr	Asp	Leu	Ser	Ala	Leu																					
				250					255																					



&lt;211&gt; 255

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 182

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Met Val Glu Gln Ser Pro Asp Phe Val Gln Ser Phe Ala Arg Gly Leu
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Ser Val Ile Arg Ser Phe Ser Ala Asp Asn Pro Ser Gln Thr Leu Ser
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Glu Val Ala Ser Gln Thr Gly Leu Ser Arg Ala Thr Ala Arg Arg Phe
          35          40          45

Leu His Thr Leu Thr Asp Leu Gly Tyr Ala Val Asn Asn Asp Ser Arg
          50          55          60

Phe Gln Leu Thr Pro Arg Val Leu Glu Leu Gly Ala Ser Tyr Leu Ser
          65          70          75          80

Ala Leu Ser Leu Pro Ala Ile Ala Gln Pro Arg Leu Glu Val Leu Ser
          85          90          95

Arg Gln Val Gly Glu Ser Ser Ser Met Ser Val Leu Asp Gly Thr Asp
          100          105          110

Ile Ile Tyr Val Cys Arg Val Pro Val Arg Arg Ile Met Thr Val Asn
          115          120          125

Ile Thr Ile Gly Thr Arg Phe Pro Ala Tyr Ala Thr Ser Met Gly Arg
          130          135          140

Ile Met Leu Ala Asn Leu Pro Glu Glu Glu Leu Asp Glu Met Leu Ala
          145          150          155          160

Ala Ala Pro Pro Glu Gln Leu Thr Thr Arg Ser Leu Thr Ser Ile Ala
          165          170          175

Ser Ile Arg Glu Glu Ile Ile Ala Thr Arg Glu Arg Gly Trp Ser Leu
          180          185          190

Val Asp Gln Glu Leu Glu Pro Gly Leu Arg Ser Leu Ala Ala Pro Ile
          195          200          205

Thr Asn Ala Gln Gly Glu Val Val Ala Ser Ile Asn Val Ser Thr Gln
          210          215          220

Ser Ala Ser His Ser Val Glu Asp Ile Arg Lys Leu Val Leu Pro Gln
          225          230          235          240

Leu Leu Glu Thr Ala Gln Ala Ile Ser Thr Asp Leu Ser Ala Leu
          245          250          255

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&lt;210&gt; 183

&lt;211&gt; 654

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(654)

&lt;223&gt; RXA01840

&lt;400&gt; 183

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Ile Ser Glu Glu Asp Gly Ala Ser Glu Pro Ala Thr Phe Ala Glu Arg	
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tcc caa cgc ctc atc cag cag gaa tgc gtt gca gcc gtg ttt ggt gga	96
Ser Gln Arg Leu Ile Gln Gln Glu Cys Val Ala Ala Val Phe Gly Gly	
20 25 30	
tgg acc tcc gcc tcc cgc aaa gca atg ctc ccc gtc ttt gag ggc aat	144
Trp Thr Ser Ala Ser Arg Lys Ala Met Leu Pro Val Phe Glu Gly Asn	
35 40 45	
aac tcc ctg ctg ttc tac ccg gtg cag tac gag ggc atg gaa tcc tcg	192
Asn Ser Leu Leu Phe Tyr Pro Val Gln Tyr Glu Gly Met Glu Ser Ser	
50 55 60	
ccg aat att ttc tac acc ggc gcc acc acc aac cag cag atc atc ccg	240
Pro Asn Ile Phe Tyr Thr Gly Ala Thr Thr Asn Gln Gln Ile Ile Pro	
65 70 75 80	
gct ctt gat tac ctg cgt gaa aac ggc ctg aac cgc ctt ttc ctt gtc	288
Ala Leu Asp Tyr Leu Arg Glu Asn Gly Leu Asn Arg Leu Phe Leu Val	
85 90 95	
ggt tcc gat tat gtt ttc cca cgc act gca aat tcc atc atc aag gac	336
Gly Ser Asp Tyr Val Phe Pro Arg Thr Ala Asn Ser Ile Ile Lys Asp	
100 105 110	
tac gcc gaa gcc aat ggt atg gaa atc gtc ggc gaa gac tac gcg ccg	384
Tyr Ala Glu Ala Asn Gly Met Glu Ile Val Gly Glu Asp Tyr Ala Pro	
115 120 125	
ttg gga tcc acc gac ttc acc acc atc gcc aac cgc atg cgt gac tcc	432
Leu Gly Ser Thr Asp Phe Thr Thr Ile Ala Asn Arg Met Arg Asp Ser	
130 135 140	
aac gca gat gcc gtg ttc aac act ttg aat ggc gat tcc aac gtg gcg	480
Asn Ala Asp Ala Val Phe Asn Thr Leu Asn Gly Asp Ser Asn Val Ala	
145 150 155 160	
ttc ttc cgc cag tac aac agc ctc ggc ttc aat gca gac acc ctt ccg	528
Phe Phe Arg Gln Tyr Asn Ser Leu Gly Phe Asn Ala Asp Thr Leu Pro	
165 170 175	
gtg atg tca gta tcc att gcg gaa gaa gaa gtc gga ggc atc ggc acc	576
Val Met Ser Val Ser Ile Ala Glu Glu Glu Val Gly Gly Ile Gly Thr	
180 185 190	
gca aat att gag ggc cag ctg gtg gcg tgg gac tac tac caa acc atc	624
Ala Asn Ile Glu Gly Gln Leu Val Ala Trp Asp Tyr Tyr Gln Thr Ile	
195 200 205	
gac acc cca gaa aac gag acc ttc gtg gag	654
Asp Thr Pro Glu Asn Glu Thr Phe Val Glu	
210 215	

<210> 184  
 <211> 218  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 184  
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 Ser Gln Arg Leu Ile Gln Gln Glu Cys Val Ala Ala Val Phe Gly Gly  
           20                  25                  30  
 Trp Thr Ser Ala Ser Arg Lys Ala Met Leu Pro Val Phe Glu Gly Asn  
           35                  40                  45  
 Asn Ser Leu Leu Phe Tyr Pro Val Gln Tyr Glu Gly Met Glu Ser Ser  
       50                  55                  60  
 Pro Asn Ile Phe Tyr Thr Gly Ala Thr Thr Asn Gln Gln Ile Ile Pro  
       65                  70                  75                  80  
 Ala Leu Asp Tyr Leu Arg Glu Asn Gly Leu Asn Arg Leu Phe Leu Val  
           85                  90                  95  
 Gly Ser Asp Tyr Val Phe Pro Arg Thr Ala Asn Ser Ile Ile Lys Asp  
          100                 105                 110  
 Tyr Ala Glu Ala Asn Gly Met Glu Ile Val Gly Glu Asp Tyr Ala Pro  
       115                 120                 125  
 Leu Gly Ser Thr Asp Phe Thr Thr Ile Ala Asn Arg Met Arg Asp Ser  
       130                 135                 140  
 Asn Ala Asp Ala Val Phe Asn Thr Leu Asn Gly Asp Ser Asn Val Ala  
      145                 150                 155                 160  
 Phe Phe Arg Gln Tyr Asn Ser Leu Gly Phe Asn Ala Asp Thr Leu Pro  
          165                 170                 175  
 Val Met Ser Val Ser Ile Ala Glu Glu Glu Val Gly Gly Ile Gly Thr  
          180                 185                 190  
 Ala Asn Ile Glu Gly Gln Leu Val Ala Trp Asp Tyr Tyr Gln Thr Ile  
      195                 200                 205  
 Asp Thr Pro Glu Asn Glu Thr Phe Val Glu  
      210                 215

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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(979)  
 <223> RXA00400

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tgagggcttc cccacccgca attaattaat tggagttttg	ttg ttc act ctt gaa	115
	Leu Phe Thr Leu Glu	
	1 5	
cag ttg cgg tgt ttt gtc gcc gtc gcc aat cat ctt cat ttc gga aaa	163	
Gln Leu Arg Cys Phe Val Ala Val Ala Asn His Leu His Phe Gly Lys		
	10 15 20	
gct gct gca gag cta tcc atg acg cag ccg ccg ttg agt cgt cag att	211	
Ala Ala Ala Glu Leu Ser Met Thr Gln Pro Pro Leu Ser Arg Gln Ile		
	25 30 35	
caa aag ctg gag aag atc gtc ggt gca acc ctg ctt gat cgt gac aac	259	
Gln Lys Leu Glu Lys Ile Val Gly Ala Thr Leu Leu Asp Arg Asp Asn		
	40 45 50	
cgc aag gtg gaa ctg acc act gcg ggt ttc gca ttt ttg aag gat gct	307	
Arg Lys Val Glu Leu Thr Thr Ala Gly Phe Ala Phe Leu Lys Asp Ala		
	55 60 65	
cgc ctc att ctc aat tcc acc gag aag gcg gct gag cgc gca cga ttg	355	
Arg Leu Ile Leu Asn Ser Thr Glu Lys Ala Ala Glu Arg Ala Arg Leu		
	70 75 80 85	
gct agc tct ggc atg tgg gga cag ctc aat att gga tac acc gct gca	403	
Ala Ser Ser Gly Met Trp Gly Gln Leu Asn Ile Gly Tyr Thr Ala Ala		
	90 95 100	
gcg ggt ttt tcc att ctg ggc ccg acg ttg aat cag ttg cat gag aag	451	
Ala Gly Phe Ser Ile Leu Gly Pro Thr Leu Asn Gln Leu His Glu Lys		
	105 110 115	
atg ccg ggg gtc agt gtc gat ctt ttt gag atg gtc tcc acc gag cag	499	
Met Pro Gly Val Ser Val Asp Leu Phe Glu Met Val Ser Thr Glu Gln		
	120 125 130	
atc gcc gcc ttg gaa tct ggg cta ctg gat ctt ggc att ggc cga ttg	547	
Ile Ala Ala Leu Glu Ser Gly Leu Leu Asp Leu Gly Ile Gly Arg Leu		
	135 140 145	
agc tcg cca gtt gag ggt ctt caa act cga cgt ctc cag gca gat tcc	595	
Ser Ser Pro Val Glu Gly Leu Gln Thr Arg Arg Leu Gln Ala Asp Ser		
	150 155 160 165	
ttg gtt ctt gca gct ccg aag ggg cat cca ctt ctt gat cag aat cga	643	
Leu Val Leu Ala Ala Pro Lys Gly His Pro Leu Leu Asp Gln Asn Arg		
	170 175 180	
cca ctg ttg cgg aag cat ctg act ggg gtt cct ttt ctg cag cac tct	691	
Pro Leu Leu Arg Lys His Leu Thr Gly Val Pro Phe Leu Gln His Ser		
	185 190 195	
ccc acc aag gcg aag tac ctc tac gac atc gtt gtt aga aac ttc acg	739	
Pro Thr Lys Ala Lys Tyr Leu Tyr Asp Ile Val Val Arg Asn Phe Thr		
	200 205 210	
atc aat gat gcg cag gtg caa cat acg ctg agc cag atc acc acg atg	787	
Ile Asn Asp Ala Gln Val Gln His Thr Leu Ser Gln Ile Thr Thr Met		
	215 220 225	

gtt agt ctg gtg gcc tct gga ctg ggt gtt gcg ctg gtt ccg gag tct 835  
 Val Ser Leu Val Ala Ser Gly Leu Gly Val Ala Leu Val Pro Glu Ser  
 230 235 240 245  
  
 gcg aaa aaa ctc aat tac agc ggt gtt gag tat cgc cat ttt tat gat 883  
 Ala Lys Lys Leu Asn Tyr Ser Gly Val Glu Tyr Arg His Phe Tyr Asp  
 250 255 260  
  
 cta cct gtt ggt tta gcg gag ctg cag gct att tat tcc acc tcg aat 931  
 Leu Pro Val Gly Leu Ala Glu Leu Gln Ala Ile Tyr Ser Thr Ser Asn  
 265 270 275  
  
 gat aat cct gcg gtg cgg aaa ttc atc aaa aac att gac gat acc ttt 979  
 Asp Asn Pro Ala Val Arg Lys Phe Ile Lys Asn Ile Asp Asp Thr Phe  
 280 285 290  
  
 taagcatttc aacatgccaa act 1002

&lt;210&gt; 186

&lt;211&gt; 293

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 186

Leu Phe Thr Leu Glu Gln Leu Arg Cys Phe Val Ala Val Ala Asn His  
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Leu His Phe Gly Lys Ala Ala Ala Glu Leu Ser Met Thr Gln Pro Pro  
 20 25 30

Leu Ser Arg Gln Ile Gln Lys Leu Glu Lys Ile Val Gly Ala Thr Leu  
 35 40 45

Leu Asp Arg Asp Asn Arg Lys Val Glu Leu Thr Thr Ala Gly Phe Ala  
 50 55 60

Phe Leu Lys Asp Ala Arg Leu Ile Leu Asn Ser Thr Glu Lys Ala Ala  
 65 70 75 80

Glu Arg Ala Arg Leu Ala Ser Ser Gly Met Trp Gly Gln Leu Asn Ile  
 85 90 95

Gly Tyr Thr Ala Ala Ala Gly Phe Ser Ile Leu Gly Pro Thr Leu Asn  
 100 105 110

Gln Leu His Glu Lys Met Pro Gly Val Ser Val Asp Leu Phe Glu Met  
 115 120 125

Val Ser Thr Glu Gln Ile Ala Ala Leu Glu Ser Gly Leu Leu Asp Leu  
 130 135 140

Gly Ile Gly Arg Leu Ser Ser Pro Val Glu Gly Leu Gln Thr Arg Arg  
 145 150 155 160

Leu Gln Ala Asp Ser Leu Val Leu Ala Ala Pro Lys Gly His Pro Leu  
 165 170 175

Leu Asp Gln Asn Arg Pro Leu Leu Arg Lys His Leu Thr Gly Val Pro  
 180 185 190

Phe Leu Gln His Ser Pro Thr Lys Ala Lys Tyr Leu Tyr Asp Ile Val  
 195 200 205  
 Val Arg Asn Phe Thr Ile Asn Asp Ala Gln Val Gln His Thr Leu Ser  
 210 215 220  
 Gln Ile Thr Thr Met Val Ser Leu Val Ala Ser Gly Leu Gly Val Ala  
 225 230 235 240  
 Leu Val Pro Glu Ser Ala Lys Lys Leu Asn Tyr Ser Gly Val Glu Tyr  
 245 250 255  
 Arg His Phe Tyr Asp Leu Pro Val Gly Leu Ala Glu Leu Gln Ala Ile  
 260 265 270  
 Tyr Ser Thr Ser Asn Asp Asn Pro Ala Val Arg Lys Phe Ile Lys Asn  
 275 280 285  
 Ile Asp Asp Thr Phe  
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 <211> 1500  
 <212> DNA  
 <213> Corynebacterium glutamicum

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 <222> (101)..(1477)  
 <223> RXA02787

<400> 187  
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 Met Ala Gln Asp Ser  
 1 5  
 ctt ttt gaa acg ccc gaa aca ccg gga tcc gca ggc aac aca agc agc 163  
 Leu Phe Glu Thr Pro Glu Thr Pro Gly Ser Ala Gly Asn Thr Ser Ser  
 10 15 20  
 gtg agc aat tcc aaa gcc gcc tcg aag tat ttt cac cca ggc gga cac 211  
 Val Ser Asn Ser Lys Ala Ala Ser Lys Tyr Phe His Pro Gly Gly His  
 25 30 35  
 gca ccc ctt gct gcc cgc atg agg cca agg acg ctt gat gaa gtg gtt 259  
 Ala Pro Leu Ala Ala Arg Met Arg Pro Arg Thr Leu Asp Glu Val Val  
 40 45 50  
 ggc caa cag cat ttg ctg ggg gag ggc agg cca ctt cgc cgg ctc att 307  
 Gly Gln Gln His Leu Leu Gly Glu Gly Arg Pro Leu Arg Arg Leu Ile  
 55 60 65  
 gaa ggt tca ggg gat gcc tcc gtc att ttg tat ggg cct ccc ggc act 355  
 Glu Gly Ser Gly Asp Ala Ser Val Ile Leu Tyr Gly Pro Pro Gly Thr  
 70 75 80 85  
 gga aaa aca acc att gcc tca ttg att tct gca gct gca ggc gat cgc 403  
 Gly Lys Thr Thr Ile Ala Ser Leu Ile Ser Ala Ala Ala Gly Asp Arg

90								95				100				
ttt	gtg	gcg	atg	tcg	gcg	ctg	tcc	tca	ggg	gtg	aaa	gaa	gtc	cgc	gcc	451
Phe	Val	Ala	Met	Ser	Ala	Leu	Ser	Ser	Gly	Val	Lys	Glu	Val	Arg	Ala	
			105						110					115		
ggt	att	gaa	cgt	gcg	agg	atg	gat	ctg	caa	tta	ggg	cag	cgc	acc	gtg	499
Val	Ile	Glu	Arg	Ala	Arg	Met	Asp	Leu	Gln	Leu	Gly	Gln	Arg	Thr	Val	
			120				125						130			
ctg	ttt	att	gat	gag	gtt	cat	agg	ttt	tcc	aaa	act	cag	cag	gac	gcg	547
Leu	Phe	Ile	Asp	Glu	Val	His	Arg	Phe	Ser	Lys	Thr	Gln	Gln	Asp	Ala	
			135				140					145				
ttg	ctc	tct	gca	gtg	gaa	aac	cgc	acc	gtg	ttg	ctc	gtt	gca	gcg	acc	595
Leu	Leu	Ser	Ala	Val	Glu	Asn	Arg	Thr	Val	Leu	Leu	Val	Ala	Ala	Thr	
						155					160				165	
act	gag	aac	ccc	tcc	ttt	tca	gtg	gtg	tct	cca	ctg	ctg	tcc	agg	tcc	643
Thr	Glu	Asn	Pro	Ser	Phe	Ser	Val	Val	Ser	Pro	Leu	Leu	Ser	Arg	Ser	
				170						175				180		
ttg	ctg	ctc	cag	ttg	gaa	tct	tta	agc	gat	gag	gat	att	aaa	aca	gtc	691
Leu	Leu	Leu	Gln	Leu	Glu	Ser	Leu	Ser	Asp	Glu	Asp	Ile	Lys	Thr	Val	
			185						190				195			
ctt	aat	aaa	gcg	ctt	gaa	gat	gag	cgt	gga	ctt	gcc	ggg	cga	atc	acc	739
Leu	Asn	Lys	Ala	Leu	Glu	Asp	Glu	Arg	Gly	Leu	Ala	Gly	Arg	Ile	Thr	
			200					205				210				
gcc	acc	gat	gaa	gca	gtt	gac	cag	ttg	gtt	ctt	ctt	gcc	ggg	ggc	gat	787
Ala	Thr	Asp	Glu	Ala	Val	Asp	Gln	Leu	Val	Leu	Leu	Ala	Gly	Gly	Asp	
			215				220					225				
gcc	cgc	cga	ggc	ctg	acc	tac	att	gaa	gcc	gct	gca	gaa	gcc	gta	gaa	835
Ala	Arg	Arg	Gly	Leu	Thr	Tyr	Ile	Glu	Ala	Ala	Ala	Glu	Ala	Val	Glu	
			230			235				240					245	
gat	ggc	ggc	gtt	tta	gat	att	gac	acc	gtc	atg	gcc	aac	gtg	aac	cgc	883
Asp	Gly	Gly	Val	Leu	Asp	Ile	Asp	Thr	Val	Met	Ala	Asn	Val	Asn	Arg	
				250					255				260			
gca	gtg	gtc	cgc	tat	gac	cgc	gat	ggc	gat	cag	cac	tat	gac	gtg	gtc	931
Ala	Val	Val	Arg	Tyr	Asp	Arg	Asp	Gly	Asp	Gln	His	Tyr	Asp	Val	Val	
			265					270					275			
agt	gcc	tgg	atc	aaa	tca	att	aga	ggc	tcc	gat	gta	gac	gca	gcc	ttg	979
Ser	Ala	Trp	Ile	Lys	Ser	Ile	Arg	Gly	Ser	Asp	Val	Asp	Ala	Ala	Leu	
			280				285					290				
cac	tac	ttg	gcg	cgc	atg	att	gat	gcc	ggg	gaa	gac	cca	cgg	ttt	att	1027
His	Tyr	Leu	Ala	Arg	Met	Ile	Asp	Ala	Gly	Glu	Asp	Pro	Arg	Phe	Ile	
			295			300				305						
gcc	cgc	cgg	ttg	gtg	gtt	cac	tca	agt	gaa	gac	atc	ggg	atg	gct	gat	1075
Ala	Arg	Arg	Leu	Val	Val	His	Ser	Ser	Glu	Asp	Ile	Gly	Met	Ala	Asp	
			310			315				320					325	
cct	tcg	gcc	atg	caa	gtg	gcc	att	gct	gca	gct	caa	gct	gtc	caa	tta	1123
Pro	Ser	Ala	Met	Gln	Val	Ala	Ile	Ala	Ala	Ala	Gln	Ala	Val	Gln	Leu	
				330					335					340		

atc ggt atg cca gag gcg cgg atc aat ttg gcg caa gcg acc att cat 1171  
 Ile Gly Met Pro Glu Ala Arg Ile Asn Leu Ala Gln Ala Thr Ile His  
 345 350 355  
 ttg gct ctt gct ccc aaa tcc aat gct gtc atc atg gcc atg gat gct 1219  
 Leu Ala Leu Ala Pro Lys Ser Asn Ala Val Ile Met Ala Met Asp Ala  
 360 365 370  
 gct ttg act gat gtt cag caa ggc cac atc ggt acc gtt cct gcg cat 1267  
 Ala Leu Thr Asp Val Gln Gln Gly His Ile Gly Thr Val Pro Ala His  
 375 380 385  
 ctt cgc gat ggt cac tat gaa ggc gcc aaa aag ctc gga aat gca gtg 1315  
 Leu Arg Asp Gly His Tyr Glu Gly Ala Lys Lys Leu Gly Asn Ala Val  
 390 395 400 405  
 gga tat tcc tat cct cac gat gat ccc agg gga gtg gtc cgg caa gaa 1363  
 Gly Tyr Ser Tyr Pro His Asp Asp Pro Arg Gly Val Val Arg Gln Glu  
 410 415 420  
 tat tta ccg gag aac ctg cgc gat cgg gtc tat tac gag ccc acc aca 1411  
 Tyr Leu Pro Glu Asn Leu Arg Asp Arg Val Tyr Tyr Glu Pro Thr Thr  
 425 430 435  
 cac ggt gga gag aag cgg att gcc gag tac att ggc agg ctt cgt cgt 1459  
 His Gly Gly Glu Lys Arg Ile Ala Glu Tyr Ile Gly Arg Leu Arg Arg  
 440 445 450  
 ata atc cgt gga acc aag tagcccggtg tgctcaacac cta 1500  
 Ile Ile Arg Gly Thr Lys  
 455

&lt;210&gt; 188

&lt;211&gt; 459

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 188

Met Ala Gln Asp Ser Leu Phe Glu Thr Pro Glu Thr Pro Gly Ser Ala  
 1 5 10 15  
 Gly Asn Thr Ser Ser Val Ser Asn Ser Lys Ala Ala Ser Lys Tyr Phe  
 20 25 30  
 His Pro Gly Gly His Ala Pro Leu Ala Ala Arg Met Arg Pro Arg Thr  
 35 40 45  
 Leu Asp Glu Val Val Gly Gln Gln His Leu Leu Gly Glu Gly Arg Pro  
 50 55 60  
 Leu Arg Arg Leu Ile Glu Gly Ser Gly Asp Ala Ser Val Ile Leu Tyr  
 65 70 75 80  
 Gly Pro Pro Gly Thr Gly Lys Thr Thr Ile Ala Ser Leu Ile Ser Ala  
 85 90 95  
 Ala Ala Gly Asp Arg Phe Val Ala Met Ser Ala Leu Ser Ser Gly Val  
 100 105 110



Lys Glu Val Arg Ala Val Ile Glu Arg Ala Arg Met Asp Leu Gln Leu  
 115 120 125  
 Gly Gln Arg Thr Val Leu Phe Ile Asp Glu Val His Arg Phe Ser Lys  
 130 135 140  
 Thr Gln Gln Asp Ala Leu Leu Ser Ala Val Glu Asn Arg Thr Val Leu  
 145 150 155 160  
 Leu Val Ala Ala Thr Thr Glu Asn Pro Ser Phe Ser Val Val Ser Pro  
 165 170 175  
 Leu Leu Ser Arg Ser Leu Leu Leu Gln Leu Glu Ser Leu Ser Asp Glu  
 180 185 190  
 Asp Ile Lys Thr Val Leu Asn Lys Ala Leu Glu Asp Glu Arg Gly Leu  
 195 200 205  
 Ala Gly Arg Ile Thr Ala Thr Asp Glu Ala Val Asp Gln Leu Val Leu  
 210 215 220  
 Leu Ala Gly Gly Asp Ala Arg Arg Gly Leu Thr Tyr Ile Glu Ala Ala  
 225 230 235 240  
 Ala Glu Ala Val Glu Asp Gly Gly Val Leu Asp Ile Asp Thr Val Met  
 245 250 255  
 Ala Asn Val Asn Arg Ala Val Val Arg Tyr Asp Arg Asp Gly Asp Gln  
 260 265 270  
 His Tyr Asp Val Val Ser Ala Trp Ile Lys Ser Ile Arg Gly Ser Asp  
 275 280 285  
 Val Asp Ala Ala Leu His Tyr Leu Ala Arg Met Ile Asp Ala Gly Glu  
 290 295 300  
 Asp Pro Arg Phe Ile Ala Arg Arg Leu Val Val His Ser Ser Glu Asp  
 305 310 315 320  
 Ile Gly Met Ala Asp Pro Ser Ala Met Gln Val Ala Ile Ala Ala Ala  
 325 330 335  
 Gln Ala Val Gln Leu Ile Gly Met Pro Glu Ala Arg Ile Asn Leu Ala  
 340 345 350  
 Gln Ala Thr Ile His Leu Ala Leu Ala Pro Lys Ser Asn Ala Val Ile  
 355 360 365  
 Met Ala Met Asp Ala Ala Leu Thr Asp Val Gln Gln Gly His Ile Gly  
 370 375 380  
 Thr Val Pro Ala His Leu Arg Asp Gly His Tyr Glu Gly Ala Lys Lys  
 385 390 395 400  
 Leu Gly Asn Ala Val Gly Tyr Ser Tyr Pro His Asp Asp Pro Arg Gly  
 405 410 415  
 Val Val Arg Gln Glu Tyr Leu Pro Glu Asn Leu Arg Asp Arg Val Tyr  
 420 425 430  
 Tyr Glu Pro Thr Thr His Gly Gly Glu Lys Arg Ile Ala Glu Tyr Ile

435

440

445

Gly Arg Leu Arg Arg Ile Ile Arg Gly Thr Lys  
 450 455

&lt;210&gt; 189

&lt;211&gt; 597

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(574)

&lt;223&gt; RXA00287

&lt;400&gt; 189

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caggaaaaat tgttgtgagg gtataaagag gacttgaaaa atg cac cat cta cgc 115  
 Met His His Leu Arg  
 1 5

tat gaa tca cca atc gga gag ctt ctt ctt gtt gca agt gac caa ggg 163  
 Tyr Glu Ser Pro Ile Gly Glu Leu Leu Leu Val Ala Ser Asp Gln Gly  
 10 15 20

cta acc tat gtg gca ttc tcc gat gaa aac tac gca gct tgt act gtc 211  
 Leu Thr Tyr Val Ala Phe Ser Asp Glu Asn Tyr Ala Ala Cys Thr Val  
 25 30 35

ggg tcg acc ccg gga acc aat gcg gtg ctg gaa cag gca gtt gct gag 259  
 Gly Ser Thr Pro Gly Thr Asn Ala Val Leu Glu Gln Ala Val Ala Glu  
 40 45 50

ctt gaa gaa tac ttc gca ggg aaa cgt aaa gag ttc agc act ccc ctg 307  
 Leu Glu Glu Tyr Phe Ala Gly Lys Arg Lys Glu Phe Ser Thr Pro Leu  
 55 60 65

gat tgg cca agc caa aat ctg ctg agc ttc cgc ggt aaa gtg cag gaa 355  
 Asp Trp Pro Ser Gln Asn Leu Leu Ser Phe Arg Gly Lys Val Gln Glu  
 70 75 80 85

ttt ttg ctg tcc att cct tat ggg gag agt aaa act tac aaa cag atc 403  
 Phe Leu Leu Ser Ile Pro Tyr Gly Glu Ser Lys Thr Tyr Lys Gln Ile  
 90 95 100

gcc gct gag ctt aat aat gtg ggc gcg gtt cgt gca gtg gga agc gcc 451  
 Ala Ala Glu Leu Asn Asn Val Gly Ala Val Arg Ala Val Gly Ser Ala  
 105 110 115

tgc gcc acc aac ccc ttg cca atc ttt gct cct tgt cac cga gta ctg 499  
 Cys Ala Thr Asn Pro Leu Pro Ile Phe Ala Pro Cys His Arg Val Leu  
 120 125 130

cgc act gat ggg gcg tta ggt ggc tac aga gga ggc ttg gaa gca aaa 547  
 Arg Thr Asp Gly Ala Leu Gly Gly Tyr Arg Gly Gly Leu Glu Ala Lys  
 135 140 145

cag tgg ctg ttg gag ctg gaa cgt cct tagtttgtgt ccgcgcacgg agc 597  
 Gln Trp Leu Leu Glu Leu Glu Arg Pro

155

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<400> 191
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gaatctaaac tattcccaaa tagaccatac ggtctaacat gtg ttc atg ctt gca 115
                                         Val Phe Met Leu Ala
                                         1                               5
cag cga aca ctc ccc att cac atc acc gcc ccc cac cta ccc gtc gcg 163
Gln Arg Thr Leu Pro Ile His Ile Thr Ala Pro His Leu Pro Val Ala
                        10                        15                        20

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cgc gta ttt cat caa att cgc gcc aca gac gcc gat cgc acc tct ctg	211
Arg Val Phe His Gln Ile Arg Ala Thr Asp Ala Asp Arg Thr Ser Leu	
25 30 35	
caa cgc gat ctt gaa ctc tcc caa gct ggc atc acg cgg cat gtg tca	259
Gln Arg Asp Leu Glu Leu Ser Gln Ala Gly Ile Thr Arg His Val Ser	
40 45 50	
gcg ctt att gat gca ggt ctc gtg gag gaa acc cga gtg gat tcc ggg	307
Ala Leu Ile Asp Ala Gly Leu Val Glu Glu Thr Arg Val Asp Ser Gly	
55 60 65	
gcg cgc tcg ggg cga ccg cgc aca aaa tta ggc atc gac ggc cgc cat	355
Ala Arg Ser Gly Arg Pro Arg Thr Lys Leu Gly Ile Asp Gly Arg His	
70 75 80 85	
ctc acc gcc tgg gga gtg cac att ggc ctg cgc agc acg gat ttt gcg	403
Leu Thr Ala Trp Gly Val His Ile Gly Leu Arg Ser Thr Asp Phe Ala	
90 95 100	
gtg tgc gat tta gcc ggc cga gtg att agg tat gag cgc gtg gac cat	451
Val Cys Asp Leu Ala Gly Arg Val Ile Arg Tyr Glu Arg Val Asp His	
105 110 115	
gaa gtt tca cac tcc acg ccg tcg gaa acg ctg aat ttt gtc gca cat	499
Glu Val Ser His Ser Thr Pro Ser Glu Thr Leu Asn Phe Val Ala His	
120 125 130	
agg tta caa aca ttg agc gcc ggc ttg ccc gag ccc cgc aat gtg ggc	547
Arg Leu Gln Thr Leu Ser Ala Gly Leu Pro Glu Pro Arg Asn Val Gly	
135 140 145	
gtg gca tta tct gcc cac tta agc gcc aac gga acc gtc act tcc gaa	595
Val Ala Leu Ser Ala His Leu Ser Ala Asn Gly Thr Val Thr Ser Glu	
150 155 160 165	
gat tat ggc tgg tca gag gtg gaa att ggg gca cac ctc ccc ttc ccc	643
Asp Tyr Gly Trp Ser Glu Val Glu Ile Gly Ala His Leu Pro Phe Pro	
170 175 180	
gcc acc atc gga tca ggt gtt gcg gcg atg gcc ggt tcg gaa att atc	691
Ala Thr Ile Gly Ser Gly Val Ala Ala Met Ala Gly Ser Glu Ile Ile	
185 190 195	
aac gcg cca ctg acc caa tcc acg cag tcc acg ctg tat ttc tac gcc	739
Asn Ala Pro Leu Thr Gln Ser Thr Gln Ser Thr Leu Tyr Phe Tyr Ala	
200 205 210	
cgc gaa atg gtc tcc cac gcc tgg att ttc aac ggc gct gtc cac cgc	787
Arg Glu Met Val Ser His Ala Trp Ile Phe Asn Gly Ala Val His Arg	
215 220 225	
ccc aac agc ggc cgc acg ccg acg gcg ttc gga aat aca aat acc tta	835
Pro Asn Ser Gly Arg Thr Pro Thr Ala Phe Gly Asn Thr Asn Thr Leu	
230 235 240 245	
aaa gat gct ttt cga cgt gga ctc aca cca aca act ttc tcc gat tta	883
Lys Asp Ala Phe Arg Arg Gly Leu Thr Pro Thr Thr Phe Ser Asp Leu	
250 255 260	

gtc caa ctc tcc cac acc aac ccg ctt gca cga cag atc ctc aac gag 931  
 Val Gln Leu Ser His Thr Asn Pro Leu Ala Arg Gln Ile Leu Asn Glu  
 265 270 275

cgc gcc cac aaa ctt gcc gac gcc gta acc acc gcc gtt gat gtt gtc 979  
 Arg Ala His Lys Leu Ala Asp Ala Val Thr Thr Ala Val Asp Val Val  
 280 285 290

gac ccc gaa gcc gtc gtc ttc gcc ggc gaa gcc ttc acc ctg gat ccg 1027  
 Asp Pro Glu Ala Val Val Phe Ala Gly Glu Ala Phe Thr Leu Asp Pro  
 295 300 305

gaa act ctt cgc att gtg gtg acc cag ctc cga gca aac acc ggc agc 1075  
 Glu Thr Leu Arg Ile Val Val Thr Gln Leu Arg Ala Asn Thr Gly Ser  
 310 315 320 325

caa ctg aga atc caa cgc gca gac gcc tac att ctc cgc acc gcg gcc 1123  
 Gln Leu Arg Ile Gln Arg Ala Asp Ala Tyr Ile Leu Arg Thr Ala Ala  
 330 335 340

atc cag gtg gcg ctg cat ccg atc cgt caa gat ccg ttg gca ttt gtg 1171  
 Ile Gln Val Ala Leu His Pro Ile Arg Gln Asp Pro Leu Ala Phe Val  
 345 350 355

taattaccac ccatgttgcg ggg 1194

<210> 192  
 <211> 357  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 192  
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His Leu Pro Val Ala Arg Val Phe His Gln Ile Arg Ala Thr Asp Ala  
 20 25 30

Asp Arg Thr Ser Leu Gln Arg Asp Leu Glu Leu Ser Gln Ala Gly Ile  
 35 40 45

Thr Arg His Val Ser Ala Leu Ile Asp Ala Gly Leu Val Glu Glu Thr  
 50 55 60

Arg Val Asp Ser Gly Ala Arg Ser Gly Arg Pro Arg Thr Lys Leu Gly  
 65 70 75 80

Ile Asp Gly Arg His Leu Thr Ala Trp Gly Val His Ile Gly Leu Arg  
 85 90 95

Ser Thr Asp Phe Ala Val Cys Asp Leu Ala Gly Arg Val Ile Arg Tyr  
 100 105 110

Glu Arg Val Asp His Glu Val Ser His Ser Thr Pro Ser Glu Thr Leu  
 115 120 125

Asn Phe Val Ala His Arg Leu Gln Thr Leu Ser Ala Gly Leu Pro Glu  
 130 135 140

Pro Arg Asn Val Gly Val Ala Leu Ser Ala His Leu Ser Ala Asn Gly

145                      150                      155                      160  
 Thr Val Thr Ser Glu Asp Tyr Gly Trp Ser Glu Val Glu Ile Gly Ala  
                                  165                                   170                                   175  
 His Leu Pro Phe Pro Ala Thr Ile Gly Ser Gly Val Ala Ala Met Ala  
                                  180                                   185                                   190  
 Gly Ser Glu Ile Ile Asn Ala Pro Leu Thr Gln Ser Thr Gln Ser Thr  
                                  195                                   200                                   205  
 Leu Tyr Phe Tyr Ala Arg Glu Met Val Ser His Ala Trp Ile Phe Asn  
                                  210                                   215                                   220  
 Gly Ala Val His Arg Pro Asn Ser Gly Arg Thr Pro Thr Ala Phe Gly  
                                  225                                   230                                   235                                   240  
 Asn Thr Asn Thr Leu Lys Asp Ala Phe Arg Arg Gly Leu Thr Pro Thr  
                                  245                                   250                                   255  
 Thr Phe Ser Asp Leu Val Gln Leu Ser His Thr Asn Pro Leu Ala Arg  
                                  260                                   265                                   270  
 Gln Ile Leu Asn Glu Arg Ala His Lys Leu Ala Asp Ala Val Thr Thr  
                                  275                                   280                                   285  
 Ala Val Asp Val Val Asp Pro Glu Ala Val Val Phe Ala Gly Glu Ala  
                                  290                                   295                                   300  
 Phe Thr Leu Asp Pro Glu Thr Leu Arg Ile Val Val Thr Gln Leu Arg  
                                  305                                   310                                   315                                   320  
 Ala Asn Thr Gly Ser Gln Leu Arg Ile Gln Arg Ala Asp Ala Tyr Ile  
                                  325                                   330                                   335  
 Leu Arg Thr Ala Ala Ile Gln Val Ala Leu His Pro Ile Arg Gln Asp  
                                  340                                   345                                   350  
 Pro Leu Ala Phe Val  
                                  355

<210> 193  
 <211> 1287  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1264)  
 <223> RXA01935

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    Met Ile Gly Tyr Gly  
    1     5  
 tta cct atg ccc aat cag gcc cac ttc tct gcg tcc ttt gcc cgc ccc 163  
 Leu Pro Met Pro Asn Gln Ala His Phe Ser Ala Ser Phe Ala Arg Pro

				10				15				20				
tct	acc	ccg	gct	gca	aag	tgc	atg	cac	cat	atc	cgc	ctc	ggc	cag	caa	211
Ser	Thr	Pro	Ala	Ala	Lys	Cys	Met	His	His	Ile	Arg	Leu	Gly	Gln	Gln	
25				30				35								
ctc	att	aga	aat	gag	ctg	gtc	gag	gcc	aca	ggg	ctg	tcc	caa	ccg	act	259
Leu	Ile	Arg	Asn	Glu	Leu	Val	Glu	Ala	Thr	Gly	Leu	Ser	Gln	Pro	Thr	
40				45				50								
gtc	acc	cgc	gca	gtc	acc	gct	tta	atg	cag	gca	ggg	ttg	gtt	cgt	gaa	307
Val	Thr	Arg	Ala	Val	Thr	Ala	Leu	Met	Gln	Ala	Gly	Leu	Val	Arg	Glu	
55				60				65								
cgc	cct	gat	ctc	aca	ctc	tca	tcg	ggc	cct	ggg	cgt	ccc	aat	att	cct	355
Arg	Pro	Asp	Leu	Thr	Leu	Ser	Ser	Gly	Pro	Gly	Arg	Pro	Asn	Ile	Pro	
70				75				80				85				
cta	gaa	ctc	gct	cca	agt	cca	tgg	att	cat	gca	ggc	gtg	gca	atc	ggc	403
Leu	Glu	Leu	Ala	Pro	Ser	Pro	Trp	Ile	His	Ala	Gly	Val	Ala	Ile	Gly	
90				95				100								
acc	aag	tct	tcc	tac	gtc	gct	ttg	ttt	gat	acc	aag	ggg	cgc	acc	ctt	451
Thr	Lys	Ser	Ser	Tyr	Val	Ala	Leu	Phe	Asp	Thr	Lys	Gly	Arg	Thr	Leu	
105				110				115								
cgt	gat	gcc	atg	ctg	gaa	atc	tca	gca	gct	gat	tta	gat	cca	gac	act	499
Arg	Asp	Ala	Met	Leu	Glu	Ile	Ser	Ala	Ala	Asp	Leu	Asp	Pro	Asp	Thr	
120				125				130								
ttc	atc	gaa	cac	ctc	att	gct	ggg	gtc	aac	cgc	ctc	acc	act	ggg	ctt	547
Phe	Ile	Glu	His	Leu	Ile	Ala	Gly	Val	Asn	Arg	Leu	Thr	Thr	Gly	Leu	
135				140				145								
gat	cta	cca	ctg	gta	ggg	att	ggg	gtt	gcc	acc	tca	gga	aaa	gtc	acc	595
Asp	Leu	Pro	Leu	Val	Gly	Ile	Gly	Val	Ala	Thr	Ser	Gly	Lys	Val	Thr	
150				155				160				165				
aac	gca	ggc	gtt	gtc	acc	gca	agc	aac	ttg	ggc	tgg	gat	ggc	gtt	gat	643
Asn	Ala	Gly	Val	Val	Thr	Ala	Ser	Asn	Leu	Gly	Trp	Asp	Gly	Val	Asp	
170				175				180								
atc	gct	ggc	cgc	ctg	aac	tac	caa	ttc	agc	gtt	cca	gca	acc	gtg	gca	691
Ile	Ala	Gly	Arg	Leu	Asn	Tyr	Gln	Phe	Ser	Val	Pro	Ala	Thr	Val	Ala	
185				190				195								
tca	gca	att	cct	gcc	atc	gca	gct	tct	gaa	ctg	cag	gct	tcc	cca	ctt	739
Ser	Ala	Ile	Pro	Ala	Ile	Ala	Ala	Ser	Glu	Leu	Gln	Ala	Ser	Pro	Leu	
200				205				210								
ccc	cac	cct	gag	cag	cca	act	ccc	atc	acc	ttg	acc	ttc	tac	gcc	gat	787
Pro	His	Pro	Glu	Gln	Pro	Thr	Pro	Ile	Thr	Leu	Thr	Phe	Tyr	Ala	Asp	
215				220				225								
gac	tct	gtg	ggc	gcg	gcc	tac	agc	aat	gat	ttg	gga	gta	cat	gtc	att	835
Asp	Ser	Val	Gly	Ala	Ala	Tyr	Ser	Asn	Asp							

gct gcc gaa gat gcg ctg agc acc caa ggt ttc tta agc agg gtt tct 931  
 Ala Ala Glu Asp Ala Leu Ser Thr Gln Gly Phe Leu Ser Arg Val Ser  
 265 270 275  
 gat cag ggt atc ttt gcc aac agc ctt ggt gag cta gtc acc att gct 979  
 Asp Gln Gly Ile Phe Ala Asn Ser Leu Gly Glu Leu Val Thr Ile Ala  
 280 285 290  
 aaa gac aat gaa acc gca cgg gaa ttc ctc aac gat cgc gcg acc ctg 1027  
 Lys Asp Asn Glu Thr Ala Arg Glu Phe Leu Asn Asp Arg Ala Thr Leu  
 295 300 305  
 ctg gct cac act gcc gca gaa gct gcc gaa aca gtt aag cca tcc acc 1075  
 Leu Ala His Thr Ala Ala Glu Ala Glu Thr Val Lys Pro Ser Thr  
 310 315 320 325  
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 Leu Val Leu Ser Gly Ser Ala Phe Ser Glu Asp Pro Gln Gly Arg Ser  
 330 335 340  
 gtg ttc gct tcc caa ttg aag aag gaa tac gac gca gac att gag ctc 1171  
 Val Phe Ala Ser Gln Leu Lys Lys Glu Tyr Asp Ala Asp Ile Glu Leu  
 345 350 355  
 cgg ttg atc ccc acc cac cgg gaa aac gtc cgc gca gca gct cga gca 1219  
 Arg Leu Ile Pro Thr His Arg Glu Asn Val Arg Ala Ala Ala Arg Ala  
 360 365 370  
 gtc gca ctt gat cga ctg ctc aac gag cca ctt act ctc gta ccc 1264  
 Val Ala Leu Asp Arg Leu Leu Asn Glu Pro Leu Thr Leu Val Pro  
 375 380 385  
 taacctcatc taagctcagt gct 1287

<210> 194  
 <211> 388  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 194  
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 35 40 45  
 Leu Ser Gln Pro Thr Val Thr Arg Ala Val Thr Ala Leu Met Gln Ala  
 50 55 60  
 Gly Leu Val Arg Glu Arg Pro Asp Leu Thr Leu Ser Ser Gly Pro Gly  
 65 70 75 80  
 Arg Pro Asn Ile Pro Leu Glu Leu Ala Pro Ser Pro Trp Ile His Ala  
 85 90 95  
 Gly Val Ala Ile Gly Thr Lys Ser Ser Tyr Val Ala Leu Phe Asp Thr



100					105					110					
Lys	Gly	Arg	Thr	Leu	Arg	Asp	Ala	Met	Leu	Glu	Ile	Ser	Ala	Ala	Asp
		115					120					125			
Leu	Asp	Pro	Asp	Thr	Phe	Ile	Glu	His	Leu	Ile	Ala	Gly	Val	Asn	Arg
	130					135					140				
Leu	Thr	Thr	Gly	Leu	Asp	Leu	Pro	Leu	Val	Gly	Ile	Gly	Val	Ala	Thr
	145					150					155				160
Ser	Gly	Lys	Val	Thr	Asn	Ala	Gly	Val	Val	Thr	Ala	Ser	Asn	Leu	Gly
				165					170					175	
Trp	Asp	Gly	Val	Asp	Ile	Ala	Gly	Arg	Leu	Asn	Tyr	Gln	Phe	Ser	Val
			180					185					190		
Pro	Ala	Thr	Val	Ala	Ser	Ala	Ile	Pro	Ala	Ile	Ala	Ala	Ser	Glu	Leu
		195					200					205			
Gln	Ala	Ser	Pro	Leu	Pro	His	Pro	Glu	Gln	Pro	Thr	Pro	Ile	Thr	Leu
	210					215					220				
Thr	Phe	Tyr	Ala	Asp	Asp	Ser	Val	Gly	Ala	Ala	Tyr	Ser	Asn	Asp	Leu
	225					230					235				240
Gly	Val	His	Val	Ile	Gly	Pro	Leu	Ala	Thr	Thr	Arg	Gly	Ser	Gly	Leu
				245					250					255	
Asp	Thr	Leu	Gly	Met	Ala	Ala	Glu	Asp	Ala	Leu	Ser	Thr	Gln	Gly	Phe
			260					265					270		
Leu	Ser	Arg	Val	Ser	Asp	Gln	Gly	Ile	Phe	Ala	Asn	Ser	Leu	Gly	Glu
		275					280					285			
Leu	Val	Thr	Ile	Ala	Lys	Asp	Asn	Glu	Thr	Ala	Arg	Glu	Phe	Leu	Asn
		290				295					300				
Asp	Arg	Ala	Thr	Leu	Leu	Ala	His	Thr	Ala	Ala	Glu	Ala	Ala	Glu	Thr
	305					310					315				320
Val	Lys	Pro	Ser	Thr	Leu	Val	Leu	Ser	Gly	Ser	Ala	Phe	Ser	Glu	Asp
				325					330					335	
Pro	Gln	Gly	Arg	Ser	Val	Phe	Ala	Ser	Gln	Leu	Lys	Lys	Glu	Tyr	Asp
			340					345					350		
Ala	Asp	Ile	Glu	Leu	Arg	Leu	Ile	Pro	Thr	His	Arg	Glu	Asn	Val	Arg
		355					360					365			
Ala	Ala	Ala	Arg	Ala	Val	Ala	Leu	Asp	Arg	Leu	Leu	Asn	Glu	Pro	Leu
		370					375					380			
Thr	Leu	Val	Pro												
				385											

&lt;210&gt; 195

&lt;211&gt; 744

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(721)

&lt;223&gt; RXN02270

&lt;400&gt; 195

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cagcttgagc aggcacgcgc cgatgacgta ccaggagttt cggcatgac cggcggcgctc 60

gcacgcgtat tgggcgcggt cgtttgtggg gtggcgggtg atg gat cag gcg cgg 115
               Met Asp Gln Ala Arg
               1 5

ccg aat cga acg cac tac gcc atg gtt gag ctg gag cag cat ggt ttt 163
Pro Asn Arg Thr His Tyr Ala Met Val Glu Leu Glu Gln His Gly Phe
               10 15 20

tta agt ggt gtg gtc acc caa aat gtc gat ggt tta cac gcg gaa gca 211
Leu Ser Gly Val Val Thr Gln Asn Val Asp Gly Leu His Ala Glu Ala
               25 30 35

ggc acg aaa aac ctg gtc gcg ctg cat ggt gat ctc gcc cat gtg atg 259
Gly Thr Lys Asn Leu Val Ala Leu His Gly Asp Leu Ala His Val Met
               40 45 50

tgt ttg aac tgc ggt ttc ggg gag gat cga cac ctc ttt gat gaa cgt 307
Cys Leu Asn Cys Gly Phe Gly Glu Asp Arg His Leu Phe Asp Glu Arg
               55 60 65

ctc gaa gcc gcc aac ccc ggc tac gtc gct tcc att cgc ctg gaa ccg 355
Leu Glu Ala Ala Asn Pro Gly Tyr Val Ala Ser Ile Arg Leu Glu Pro
               70 75 80 85

ggc gca gtc aac ccc gac ggc gac gtc ttc ctc gac gaa gaa caa gta 403
Gly Ala Val Asn Pro Asp Gly Asp Val Phe Leu Asp Glu Glu Gln Val
               90 95 100

cgc cgc ttc acc atg atc ggc tgc ttg cgc tgc ggc tcg ctc atg ctc 451
Arg Arg Phe Thr Met Ile Gly Cys Leu Arg Cys Gly Ser Leu Met Leu
               105 110 115

aaa cca gac gtg gtt tac ttc ggc gaa ccc gtg ccc gcc gcg cgc aaa 499
Lys Pro Asp Val Val Tyr Phe Gly Glu Pro Val Pro Ala Ala Arg Lys
               120 125 130

aaa gat tta aaa aag ctt ctc gac gcc tcc tcc agc ctc tta atc gcc 547
Lys Asp Leu Lys Lys Leu Leu Asp Ala Ser Ser Ser Leu Leu Ile Ala
               135 140 145

ggc tcc tcc cta gcc gtc atg agt gga tac cgg atc gtc atc gaa gcg 595
Gly Ser Ser Leu Ala Val Met Ser Gly Tyr Arg Ile Val Ile Glu Ala
               150 155 160 165

caa cgt caa gga aaa caa gtg tct gtc atc aac ggc ggc cca ggt cgg 643
Gln Arg Gln Gly Lys Gln Val Ser Val Ile Asn Gly Gly Pro Gly Arg
               170 175 180

gcg gat tcc cgc gtg gac att ttg tgg cgc acc cgc gtt gca ccg gcc 691
Ala Asp Ser Arg Val Asp Ile Leu Trp Arg Thr Arg Val Ala Pro Ala
               185 190 195

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ttt gat gac att ttg gac gcg ctg gac ctt tagacttttg gtggcttaag ttc 744  
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<210> 196

<211> 207

<212> PRT

<213> Corynebacterium glutamicum

<400> 196

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Glu Gln His Gly Phe Leu Ser Gly Val Val Thr Gln Asn Val Asp Gly  
                   20                          25                          30

Leu His Ala Glu Ala Gly Thr Lys Asn Leu Val Ala Leu His Gly Asp  
           35                          40                          45

Leu Ala His Val Met Cys Leu Asn Cys Gly Phe Gly Glu Asp Arg His  
       50                          55                          60

Leu Phe Asp Glu Arg Leu Glu Ala Ala Asn Pro Gly Tyr Val Ala Ser  
       65                          70                          75                          80

Ile Arg Leu Glu Pro Gly Ala Val Asn Pro Asp Gly Asp Val Phe Leu  
                           85                          90                          95

Asp Glu Glu Gln Val Arg Arg Phe Thr Met Ile Gly Cys Leu Arg Cys  
                   100                          105                          110

Gly Ser Leu Met Leu Lys Pro Asp Val Val Tyr Phe Gly Glu Pro Val  
       115                          120                          125

Pro Ala Ala Arg Lys Lys Asp Leu Lys Lys Leu Leu Asp Ala Ser Ser  
       130                          135                          140

Ser Leu Leu Ile Ala Gly Ser Ser Leu Ala Val Met Ser Gly Tyr Arg  
       145                          150                          155                          160

Ile Val Ile Glu Ala Gln Arg Gln Gly Lys Gln Val Ser Val Ile Asn  
                   165                          170                          175

Gly Gly Pro Gly Arg Ala Asp Ser Arg Val Asp Ile Leu Trp Arg Thr  
                   180                          185                          190

Arg Val Ala Pro Ala Phe Asp Asp Ile Leu Asp Ala Leu Asp Leu  
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<210> 197

<211> 744

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(721)

<223> FRXA02270

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gcacgcgtat tgggcgcggt cgtttgtggg gtggcgggtg atg gat cag gcg cgg Met Asp Gln Ala Arg 1 5															115
ccg aat cga acg cac tac gcc atg gtt gag ctg gag cag cat ggt ttt Pro Asn Arg Thr His Tyr Ala Met Val Glu Leu Glu Gln His Gly Phe 10 15 20															163
tta agt ggt gtg gtc acc caa aat gtc gat ggt tta cac gcg gaa gca Leu Ser Gly Val Val Thr Gln Asn Val Asp Gly Leu His Ala Glu Ala 25 30 35															211
ggc acg aaa aac ctg gtc gcg ctg cat ggt gat ctc gcc cat gtg atg Gly Thr Lys Asn Leu Val Ala Leu His Gly Asp Leu Ala His Val Met 40 45 50															259
tgt ttg aac tgc ggt ttc ggg gag gat cga cac ctc ttt gat gaa cgt Cys Leu Asn Cys Gly Phe Gly Glu Asp Arg His Leu Phe Asp Glu Arg 55 60 65															307
ctc gaa gcc gcc aac ccc ggc tac gtc gct tcc att cgc ctg gaa ccg Leu Glu Ala Ala Asn Pro Gly Tyr Val Ala Ser Ile Arg Leu Glu Pro 70 75 80 85															355
ggc gca gtc aac ccc gac ggc gac gtc ttc ctc gac gaa gaa caa gta Gly Ala Val Asn Pro Asp Gly Asp Val Phe Leu Asp Glu Glu Gln Val 90 95 100															403
cgc cgc ttc acc atg atc ggc tgc ttg cgc tgc ggc tcg ctc atg ctc Arg Arg Phe Thr Met Ile Gly Cys Leu Arg Cys Gly Ser Leu Met Leu 105 110 115															451
aaa cca gac gtg gtt tac ttc ggc gaa ccc gtg ccc gcc gcg cgc aaa Lys Pro Asp Val Val Tyr Phe Gly Glu Pro Val Pro Ala Ala Arg Lys 120 125 130															499
aaa gat tta aaa aag ctt ctc gac gcc tcc tcc agc ctc tta atc gcc Lys Asp Leu Lys Lys Leu Leu Asp Ala Ser Ser Ser Leu Leu Ile Ala 135 140 145															547
ggc tcc tcc cta gcc gtc atg agt gga tac cgg atc gtc atc gaa gcg Gly Ser Ser Leu Ala Val Met Ser Gly Tyr Arg Ile Val Ile Glu Ala 150 155 160 165															595
caa cgt caa gga aaa caa gtg tct gtc atc aac ggc ggc cca ggt cgg Gln Arg Gln Gly Lys Gln Val Ser Val Ile Asn Gly Gly Pro Gly Arg 170 175 180															643
gcg gat tcc cgc gtg gac att ttg tgg cgc acc cgc gtt gca ccg gcc Ala Asp Ser Arg Val Asp Ile Leu Trp Arg Thr Arg Val Ala Pro Ala 185 190 195															691
ttt gat gac att ttg gac gcg ctg gac ctt tagacttttg gtggcttaag ttc Phe Asp Asp Ile Leu Asp Ala Leu Asp Leu 200 205															744

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 <212> PRT  
 <213> Corynebacterium glutamicum

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             20                    25                    30  
 Leu His Ala Glu Ala Gly Thr Lys Asn Leu Val Ala Leu His Gly Asp  
             35                    40                    45  
 Leu Ala His Val Met Cys Leu Asn Cys Gly Phe Gly Glu Asp Arg His  
             50                    55                    60  
 Leu Phe Asp Glu Arg Leu Glu Ala Ala Asn Pro Gly Tyr Val Ala Ser  
             65                    70                    75                    80  
 Ile Arg Leu Glu Pro Gly Ala Val Asn Pro Asp Gly Asp Val Phe Leu  
                     85                    90                    95  
 Asp Glu Glu Gln Val Arg Arg Phe Thr Met Ile Gly Cys Leu Arg Cys  
             100                    105                    110  
 Gly Ser Leu Met Leu Lys Pro Asp Val Val Tyr Phe Gly Glu Pro Val  
             115                    120                    125  
 Pro Ala Ala Arg Lys Lys Asp Leu Lys Lys Leu Leu Asp Ala Ser Ser  
             130                    135                    140  
 Ser Leu Leu Ile Ala Gly Ser Ser Leu Ala Val Met Ser Gly Tyr Arg  
             145                    150                    155                    160  
 Ile Val Ile Glu Ala Gln Arg Gln Gly Lys Gln Val Ser Val Ile Asn  
                     165                    170                    175  
 Gly Gly Pro Gly Arg Ala Asp Ser Arg Val Asp Ile Leu Trp Arg Thr  
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 Arg Val Ala Pro Ala Phe Asp Asp Ile Leu Asp Ala Leu Asp Leu  
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<210> 199  
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	Val	Asp	Val	Arg	His	
	1				5	
ctt cca gaa act gaa agc cgt tcc tcc aag gct gct aca cag gca aag						163
Leu Pro Glu Thr Glu Ser Arg Ser Ser Lys Ala Ala Thr Gln Ala Lys						
			10		15	20
agc aag gcc cct cag gcc ggg gtc cat gat cct gag tta gct ggc cag						211
Ser Lys Ala Pro Gln Ala Gly Val His Asp Pro Glu Leu Ala Gly Gln			25		30	35
acc tca ttt gtc cca gtg gtg ggc aaa att gcc gct ggt agc ccg atc						259
Thr Ser Phe Val Pro Val Val Gly Lys Ile Ala Ala Gly Ser Pro Ile			40		45	50
acc gct gag cag aac atc gaa gag tac tac cca ctc ccc gca gaa atc						307
Thr Ala Glu Gln Asn Ile Glu Glu Tyr Tyr Pro Leu Pro Ala Glu Ile			55		60	65
gtc gga gac ggt gac ttg ttc atg ctc cag gtt gtt ggc gag tcc atg						355
Val Gly Asp Gly Asp Leu Phe Met Leu Gln Val Val Gly Glu Ser Met			70		75	80
					85	
agg gat gct ggc atc ctc acc ggc gac tgg gtt gtt gtt cgt tcc cag						403
Arg Asp Ala Gly Ile Leu Thr Gly Asp Trp Val Val Val Arg Ser Gln			90		95	100
ccg gta gct gag cag gcc gag ttc gtc gcg gca atg att gac ggt gaa						451
Pro Val Ala Glu Gln Gly Glu Phe Val Ala Ala Met Ile Asp Gly Glu			105		110	115
gcc acc gtg aag gaa ttc cac aag gat tca tct ggc atc tgg ctc ctg						499
Ala Thr Val Lys Glu Phe His Lys Asp Ser Ser Gly Ile Trp Leu Leu			120		125	130
cca cac aac gat acg ttt gcc cca att cct gct gag aat gca gaa atc						547
Pro His Asn Asp Thr Phe Ala Pro Ile Pro Ala Glu Asn Ala Glu Ile			135		140	145
atg ggc aag gtt gtt tcc gtg atg cgc aag ctt taagtcgctt ttcaggttcc						600
Met Gly Lys Val Val Ser Val Met Arg Lys Leu			150		155	160
cgc						603

&lt;210&gt; 200

&lt;211&gt; 160

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 200

Val	Asp	Val	Arg	His	Leu	Pro	Glu	Thr	Glu	Ser	Arg	Ser	Ser	Lys	Ala
1				5					10					15	

Ala	Thr	Gln	Ala	Lys	Ser	Lys	Ala	Pro	Gln	Ala	Gly	Val	His	Asp	Pro
		20					25						30		

Glu	Leu	Ala	Gly	Gln	Thr	Ser	Phe	Val	Pro	Val	Val	Gly	Lys	Ile	Ala
		35					40					45			

Ala Gly Ser Pro Ile Thr Ala Glu Gln Asn Ile Glu Glu Tyr Tyr Pro  
 50 55 60

Leu Pro Ala Glu Ile Val Gly Asp Gly Asp Leu Phe Met Leu Gln Val  
 65 70 75 80

Val Gly Glu Ser Met Arg Asp Ala Gly Ile Leu Thr Gly Asp Trp Val  
 85 90 95

Val Val Arg Ser Gln Pro Val Ala Glu Gln Gly Glu Phe Val Ala Ala  
 100 105 110

Met Ile Asp Gly Glu Ala Thr Val Lys Glu Phe His Lys Asp Ser Ser  
 115 120 125

Gly Ile Trp Leu Leu Pro His Asn Asp Thr Phe Ala Pro Ile Pro Ala  
 130 135 140

Glu Asn Ala Glu Ile Met Gly Lys Val Val Ser Val Met Arg Lys Leu  
 145 150 155 160

<210> 201  
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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(754)  
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tgagggaaca tcccaaacc aaagaacctt ggagaacatt atg agt gag aca gtt 115  
 Met Ser Glu Thr Val  
 1 5

tta gtc ata gga gca aca gga agc ata ggc cga cat gtt gtc tcg gaa 163  
 Leu Val Ile Gly Ala Thr Gly Ser Ile Gly Arg His Val Val Ser Glu  
 10 15 20

gca ctt aac cag gga tac caa gtt aag gca ttt gtc cgt agc aag tcc 211  
 Ala Leu Asn Gln Gly Tyr Gln Val Lys Ala Phe Val Arg Ser Lys Ser  
 25 30 35

cgt gca cgg gtg ctt cca gct gag gca gag att atc gta gga gac ctg 259  
 Arg Ala Arg Val Leu Pro Ala Glu Ala Glu Ile Ile Val Gly Asp Leu  
 40 45 50

ctt gat cct tcc tcg att gag aaa gct gta aaa ggc gtc gag gga atc 307  
 Leu Asp Pro Ser Ser Ile Glu Lys Ala Val Lys Gly Val Glu Gly Ile  
 55 60 65

att ttc act cac ggc acc tcc act cgt aaa agc gat gtg cgg gat gtt 355  
 Ile Phe Thr His Gly Thr Ser Thr Arg Lys Ser Asp Val Arg Asp Val  
 70 75 80 85

gat tac acc ggc gtt gcc aac acg ttg aag gca gtc aag gga aaa gat 403  
Asp Tyr Thr Gly Val Ala Asn Thr Leu Lys Ala Val Lys Gly Lys Asp  
90 95 100  
gta aaa att gtg ctg atg acc gcc gtt gga acg acc cgc cca ggt gtg 451  
Val Lys Ile Val Leu Met Thr Ala Val Gly Thr Thr Arg Pro Gly Val  
105 110 115  
gct tat gcc gag tgg aag cga cat ggc gag caa ctt gtt cga gct agc 499  
Ala Tyr Ala Glu Trp Lys Arg His Gly Glu Gln Leu Val Arg Ala Ser  
120 125 130  
gga cac ggt tac acc att gtt cgc cct ggt tgg ttt gat tac aac aac 547  
Gly His Gly Tyr Thr Ile Val Arg Pro Gly Trp Phe Asp Tyr Asn Asn  
135 140 145  
gat gac gag cgt cag atc gtc atg ctt caa ggc gac acc aat cag tcg 595  
Asp Asp Glu Arg Gln Ile Val Met Leu Gln Gly Asp Thr Asn Gln Ser  
150 155 160 165  
ggt ggc cca gcc gat ggc gtg att gcg cgt gat caa atc gcg cga gtt 643  
Gly Gly Pro Ala Asp Gly Val Ile Ala Arg Asp Gln Ile Ala Arg Val  
170 175 180  
ttg gtt agc agt ttg aat gat gca aaa gca cga aac aaa acc ttc gag 691  
Leu Val Ser Ser Leu Asn Asp Ala Lys Ala Arg Asn Lys Thr Phe Glu  
185 190 195  
ctt tct gcc act tat gga cct gcc caa gga aag cct gac cgc aac ttt 739  
Leu Ser Ala Thr Tyr Gly Pro Ala Gln Gly Lys Pro Asp Arg Asn Phe  
200 205 210  
tgc agc act tcg ggc tgacgatacc gatgatattg acg 777  
Cys Ser Thr Ser Gly  
215

&lt;210&gt; 202

&lt;211&gt; 218

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 202

Met Ser Glu Thr Val Leu Val Ile Gly Ala Thr Gly Ser Ile Gly Arg  
1 5 10 15  
His Val Val Ser Glu Ala Leu Asn Gln Gly Tyr Gln Val Lys Ala Phe  
20 25 30  
Val Arg Ser Lys Ser Arg Ala Arg Val Leu Pro Ala Glu Ala Glu Ile  
35 40 45  
Ile Val Gly Asp Leu Leu Asp Pro Ser Ser Ile Glu Lys Ala Val Lys  
50 55 60  
Gly Val Glu Gly Ile Ile Phe Thr His Gly Thr Ser Thr Arg Lys Ser  
65 70 75 80  
Asp Val Arg Asp Val Asp Tyr Thr Gly Val Ala Asn Thr Leu Lys Ala  
85 90 95



Val Lys Gly Lys Asp Val Lys Ile Val Leu Met Thr Ala Val Gly Thr  
 100 105 110

Thr Arg Pro Gly Val Ala Tyr Ala Glu Trp Lys Arg His Gly Glu Gln  
 115 120 125

Leu Val Arg Ala Ser Gly His Gly Tyr Thr Ile Val Arg Pro Gly Trp  
 130 135 140

Phe Asp Tyr Asn Asn Asp Asp Glu Arg Gln Ile Val Met Leu Gln Gly  
 145 150 155 160

Asp Thr Asn Gln Ser Gly Gly Pro Ala Asp Gly Val Ile Ala Arg Asp  
 165 170 175

Gln Ile Ala Arg Val Leu Val Ser Ser Leu Asn Asp Ala Lys Ala Arg  
 180 185 190

Asn Lys Thr Phe Glu Leu Ser Ala Thr Tyr Gly Pro Ala Gln Gly Lys  
 195 200 205

Pro Asp Arg Asn Phe Cys Ser Thr Ser Gly  
 210 215

<210> 203  
 <211> 861  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(838)  
 <223> RXA00583

<400> 203  
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actgttaaata gtgttaaacc tgcccagact gctgtaccgc gtg tat gag cgc cgt 115  
 Val Tyr Glu Arg Arg  
 1 5

ctt tta aga gaa cta gac ggc gcc aaa cag ccc ggt cac gtt gcc atc 163  
 Leu Leu Arg Glu Leu Asp Gly Ala Lys Gln Pro Gly His Val Ala Ile  
 10 15 20

atg tgt gat ggc aac cga cgc tgg gcc cgg gaa gcg ggc ttc act gat 211  
 Met Cys Asp Gly Asn Arg Arg Trp Ala Arg Glu Ala Gly Phe Thr Asp  
 25 30 35

gtc agc cat ggg cac cga gtg ggt gcc aaa aag atc ggc gag atg gtc 259  
 Val Ser His Gly His Arg Val Gly Ala Lys Lys Ile Gly Glu Met Val  
 40 45 50

cgc tgg tgt gat gat gta gac gtc aat ctc gtg acc gtt tat ttg ctg 307  
 Arg Trp Cys Asp Asp Val Asp Val Asn Leu Val Thr Val Tyr Leu Leu  
 55 60 65

tct atg gaa aac ctt ggg cga tcc tcc gaa gag ctg caa ttg ctg ttc 355  
 Ser Met Glu Asn Leu Gly Arg Ser Ser Glu Glu Leu Gln Leu Leu Phe

70	75	80	85	
gat atc atc gcc gat gtc gct gat gaa ctc gcg cgt cct gaa acc aac				403
Asp Ile Ile Ala Asp Val Ala Asp Glu Leu Ala Arg Pro Glu Thr Asn	90	95	100	
tgt cga gtc cgc ctc gtt ggt cat tta gat ctg ctc cca gac cca gtt				451
Cys Arg Val Arg Leu Val Gly His Leu Asp Leu Leu Pro Asp Pro Val	105	110	115	
gct tgt cgt tta cgc aaa gct gaa gaa gct acc gtt aac aac aca ggc				499
Ala Cys Arg Leu Arg Lys Ala Glu Glu Ala Thr Val Asn Asn Thr Gly	120	125	130	
atc gca gtc aac atg gct gtc ggt tat ggc gga cgc cag gaa atc gtt				547
Ile Ala Val Asn Met Ala Val Gly Tyr Gly Gly Arg Gln Glu Ile Val	135	140	145	
gat gcc gtg caa aaa ctt ctg acc atc ggc aag gac gag ggc cta agc				595
Asp Ala Val Gln Lys Leu Leu Thr Ile Gly Lys Asp Glu Gly Leu Ser	150	155	160	165
gtt gat gaa ctg atc gaa tcc gtc aag gta gat gcg atc tcc act cac				643
Val Asp Glu Leu Ile Glu Ser Val Lys Val Asp Ala Ile Ser Thr His	170	175	180	
ctg tac acc tct ggc caa cca gac cca gac ctg gtg atc cgc acc tct				691
Leu Tyr Thr Ser Gly Gln Pro Asp Pro Asp Leu Val Ile Arg Thr Ser	185	190	195	
ggt gag cag cga ctt tcc gga ttc atg ctg tgg caa tct gcc tac tcc				739
Gly Glu Gln Arg Leu Ser Gly Phe Met Leu Trp Gln Ser Ala Tyr Ser	200	205	210	
gaa atc tgg ttc aca gac acc tac tgg cca gcc ttc cga cgc atc gac				787
Glu Ile Trp Phe Thr Asp Thr Tyr Trp Pro Ala Phe Arg Arg Ile Asp	215	220	225	
ttc ctc cgc gcc att cgc gac tac tcg cag cgc agc aga aga ttc ggt				835
Phe Leu Arg Ala Ile Arg Asp Tyr Ser Gln Arg Ser Arg Arg Phe Gly	230	235	240	245
aaa taacttattc tccaaggaga gac				861
Lys				

&lt;210&gt; 204

&lt;211&gt; 246

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 204

Val Tyr Glu Arg Arg Leu Leu Arg Glu Leu Asp Gly Ala Lys Gln Pro	
1 5 10 15	

Gly His Val Ala Ile Met Cys Asp Gly Asn Arg Arg Trp Ala Arg Glu	
20 25 30	

Ala Gly Phe Thr Asp Val Ser His Gly His Arg Val Gly Ala Lys Lys	
35 40 45	

Ile Gly Glu Met Val Arg Trp Cys Asp Asp Val Asp Val Asn Leu Val  
 50 55 60  
 Thr Val Tyr Leu Leu Ser Met Glu Asn Leu Gly Arg Ser Ser Glu Glu  
 65 70 75 80  
 Leu Gln Leu Leu Phe Asp Ile Ile Ala Asp Val Ala Asp Glu Leu Ala  
 85 90 95  
 Arg Pro Glu Thr Asn Cys Arg Val Arg Leu Val Gly His Leu Asp Leu  
 100 105 110  
 Leu Pro Asp Pro Val Ala Cys Arg Leu Arg Lys Ala Glu Glu Ala Thr  
 115 120 125  
 Val Asn Asn Thr Gly Ile Ala Val Asn Met Ala Val Gly Tyr Gly Gly  
 130 135 140  
 Arg Gln Glu Ile Val Asp Ala Val Gln Lys Leu Leu Thr Ile Gly Lys  
 145 150 155 160  
 Asp Glu Gly Leu Ser Val Asp Glu Leu Ile Glu Ser Val Lys Val Asp  
 165 170 175  
 Ala Ile Ser Thr His Leu Tyr Thr Ser Gly Gln Pro Asp Pro Asp Leu  
 180 185 190  
 Val Ile Arg Thr Ser Gly Glu Gln Arg Leu Ser Gly Phe Met Leu Trp  
 195 200 205  
 Gln Ser Ala Tyr Ser Glu Ile Trp Phe Thr Asp Thr Tyr Trp Pro Ala  
 210 215 220  
 Phe Arg Arg Ile Asp Phe Leu Arg Ala Ile Arg Asp Tyr Ser Gln Arg  
 225 230 235 240  
 Ser Arg Arg Phe Gly Lys  
 245

<210> 205  
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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <223> RXA00592

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 Met Ala Ser Asn Ser  
 1 5  
 gaa cgc ctt gca gag ctg ggc att tct ctt cct tcc gtt gca gcg cct 163  
 Glu Arg Leu Ala Glu Leu Gly Ile Ser Leu Pro Ser Val Ala Ala Pro  
 10 15 20

gtt gct gcg tat gtt cct gcg att cag acc ggt aac cag gtg tgg act 211  
 Val Ala Ala Tyr Val Pro Ala Ile Gln Thr Gly Asn Gln Val Trp Thr  
 25 30 35  
 tct ggt cag ctg cct ttc gtt gat ggt cag ctt ccg gcc acc ggc aag 259  
 Ser Gly Gln Leu Pro Phe Val Asp Gly Gln Leu Pro Ala Thr Gly Lys  
 40 45 50  
 gtt ggc gct gag gtt tcc gct gag gat gcg gag aag ttg gct cgt gcg 307  
 Val Gly Ala Glu Val Ser Ala Glu Asp Ala Glu Lys Leu Ala Arg Ala  
 55 60 65  
 gct gcg cta aac gct ctt gct gcg att gat gcg ctt gtt ggc att gat 355  
 Ala Ala Leu Asn Ala Leu Ala Ala Ile Asp Ala Leu Val Gly Ile Asp  
 70 75 80 85  
 aag gtc act cgc gtt ttg aag att gtt ggt ttc gtg gcg tct gct gat 403  
 Lys Val Thr Arg Val Leu Lys Ile Val Gly Phe Val Ala Ser Ala Asp  
 90 95 100  
 gat ttc agt ggt cag cct gct gtc gtc aac ggt gct tcc aat ttg atg 451  
 Asp Phe Ser Gly Gln Pro Ala Val Val Asn Gly Ala Ser Asn Leu Met  
 105 110 115  
 ggt gag gtt ttc ggc gag gct ggg gcg cat gcg cgt tct gct gtg ggc 499  
 Gly Glu Val Phe Gly Glu Ala Gly Ala His Ala Arg Ser Ala Val Gly  
 120 125 130  
 gtg gcg gag ttg ccg ctc aac tcg cct gtc gag gtc gag gtt atc gtc 547  
 Val Ala Glu Leu Pro Leu Asn Ser Pro Val Glu Val Glu Val Ile Val  
 135 140 145  
 gag atc gcg cag tagcacgctt ttcgacgcaa aat 582  
 Glu Ile Ala Gln  
 150

&lt;210&gt; 206

&lt;211&gt; 153

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 206

Met Ala Ser Asn Ser Glu Arg Leu Ala Glu Leu Gly Ile Ser Leu Pro  
 1 5 10 15  
 Ser Val Ala Ala Pro Val Ala Ala Tyr Val Pro Ala Ile Gln Thr Gly  
 20 25 30  
 Asn Gln Val Trp Thr Ser Gly Gln Leu Pro Phe Val Asp Gly Gln Leu  
 35 40 45  
 Pro Ala Thr Gly Lys Val Gly Ala Glu Val Ser Ala Glu Asp Ala Glu  
 50 55 60  
 Lys Leu Ala Arg Ala Ala Ala Leu Asn Ala Leu Ala Ala Ile Asp Ala  
 65 70 75 80  
 Leu Val Gly Ile Asp Lys Val Thr Arg Val Leu Lys Ile Val Gly Phe  
 85 90 95

Val Ala Ser Ala Asp Asp Phe Ser Gly Gln Pro Ala Val Val Asn Gly  
 100 105 110

Ala Ser Asn Leu Met Gly Glu Val Phe Gly Glu Ala Gly Ala His Ala  
 115 120 125

Arg Ser Ala Val Gly Val Ala Glu Leu Pro Leu Asn Ser Pro Val Glu  
 130 135 140

Val Glu Val Ile Val Glu Ile Ala Gln  
 145 150

<210> 207  
 <211> 182  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(159)  
 <223> RXA00630

<400> 207  
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 Ala Lys Ile Leu Asp Asn Val Trp His Tyr Asp Phe Gly Gly Asp Gly  
 1 5 10 15

aac gtc gtg gaa tcc tac atc tcc tac ctg cgc cgc aag gtg gac acc 96  
 Asn Val Val Glu Ser Tyr Ile Ser Tyr Leu Arg Arg Lys Val Asp Thr  
 20 25 30

cag gat ccg cag cta att cag act gtt cgt ggc gtt gga tat gtt ctg 144  
 Gln Asp Pro Gln Leu Ile Gln Thr Val Arg Gly Val Gly Tyr Val Leu  
 35 40 45

cgc acc cca cgt agc taaattctcc tatggaaaat cct 182  
 Arg Thr Pro Arg Ser  
 50

<210> 208  
 <211> 53  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 208  
 Ala Lys Ile Leu Asp Asn Val Trp His Tyr Asp Phe Gly Gly Asp Gly  
 1 5 10 15

Asn Val Val Glu Ser Tyr Ile Ser Tyr Leu Arg Arg Lys Val Asp Thr  
 20 25 30

Gln Asp Pro Gln Leu Ile Gln Thr Val Arg Gly Val Gly Tyr Val Leu  
 35 40 45

Arg Thr Pro Arg Ser  
 50

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<400> 210
Met Glu Glu Ile Lys Met Asp Asn Gln Ser Asp Gly Gln Ile Arg Val
  1             5             10            15
Leu Val Val Asp Asp Glu Pro Asn Ile Val Glu Leu Leu Thr Val Ser
          20          25          30

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Leu Lys Phe Gln Gly Phe Ala Val Met Thr Ala Asn Asp Gly Asn Glu  
           35                                  40                                  45  
 Ala Leu Lys Ile Ala Arg Glu Phe Arg Pro Asp Ala Tyr Ile Leu Asp  
           50                                  55                                  60  
 Val Met Met Pro Gly Met Asp Gly Phe Glu Leu Leu Thr Lys Leu Arg  
           65                                  70                                  75                                  80  
 Gly Glu Gly Leu Asp Ser Pro Val Leu Tyr Leu Thr Ala Lys Asp Ala  
                                   85                                  90                                  95  
 Val Glu His Arg Ile His Gly Leu Thr Ile Gly Ala Asp Asp Tyr Val  
                                   100                                  105                                  110  
 Thr Lys Pro Phe Ser Leu Glu Glu Val Ile Thr Arg Leu Arg Val Ile  
           115                                  120                                  125

<210> 211  
 <211> 1251  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(1228)  
 <223> RXA00894

<400> 211  
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   Met Gly Ile Glu Phe  
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 aag cgt tca ccg cga ccc acc ctg ggc gtt gag tgg gaa att gca ctt 163  
 Lys Arg Ser Pro Arg Pro Thr Leu Gly Val Glu Trp Glu Ile Ala Leu  
                                   10                                  15                                  20  
 gtt gat cca gaa aca cgt gat cta gcc ccg cgc gct gca gaa ata cta 211  
 Val Asp Pro Glu Thr Arg Asp Leu Ala Pro Arg Ala Ala Glu Ile Leu  
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 gag att gtg gcc aag aac cac cct gag gtg cac ctc gag cgc gaa ttc 259  
 Glu Ile Val Ala Lys Asn His Pro Glu Val His Leu Glu Arg Glu Phe  
                                   40                                  45                                  50  
 ctc caa aac acc gtg gag ctt gtc acc gga gtg tgc gac acc gtc ccc 307  
 Leu Gln Asn Thr Val Glu Leu Val Thr Gly Val Cys Asp Thr Val Pro  
                                   55                                  60                                  65  
 gaa gcg gtg gca gag ctt tcc cac gat cta gat gcg ctg aaa gaa gca 355  
 Glu Ala Val Ala Glu Leu Ser His Asp Leu Asp Ala Leu Lys Glu Ala  
           70                                  75                                  80                                  85  
 gcg gat tct ctc ggg ctt cgg ttg tgg acc tct gga tcc cac cca ttt 403

Ala	Asp	Ser	Leu	Gly	Leu	Arg	Leu	Trp	Thr	Ser	Gly	Ser	His	Pro	Phe	
				90					95					100		
tcg	gat	ttc	cgc	gaa	aac	cca	gta	tct	gaa	aaa	ggc	tcc	tac	gac	gag	451
Ser	Asp	Phe	Arg	Glu	Asn	Pro	Val	Ser	Glu	Lys	Gly	Ser	Tyr	Asp	Glu	
			105					110					115			
atc	atc	gcg	cgc	acc	caa	tac	tgg	gga	aac	cag	atg	ttg	att	tgg	ggc	499
Ile	Ile	Ala	Arg	Thr	Gln	Tyr	Trp	Gly	Asn	Gln	Met	Leu	Ile	Trp	Gly	
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Ile	His	Val	His	Val	Gly	Ile	Ser	His	Glu	Asp	Arg	Val	Trp	Pro	Ile	
	135					140					145					
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Ile	Asn	Ala	Leu	Leu	Thr	Asn	Tyr	Pro	His	Leu	Leu	Ala	Leu	Ser	Ala	
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agc	tct	cca	gca	tgg	gac	gga	ctt	gat	acc	ggt	tat	gcc	tcc	aac	cgg	643
Ser	Ser	Pro	Ala	Trp	Asp	Gly	Leu	Asp	Thr	Gly	Tyr	Ala	Ser	Asn	Arg	
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acg	atg	ctc	tac	caa	cag	ctg	cct	aca	gcc	gga	ctg	cca	tac	caa	ttc	691
Thr	Met	Leu	Tyr	Gln	Gln	Leu	Pro	Thr	Ala	Gly	Leu	Pro	Tyr	Gln	Phe	
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caa	agc	tgg	gat	gaa	tgg	tgc	agc	tac	atg	gcg	gat	caa	gat	aaa	tcc	739
Gln	Ser	Trp	Asp	Glu	Trp	Cys	Ser	Tyr	Met	Ala	Asp	Gln	Asp	Lys	Ser	
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Gly	Val	Ile	Asn	His	Thr	Gly	Ser	Met	His	Phe	Asp	Ile	Arg	Pro	Ala	
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tcc	aaa	tgg	gga	acc	atc	gaa	gtc	cgc	gtg	gcc	gat	tct	acc	tcc	aac	835
Ser	Lys	Trp	Gly	Thr	Ile	Glu	Val	Arg	Val	Ala	Asp	Ser	Thr	Ser	Asn	
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ctg	cgg	gaa	ctg	tct	gcc	atc	gtg	gcg	ttg	acc	cac	tgt	ctc	gtg	gtg	883
Leu	Arg	Glu	Leu	Ser	Ala	Ile	Val	Ala	Leu	Thr	His	Cys	Leu	Val	Val	
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His	Tyr	Asp	Arg	Met	Ile	Asp	Ala	Gly	Glu	Glu	Leu	Pro	Ser	Leu	Gln	
			265					270					275			
caa	tgg	cac	gtt	tcg	gaa	aat	aaa	tgg	cgc	gcg	gct	agg	tat	ggt	ctg	979
Gln	Trp	His	Val	Ser	Glu	Asn	Lys	Trp	Arg	Ala	Ala	Arg	Tyr	Gly	Leu	
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Asp	Ala	Glu	Ile	Ile	Ile	Ser	Arg	Asp	Thr	Asp	Glu	Ala	Met	Val	Gln	
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gac	gaa	ctc	cgc	cga	cta	gta	gcg	caa	ttg	atg	cct	cta	gcc	aac	gaa	1075
Asp	Glu	Leu	Arg	Arg	Leu	Val	Ala	Gln	Leu	Met	Pro	Leu	Ala	Asn	Glu	
310					315					320					325	
ctc	ggc	tgc	gct	cgt	gag	ctt	gaa	ctt	gtg	ttg	gaa	atc	ctg	gaa	cgt	1123
Leu	Gly	Cys	Ala	Arg	Glu	Leu	Glu	Leu	Val	Leu	Glu	Ile	Leu	Glu	Arg	



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Gly Gly Gly Tyr Glu Arg Gln Arg Arg Val Phe Lys Glu Thr Gly Ser
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tgg aaa gct gca gtt gat tta gcc tgc gac gaa ctc aac gac ctc aaa 1219
Trp Lys Ala Ala Val Asp Leu Ala Cys Asp Glu Leu Asn Asp Leu Lys
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gca ctg gac taaatagcta tgggtggaatc cca 1251
Ala Leu Asp
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Leu Glu Arg Glu Phe Leu Gln Asn Thr Val Glu Leu Val Thr Gly Val
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Cys Asp Thr Val Pro Glu Ala Val Ala Glu Leu Ser His Asp Leu Asp
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Ala Leu Lys Glu Ala Ala Asp Ser Leu Gly Leu Arg Leu Trp Thr Ser
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Gly Ser His Pro Phe Ser Asp Phe Arg Glu Asn Pro Val Ser Glu Lys
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Gly Ser Tyr Asp Glu Ile Ile Ala Arg Thr Gln Tyr Trp Gly Asn Gln
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Met Leu Ile Trp Gly Ile His Val His Val Gly Ile Ser His Glu Asp
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Arg Val Trp Pro Ile Ile Asn Ala Leu Leu Thr Asn Tyr Pro His Leu
      145              150              155              160

Leu Ala Leu Ser Ala Ser Ser Pro Ala Trp Asp Gly Leu Asp Thr Gly
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Tyr Ala Ser Asn Arg Thr Met Leu Tyr Gln Gln Leu Pro Thr Ala Gly
      180              185              190

Leu Pro Tyr Gln Phe Gln Ser Trp Asp Glu Trp Cys Ser Tyr Met Ala
      195              200              205

Asp Gln Asp Lys Ser Gly Val Ile Asn His Thr Gly Ser Met His Phe

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210	215	220
Asp Ile Arg Pro Ala Ser Lys Trp Gly Thr Ile Glu Val Arg Val Ala 225 230 235 240		
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His Cys Leu Val Val His Tyr Asp Arg Met Ile Asp Ala Gly Glu Glu 260 265 270		
Leu Pro Ser Leu Gln Gln Trp His Val Ser Glu Asn Lys Trp Arg Ala 275 280 285		
Ala Arg Tyr Gly Leu Asp Ala Glu Ile Ile Ile Ser Arg Asp Thr Asp 290 295 300		
Glu Ala Met Val Gln Asp Glu Leu Arg Arg Leu Val Ala Gln Leu Met 305 310 315 320		
Pro Leu Ala Asn Glu Leu Gly Cys Ala Arg Glu Leu Glu Leu Val Leu 325 330 335		
Glu Ile Leu Glu Arg Gly Gly Gly Tyr Glu Arg Gln Arg Arg Val Phe 340 345 350		
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 Val Pro Val Thr Leu  
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 act ctt gga atc gtc ggc ctg ccc aac gtt ggc aag tcc acc ctg ttc 163  
 Thr Leu Gly Ile Val Gly Leu Pro Asn Val Gly Lys Ser Thr Leu Phe  
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 acc atc gag cca aac gtg ggc ctt gtc gag ctt cca gac gct cgc ctt 259  
 Thr Ile Glu Pro Asn Val Gly Leu Val Glu Leu Pro Asp Ala Arg Leu  
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gaa cgc ctt tct gaa atc ttc ggc tct gag cgc atc ctg cca gca acc 307  
 Glu Arg Leu Ser Glu Ile Phe Gly Ser Glu Arg Ile Leu Pro Ala Thr  
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 Val Ser Phe Val Asp Ile Ala Gly Ile Val Lys Gly Ala Ser Glu Gly  
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 Glu Gly Met Gly Asn Ala Phe Leu Ala Asn Ile Arg Glu Ala Asp Ala  
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 Ile Cys Gln Val Val Arg Ala Phe Ala Asp Glu Asn Val Ile His Val  
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ctg atc ctc gcc gac ctg cag acc gtg gaa aaa gca ctc cca cgc ctc 547  
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 135 140 145

gaa aag gat gca cgc aaa gac aag gga ctt ggc gaa gtc gta gat gag 595  
 Glu Lys Asp Ala Arg Lys Asp Lys Gly Leu Gly Glu Val Val Asp Glu  
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acc aaa aaa gcc ctt gcg atc ttg agc gat gac cgc acc ttg ttt ctc 643  
 Thr Lys Lys Ala Leu Ala Ile Leu Ser Asp Asp Arg Thr Leu Phe Leu  
 170 175 180

tgc agc aaa agc tgg cga cat tgatctggcc ctccctgcgcg atc 687  
 Cys Ser Lys Ser Trp Arg His  
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&lt;210&gt; 214

&lt;211&gt; 188

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 214

Val Pro Val Thr Leu Thr Leu Gly Ile Val Gly Leu Pro Asn Val Gly  
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Lys Ser Thr Leu Phe Asn Ala Leu Thr Arg Asn Asp Val Leu Ala Ala  
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Asn Tyr Pro Phe Ala Thr Ile Glu Pro Asn Val Gly Leu Val Glu Leu  
 35 40 45

Pro Asp Ala Arg Leu Glu Arg Leu Ser Glu Ile Phe Gly Ser Glu Arg  
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Ile Leu Pro Ala Thr Val Ser Phe Val Asp Ile Ala Gly Ile Val Lys  
 65 70 75 80

Gly Ala Ser Glu Gly Glu Gly Met Gly Asn Ala Phe Leu Ala Asn Ile  
 85 90 95

Arg Glu Ala Asp Ala Ile Cys Gln Val Val Arg Ala Phe Ala Asp Glu  
 100 105 110  
 Asn Val Ile His Val Asp Gly Glu Val Asn Pro Ala Thr Asp Ile Ser  
 115 120 125  
 Val Ile Asn Thr Glu Leu Ile Leu Ala Asp Leu Gln Thr Val Glu Lys  
 130 135 140  
 Ala Leu Pro Arg Leu Glu Lys Asp Ala Arg Lys Asp Lys Gly Leu Gly  
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 Met Thr Ala Pro Cys  
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 ttc tct gca gca aaa gct ggc gac att gat ctg gcc ctc ctg cgc gat 163  
 Phe Ser Ala Ala Lys Ala Gly Asp Ile Asp Leu Ala Leu Leu Arg Asp  
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 Glu Lys Val Leu Thr Asp Asp Ala Lys Lys Asp Glu Leu Arg Ala Leu  
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 Val Ala Pro Ala Asp Cys Val Phe Leu Asp Ala Gln Thr Glu Thr Glu  
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 Leu Leu Glu Leu Glu Glu Asp Glu Ala Ala Glu Leu Leu Glu Ala Val  
 70 75 80 85  
 ggc caa acg gaa cca ggc cta cac tcc ctc gca cgt gca gga ttt gaa 403  
 Gly Gln Thr Glu Pro Gly Leu His Ser Leu Ala Arg Ala Gly Phe Glu  
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acc ctc gga cta cag acc tac ctc acc gcg ggt cct aag gaa tca cgc 451  
 Thr Leu Gly Leu Gln Thr Tyr Leu Thr Ala Gly Pro Lys Glu Ser Arg  
 105 110 115

gcc tgg acc atc cac aag ggc gac acc gct cca cag gca gca ggc gtt 499  
 Ala Trp Thr Ile His Lys Gly Asp Thr Ala Pro Gln Ala Ala Gly Val  
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atc cat tct gac ttc gaa cgc ggc ttc atc aag gct gaa atc gtc tcc 547  
 Ile His Ser Asp Phe Glu Arg Gly Phe Ile Lys Ala Glu Ile Val Ser  
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 Phe Glu Asp Leu Asp Ala Ala Gly Ser Met Ala Glu Ala Lys Ala Gln  
 150 155 160 165

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 Gly Lys Val Arg Gln Glu Gly Lys Asp Tyr Val Met Val Asp Gly Asp  
 170 175 180

gtt gtg gag ttc cgg ttt aac gtc tagcggttatt gacgctcctc gtt 690  
 Val Val Glu Phe Arg Phe Asn Val  
 185

&lt;210&gt; 216

&lt;211&gt; 189

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 216

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Ala Leu Leu Arg Asp Leu His Leu Met Thr Ala Lys Pro Phe Leu Tyr  
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Val Phe Asn Ser Asp Glu Lys Val Leu Thr Asp Asp Ala Lys Lys Asp  
 35 40 45

Glu Leu Arg Ala Leu Val Ala Pro Ala Asp Cys Val Phe Leu Asp Ala  
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Gln Thr Glu Thr Glu Leu Leu Glu Leu Glu Glu Asp Glu Ala Ala Glu  
 65 70 75 80

Leu Leu Glu Ala Val Gly Gln Thr Glu Pro Gly Leu His Ser Leu Ala  
 85 90 95

Arg Ala Gly Phe Glu Thr Leu Gly Leu Gln Thr Tyr Leu Thr Ala Gly  
 100 105 110

Pro Lys Glu Ser Arg Ala Trp Thr Ile His Lys Gly Asp Thr Ala Pro  
 115 120 125

Gln Ala Ala Gly Val Ile His Ser Asp Phe Glu Arg Gly Phe Ile Lys  
 130 135 140

Ala Glu Ile Val Ser Phe Glu Asp Leu Asp Ala Ala Gly Ser Met Ala  
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Glu Ala Lys Ala Gln Gly Lys Val Arg Gln Glu Gly Lys Asp Tyr Val  
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Met Val Asp Gly Asp Val Val Glu Phe Arg Phe Asn Val  
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 Gly Asn Gly Gly His Gly Gly Asp Ile Ile Leu Glu Val Thr Ala Gln  
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 Val His Thr Leu Leu Asp Phe His Phe His Pro His Val Lys Ala Glu  
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 Arg Gly Ala Asn Gly Ala Gly Asp His Arg Asn Gly Ala Arg Gly Lys  
 70 75 80 85  
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 Gly Glu Thr Leu Ala Asp Leu Thr Ser Val Gly Met Lys Phe Ile Ala  
 105 110 115  
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 Ala Ala Gly Gly Asn Gly Gly Leu Gly Asn Ala Ala Leu Ala Ser Lys  
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 Ala Arg Lys Ala Pro Gly Phe Ala Leu Ile Gly Glu Pro Gly Glu Ala  
 135 140 145  
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Pro	Gly 215	Leu	Ile	Pro	Gly	Ala 220	Ser	Glu	Gly	Lys	Gly 225	Leu	Gly	Leu	Asp	
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Phe	Leu	Arg	His	Ile	Glu 235	Arg	Thr	Ser	Val	Leu 240	Val	His	Val	Val	Asp 245	
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Tyr Leu Ala Asp	Arg Leu Ala Lys Leu Gly Ile Glu Asp Gly Leu Arg			
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Gly Arg Gly Thr Asp Val Arg Leu Glu Gln Thr Ser Arg Ile Ser Ala				
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Leu Asp Tyr Gly Glu Asp Gln Glu Ala Ser Arg Glu Arg Trp Glu Gly				
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taaaaccgag cacttttcag gtc				1626

&lt;210&gt; 218

&lt;211&gt; 501

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 218

Met Asn Arg Phe Ile Asp Arg Val Val Leu His Leu Ala Ala Gly Asp	
1 5 10 15	
Gly Gly Asn Gly Cys Val Ser Val His Arg Glu Lys Phe Lys Pro Leu	
20 25 30	
Gly Gly Pro Asp Gly Gly Asn Gly Gly His Gly Gly Asp Ile Ile Leu	
35 40 45	
Glu Val Thr Ala Gln Val His Thr Leu Leu Asp Phe His Phe His Pro	
50 55 60	
His Val Lys Ala Glu Arg Gly Ala Asn Gly Ala Gly Asp His Arg Asn	
65 70 75 80	
Gly Ala Arg Gly Lys Asp Leu Val Leu Glu Val Pro Pro Gly Thr Val	
85 90 95	
Val Leu Asn Glu Lys Gly Glu Thr Leu Ala Asp Leu Thr Ser Val Gly	
100 105 110	
Met Lys Phe Ile Ala Ala Ala Gly Gly Asn Gly Gly Leu Gly Asn Ala	
115 120 125	
Ala Leu Ala Ser Lys Ala Arg Lys Ala Pro Gly Phe Ala Leu Ile Gly	
130 135 140	



Glu	Pro	Gly	Glu	Ala	His	Asp	Leu	Ile	Leu	Glu	Leu	Lys	Ser	Met	Ala	
145					150					155					160	
Asp	Val	Gly	Leu	Val	Gly	Phe	Pro	Ser	Ala	Gly	Lys	Ser	Ser	Leu	Ile	
				165					170					175		
Ser	Val	Met	Ser	Ala	Ala	Lys	Pro	Lys	Ile	Gly	Asp	Tyr	Pro	Phe	Thr	
			180					185					190			
Thr	Leu	Gln	Pro	Asn	Leu	Gly	Val	Val	Asn	Val	Gly	His	Glu	Thr	Phe	
		195					200					205				
Thr	Met	Ala	Asp	Val	Pro	Gly	Leu	Ile	Pro	Gly	Ala	Ser	Glu	Gly	Lys	
	210					215					220					
Gly	Leu	Gly	Leu	Asp	Phe	Leu	Arg	His	Ile	Glu	Arg	Thr	Ser	Val	Leu	
225					230					235					240	
Val	His	Val	Val	Asp	Thr	Ala	Thr	Met	Asp	Pro	Gly	Arg	Asp	Pro	Ile	
				245					250					255		
Ser	Asp	Ile	Glu	Ala	Leu	Glu	Ala	Glu	Leu	Ala	Ala	Tyr	Gln	Ser	Ala	
			260					265					270			
Leu	Asp	Glu	Asp	Thr	Gly	Leu	Gly	Asp	Leu	Ser	Gln	Arg	Pro	Arg	Leu	
	275						280					285				
Val	Val	Leu	Asn	Lys	Ala	Asp	Val	Pro	Glu	Ala	Glu	Glu	Leu	Ala	Glu	
	290					295					300					
Phe	Leu	Lys	Glu	Asp	Ile	Glu	Lys	Gln	Phe	Gly	Trp	Pro	Val	Phe	Ile	
305					310					315					320	
Ile	Ser	Ala	Val	Ala	Arg	Lys	Gly	Leu	Asp	Pro	Leu	Lys	Tyr	Lys	Leu	
				325					330					335		
Leu	Glu	Ile	Val	Gln	Asp	Ala	Arg	Lys	Lys	Arg	Pro	Lys	Glu	Lys	Ala	
			340					345					350			
Glu	Ser	Val	Ile	Ile	Lys	Pro	Lys	Ala	Val	Asp	His	Arg	Thr	Lys	Gly	
		355					360					365				
Gln	Phe	Gln	Ile	Lys	Pro	Asp	Pro	Glu	Val	Gln	Gly	Gly	Phe	Ile	Ile	
	370					375					380					
Thr	Gly	Glu	Lys	Pro	Glu	Arg	Trp	Ile	Leu	Gln	Thr	Asp	Phe	Glu	Asn	
385					390					395					400	
Asp	Glu	Ala	Val	Gly	Tyr	Leu	Ala	Asp	Arg	Leu	Ala	Lys	Leu	Gly	Ile	
				405					410					415		
Glu	Asp	Gly	Leu	Arg	Lys	Ala	Gly	Ala	His	Val	Gly	Ala	Asn	Val	Thr	
			420					425					430			
Ile	Gly	Gly	Ile	Ser	Phe	Glu	Trp	Glu	Pro	Met	Thr	Thr	Ala	Gly	Asp	
		435					440					445				
Asp	Pro	Val	Leu	Thr	Gly	Arg	Gly	Thr	Asp	Val	Arg	Leu	Glu	Gln	Thr	
	450					455					460					

Ser Arg Ile Ser Ala Ala Glu Arg Lys Arg Ala Ser Gln Val Arg Arg  
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Gly Leu Ile Asp Glu Leu Asp Tyr Gly Glu Asp Gln Glu Ala Ser Arg  
485 490 495

Glu Arg Trp Glu Gly  
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<210> 219

<211> 605

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(582)

<223> RXA01065

<400> 219

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Ile Leu Glu Ala Val Arg Lys Val Ser Pro Lys Thr Pro Ile Leu Gly	
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atc atc acc aaa gca gac agc gtc tca cgt gac ttg gtt gcg gcc caa	96
Ile Ile Thr Lys Ala Asp Ser Val Ser Arg Asp Leu Val Ala Ala Gln	
20 25 30	
ctg atg gct gtc cat gag ctg ctc ggc gga aac agc gag gta gtc cca	144
Leu Met Ala Val His Glu Leu Leu Gly Gly Asn Ser Glu Val Val Pro	
35 40 45	
gtg tct tcc acc tgc ggg gaa aac gtc gaa acg ctt att aag gtc atg	192
Val Ser Ser Thr Ser Gly Glu Asn Val Glu Thr Leu Ile Lys Val Met	
50 55 60	
acc gac ctg ctg cct gaa ggc ccc aag ttc tac ccg gat gat cac atc	240
Thr Asp Leu Leu Pro Glu Gly Pro Lys Phe Tyr Pro Asp Asp His Ile	
65 70 75 80	
acc gat gag gac acc aac acc cgc atc gcg gaa gcc atc cgc gaa gca	288
Thr Asp Glu Asp Thr Asn Thr Arg Ile Ala Glu Ala Ile Arg Glu Ala	
85 90 95	
gca ctg tct ggc ttg aag aac gaa ctg ccg cac tcc gtc gca gtt gag	336
Ala Leu Ser Gly Leu Lys Asn Glu Leu Pro His Ser Val Ala Val Glu	
100 105 110	
gtt gat gaa atc ctg cca gac cca gaa cgc aac ggt gtc ctg gct gtg	384
Val Asp Glu Ile Leu Pro Asp Pro Glu Arg Asn Gly Val Leu Ala Val	
115 120 125	
cac gcc atc atc tac gtc gag cgt gtt ggt cag aaa gac atc atc gtc	432
His Ala Ile Ile Tyr Val Glu Arg Val Gly Gln Lys Asp Ile Ile Val	
130 135 140	
gga cac aag gga cag cgc ctg ggg cgc atc atc cac acc tca cgc caa	480
Gly His Lys Gly Gln Arg Leu Gly Arg Ile Ile His Thr Ser Arg Gln	
145 150 155 160	

gac atc atc aag atc ctc ggc caa aac gta ttc ctt gac ctg cgc atc 528  
 Asp Ile Ile Lys Ile Leu Gly Gln Asn Val Phe Leu Asp Leu Arg Ile  
                   165                                  170                                  175

aag gtg ctg aag aac tgg caa tcc gat cca aag gct ttg aac cgc ctg 576  
 Lys Val Leu Lys Asn Trp Gln Ser Asp Pro Lys Ala Leu Asn Arg Leu  
                   180                                  185                                  190

ggc ttc tagctttaag ggggtgagtt cat 605  
 Gly Phe

<210> 220

<211> 194

<212> PRT

<213> Corynebacterium glutamicum

<400> 220

Ile Leu Glu Ala Val Arg Lys Val Ser Pro Lys Thr Pro Ile Leu Gly  
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Ile Ile Thr Lys Ala Asp Ser Val Ser Arg Asp Leu Val Ala Ala Gln  
                   20                                  25                                  30

Leu Met Ala Val His Glu Leu Leu Gly Gly Asn Ser Glu Val Val Pro  
                   35                                  40                                  45

Val Ser Ser Thr Ser Gly Glu Asn Val Glu Thr Leu Ile Lys Val Met  
   50                                  55                                  60

Thr Asp Leu Leu Pro Glu Gly Pro Lys Phe Tyr Pro Asp Asp His Ile  
   65                                  70                                  75                                  80

Thr Asp Glu Asp Thr Asn Thr Arg Ile Ala Glu Ala Ile Arg Glu Ala  
                   85                                  90                                  95

Ala Leu Ser Gly Leu Lys Asn Glu Leu Pro His Ser Val Ala Val Glu  
                   100                                  105                                  110

Val Asp Glu Ile Leu Pro Asp Pro Glu Arg Asn Gly Val Leu Ala Val  
   115                                  120                                  125

His Ala Ile Ile Tyr Val Glu Arg Val Gly Gln Lys Asp Ile Ile Val  
   130                                  135                                  140

Gly His Lys Gly Gln Arg Leu Gly Arg Ile Ile His Thr Ser Arg Gln  
   145                                  150                                  155                                  160

Asp Ile Ile Lys Ile Leu Gly Gln Asn Val Phe Leu Asp Leu Arg Ile  
                   165                                  170                                  175

Lys Val Leu Lys Asn Trp Gln Ser Asp Pro Lys Ala Leu Asn Arg Leu  
                   180                                  185                                  190

Gly Phe

<210> 221

<211> 1650

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1627)

&lt;223&gt; RXA02232

&lt;400&gt; 221

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aatagagcgc tcaatttagg tgtttatggt ggcttgatcg ctcacggcgt tgcccgaacac 60

ctagccttgg cgacagcaga cgtgaaacaa tagataaaca atg gat gaa aag aaa 115
                                         Met Asp Glu Lys Lys
                                         1 5

aac tta agt cat gat gaa ctt ctc gct cag gcc ttc cgc ggt cac aaa 163
Asn Leu Ser His Asp Glu Leu Leu Ala Gln Ala Phe Arg Gly His Lys
                        10 15 20

aat acc gtg cgc cca gga tct gac gag acc tca ggt ttt gat ctc agt 211
Asn Thr Val Arg Pro Gly Ser Asp Glu Thr Ser Gly Phe Asp Leu Ser
                        25 30 35

ggt ttt atc cga gct gaa gaa cca tca act ggt gat ctc gac cta gag 259
Gly Phe Ile Arg Ala Glu Glu Pro Ser Thr Gly Asp Leu Asp Leu Glu
                        40 45 50

gcc cgc gat gcc caa cgt cgc cgg gac acc gaa atc cac gct gat gaa 307
Ala Arg Asp Ala Gln Arg Arg Arg Asp Thr Glu Ile His Ala Asp Glu
                        55 60 65

gca gca gat ggc tac gag gtt gag tac cga aag ctg cga ctt gag cgc 355
Ala Ala Asp Gly Tyr Glu Val Glu Tyr Arg Lys Leu Arg Leu Glu Arg
                        70 75 80 85

gtt atc tta gtg ggc gtg tgg acc gaa ggt acc acc gca gaa att gac 403
Val Ile Leu Val Gly Val Trp Thr Glu Gly Thr Thr Ala Glu Ile Asp
                        90 95 100

gcc agc ctt gcg gaa ctt gca gcg ttg gct gat acc gcc ggc gct gag 451
Ala Ser Leu Ala Glu Leu Ala Ala Leu Ala Asp Thr Ala Gly Ala Glu
                        105 110 115

gtt att gaa acg ctg tac caa aag cgc gat aaa cca gat cct gga acc 499
Val Ile Glu Thr Leu Tyr Gln Lys Arg Asp Lys Pro Asp Pro Gly Thr
                        120 125 130

tac att ggt tcc ggc aag gtt cgg gag tta aag gag atc atc gaa gcc 547
Tyr Ile Gly Ser Gly Lys Val Arg Glu Leu Lys Glu Ile Ile Glu Ala
                        135 140 145

act agt gca gat acc gtg gtg tgc gat ggt gaa ctt agc cct tcc cag 595
Thr Ser Ala Asp Thr Val Val Cys Asp Gly Glu Leu Ser Pro Ser Gln
                        150 155 160 165

ctc gtg gca tta gag cgc gaa ctt gat atc aag gtc att gac cgc acc 643
Leu Val Ala Leu Glu Arg Glu Leu Asp Ile Lys Val Ile Asp Arg Thr
                        170 175 180

atg ctg att ctg gat atc ttc gcc cag cac gct aaa tcg cgc gaa ggt 691
Met Leu Ile Leu Asp Ile Phe Ala Gln His Ala Lys Ser Arg Glu Gly

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185					190					195					
aaa gcc caa gtc gcg ttg gcg cag atg gaa tac ctg att agc cgt gtg	739														
Lys Ala Gln Val Ala Leu Ala Gln Met Glu Tyr Leu Ile Ser Arg Val															
200	205					210									
cgt ggt tgg ggt gga aac ctc tcc agg cag gcc ggt ggt cgt gca ggt	787														
Arg Gly Trp Gly Gly Asn Leu Ser Arg Gln Ala Gly Gly Arg Ala Gly															
215	220					225									
tct aat ggt ggt gtg ggt ctg cgt ggt cca ggt gaa acc aaa att gaa	835														
Ser Asn Gly Gly Val Gly Leu Arg Gly Pro Gly Glu Thr Lys Ile Glu															
230	235					240					245				
gca gac cgc cgt cgt ctt cga tcg gat atg gct cgc ctg cgc agg gaa	883														
Ala Asp Arg Arg Leu Arg Ser Asp Met Ala Arg Leu Arg Arg Glu															
250	255					260									
ctt tcg ggg ctg gat acg tcg aga agc att aaa aga gcg caa cgc gca	931														
Leu Ser Gly Leu Asp Thr Ser Arg Ser Ile Lys Arg Ala Gln Arg Ala															
265	270					275									
gcc tcc ctg gtg ccg cag atc gcc atc gct ggc tac acg aac gcc ggc	979														
Ala Ser Leu Val Pro Gln Ile Ala Ile Ala Gly Tyr Thr Asn Ala Gly															
280	285					290									
aaa tct tcg ctg att aac gcg atg acc ggc gcg ggt gtg ctg gtg gag	1027														
Lys Ser Ser Leu Ile Asn Ala Met Thr Gly Ala Gly Val Leu Val Glu															
295	300					305									
aac gcg ctg ttc gcc acg ctt gat cca aca acc aga aaa gcc gag ctt	1075														
Asn Ala Leu Phe Ala Thr Leu Asp Pro Thr Thr Arg Lys Ala Glu Leu															
310	315					320					325				
gcc gac ggc cga cac gtc gtg ttc acg gac acc gtc ggc ttt gtg cga	1123														
Ala Asp Gly Arg His Val Val Phe Thr Asp Thr Val Gly Phe Val Arg															
330	335					340									
cac ctg ccg acc tct ctg gtt gag gcg ttc aaa tct acg ctg gaa gaa	1171														
His Leu Pro Thr Ser Leu Val Glu Ala Phe Lys Ser Thr Leu Glu Glu															
345	350					355									
gtc gtg gag gcg gac ctc atg ctg cac gtg gtg gat gga tcc gat ccg	1219														
Val Val Glu Ala Asp Leu Met Leu His Val Val Asp Gly Ser Asp Pro															
360	365					370									
ttc ccg ctg aag cag atc gac gct gtg aac acc gtg att agc gat att	1267														
Phe Pro Leu Lys Gln Ile Asp Ala Val Asn Thr Val Ile Ser Asp Ile															
375	380					385									
gtg cga tcc acc ggt gcg gtg cca cca cca gag atc atc gtg gtg aac	1315														
Val Arg Ser Thr Gly Ala Val Pro Pro Pro Glu Ile Ile Val Val Asn															
390	395					400					405				
aaa att gac caa gct gat ccg ctg acg ctg gca gaa cta cgc cac gcc	1363														
Lys Ile Asp Gln Ala Asp Pro Leu Thr Leu Ala Glu Leu Arg His Ala															
410	415					420									
gtc gac gat gtg gtg ttt gtc tct gcg ctg aca ggg gag gga att aag	1411														
Val Asp Asp Val Val Phe Val Ser Ala Leu Thr Gly Glu Gly Ile Lys															
425	430					435									

gag ctg gaa gct cgc atc gaa cta ttc ctc aac tcc agg gac gcg cac 1459  
 Glu Leu Glu Ala Arg Ile Glu Leu Phe Leu Asn Ser Arg Asp Ala His  
           440                                  445                                  450

cta ctg ctg aaa atc ccg ttc acc cgt ggc gat att gtg tcc cgc ctg 1507  
 Leu Leu Leu Lys Ile Pro Phe Thr Arg Gly Asp Ile Val Ser Arg Leu  
           455                                  460                                  465

cac cag cat ggc acc gtt ctc agc gaa gac tac gcc gaa gac ggc acc 1555  
 His Gln His Gly Thr Val Leu Ser Glu Asp Tyr Ala Glu Asp Gly Thr  
           470                                  475                                  480                                  485

ttg atg gat gtg cgt atc ccc acc caa ttg gcc caa gag ctg cag agt 1603  
 Leu Met Asp Val Arg Ile Pro Thr Gln Leu Ala Gln Glu Leu Gln Ser  
                                   490                                  495                                  500

tac gtt gta gaa ccc acc tct gcc taactgtcga tttccaaga gcc 1650  
 Tyr Val Val Glu Pro Thr Ser Ala  
                                   505

<210> 222

<211> 509

<212> PRT

<213> Corynebacterium glutamicum

<400> 222

Met Asp Glu Lys Lys Asn Leu Ser His Asp Glu Leu Leu Ala Gln Ala  
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Phe Arg Gly His Lys Asn Thr Val Arg Pro Gly Ser Asp Glu Thr Ser  
           20                                  25                                  30

Gly Phe Asp Leu Ser Gly Phe Ile Arg Ala Glu Glu Pro Ser Thr Gly  
           35                                  40                                  45

Asp Leu Asp Leu Glu Ala Arg Asp Ala Gln Arg Arg Arg Asp Thr Glu  
           50                                  55                                  60

Ile His Ala Asp Glu Ala Ala Asp Gly Tyr Glu Val Glu Tyr Arg Lys  
           65                                  70                                  75                                  80

Leu Arg Leu Glu Arg Val Ile Leu Val Gly Val Trp Thr Glu Gly Thr  
                                   85                                  90                                  95

Thr Ala Glu Ile Asp Ala Ser Leu Ala Glu Leu Ala Ala Leu Ala Asp  
           100                                  105                                  110

Thr Ala Gly Ala Glu Val Ile Glu Thr Leu Tyr Gln Lys Arg Asp Lys  
           115                                  120                                  125

Pro Asp Pro Gly Thr Tyr Ile Gly Ser Gly Lys Val Arg Glu Leu Lys  
           130                                  135                                  140

Glu Ile Ile Glu Ala Thr Ser Ala Asp Thr Val Val Cys Asp Gly Glu  
           145                                  150                                  155                                  160

Leu Ser Pro Ser Gln Leu Val Ala Leu Glu Arg Glu Leu Asp Ile Lys  
                                   165                                  170                                  175

Val Ile Asp Arg Thr Met Leu Ile Leu Asp Ile Phe Ala Gln His Ala  
 180 185 190  
 Lys Ser Arg Glu Gly Lys Ala Gln Val Ala Leu Ala Gln Met Glu Tyr  
 195 200 205  
 Leu Ile Ser Arg Val Arg Gly Trp Gly Gly Asn Leu Ser Arg Gln Ala  
 210 215 220  
 Gly Gly Arg Ala Gly Ser Asn Gly Gly Val Gly Leu Arg Gly Pro Gly  
 225 230 235 240  
 Glu Thr Lys Ile Glu Ala Asp Arg Arg Arg Leu Arg Ser Asp Met Ala  
 245 250 255  
 Arg Leu Arg Arg Glu Leu Ser Gly Leu Asp Thr Ser Arg Ser Ile Lys  
 260 265 270  
 Arg Ala Gln Arg Ala Ala Ser Leu Val Pro Gln Ile Ala Ile Ala Gly  
 275 280 285  
 Tyr Thr Asn Ala Gly Lys Ser Ser Leu Ile Asn Ala Met Thr Gly Ala  
 290 295 300  
 Gly Val Leu Val Glu Asn Ala Leu Phe Ala Thr Leu Asp Pro Thr Thr  
 305 310 315 320  
 Arg Lys Ala Glu Leu Ala Asp Gly Arg His Val Val Phe Thr Asp Thr  
 325 330 335  
 Val Gly Phe Val Arg His Leu Pro Thr Ser Leu Val Glu Ala Phe Lys  
 340 345 350  
 Ser Thr Leu Glu Glu Val Val Glu Ala Asp Leu Met Leu His Val Val  
 355 360 365  
 Asp Gly Ser Asp Pro Phe Pro Leu Lys Gln Ile Asp Ala Val Asn Thr  
 370 375 380  
 Val Ile Ser Asp Ile Val Arg Ser Thr Gly Ala Val Pro Pro Pro Glu  
 385 390 395 400  
 Ile Ile Val Val Asn Lys Ile Asp Gln Ala Asp Pro Leu Thr Leu Ala  
 405 410 415  
 Glu Leu Arg His Ala Val Asp Asp Val Val Phe Val Ser Ala Leu Thr  
 420 425 430  
 Gly Glu Gly Ile Lys Glu Leu Glu Ala Arg Ile Glu Leu Phe Leu Asn  
 435 440 445  
 Ser Arg Asp Ala His Leu Leu Leu Lys Ile Pro Phe Thr Arg Gly Asp  
 450 455 460  
 Ile Val Ser Arg Leu His Gln His Gly Thr Val Leu Ser Glu Asp Tyr  
 465 470 475 480  
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 485 490 495  
 Gln Glu Leu Gln Ser Tyr Val Val Glu Pro Thr Ser Ala

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505

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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (1)..(171)  
 <223> RXA00848

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 1 5 10 15  
 ctg gag ttc tgt ggc gtc gac gag tgc gtc gag gtt acc cct gat gtt 96  
 Leu Glu Phe Cys Gly Val Asp Glu Cys Val Glu Val Thr Pro Asp Val  
 20 25 30  
 ctg cgc atc cgc aag gtc atc ctg aac gct act gag cgt ggc cgt gca 144  
 Leu Arg Ile Arg Lys Val Ile Leu Asn Ala Thr Glu Arg Gly Arg Ala  
 35 40 45  
 cgt tcc cgt gcg aag agc ctg aac aag taattctctt ttagttaaga gtt 194  
 Arg Ser Arg Ala Lys Ser Leu Asn Lys  
 50 55

<210> 224  
 <211> 57  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 224  
 Thr Thr Val Thr Leu Ala Lys Ala Arg Ser Leu Ser Leu Asp Glu Ala  
 1 5 10 15  
 Leu Glu Phe Cys Gly Val Asp Glu Cys Val Glu Val Thr Pro Asp Val  
 20 25 30  
 Leu Arg Ile Arg Lys Val Ile Leu Asn Ala Thr Glu Arg Gly Arg Ala  
 35 40 45  
 Arg Ser Arg Ala Lys Ser Leu Asn Lys  
 50 55

<210> 225  
 <211> 469  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(469)  
 <223> FRXA00839



&lt;400&gt; 225

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cggttttataa gtcctccata cttctttatc cggcaggaga atg ccc cca gtg acc 115  
 Met Pro Pro Val Thr  
 1 5

cac cca gag ttt cgt aac gta gcg att gtc gcg cac gtt gac cac gga 163  
 His Pro Glu Phe Arg Asn Val Ala Ile Val Ala His Val Asp His Gly  
 10 15 20

aag acc aca ctc gtt aat gcc atg ctt gaa cag tct ggc gta ttc agt 211  
 Lys Thr Thr Leu Val Asn Ala Met Leu Glu Gln Ser Gly Val Phe Ser  
 25 30 35

gac cac ggt gaa gta gcc gac cgt gtg atg gac tcc ggt gac ctg gaa 259  
 Asp His Gly Glu Val Ala Asp Arg Val Met Asp Ser Gly Asp Leu Glu  
 40 45 50

aag gaa aag ggc atc acc atc ctt gcc aag aac acc gcg att cgt cgt 307  
 Lys Glu Lys Gly Ile Thr Ile Leu Ala Lys Asn Thr Ala Ile Arg Arg  
 55 60 65

aaa ggc gct ggc aag gac ggc aat gac ctg att atc aac gtc att gac 355  
 Lys Gly Ala Gly Lys Asp Gly Asn Asp Leu Ile Ile Asn Val Ile Asp  
 70 75 80 85

acc cca ggc cac gct gac ttc ggt ggc gaa gtt gag cgc gca ctg tcc 403  
 Thr Pro Gly His Ala Asp Phe Gly Gly Glu Val Glu Arg Ala Leu Ser  
 90 95 100

atg gtt gac ggc gtt gtc ctt ctg gtt gac gca tct gaa ggc cca ctg 451  
 Met Val Asp Gly Val Val Leu Leu Val Asp Ala Ser Glu Gly Pro Leu  
 105 110 115

cct cag acc cga ttc gtg 469  
 Pro Gln Thr Arg Phe Val  
 120

&lt;210&gt; 226

&lt;211&gt; 123

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 226

Met Pro Pro Val Thr His Pro Glu Phe Arg Asn Val Ala Ile Val Ala  
 1 5 10 15

His Val Asp His Gly Lys Thr Thr Leu Val Asn Ala Met Leu Glu Gln  
 20 25 30

Ser Gly Val Phe Ser Asp His Gly Glu Val Ala Asp Arg Val Met Asp  
 35 40 45

Ser Gly Asp Leu Glu Lys Glu Lys Gly Ile Thr Ile Leu Ala Lys Asn  
 50 55 60

Thr Ala Ile Arg Arg Lys Gly Ala Gly Lys Asp Gly Asn Asp Leu Ile  
 65 70 75 80

Ile Asn Val Ile Asp Thr Pro Gly His Ala Asp Phe Gly Gly Glu Val  
85 90 95

Glu Arg Ala Leu Ser Met Val Asp Gly Val Val Leu Leu Val Asp Ala  
100 105 110

Ser Glu Gly Pro Leu Pro Gln Thr Arg Phe Val  
115 120

<210> 227

<211> 903

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(903)

<223> FRXA00845

<400> 227

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ttg cgt aag ggc cag cag gtt gca tgg att cac tac gat gaa gaa ggt	96
Leu Arg Lys Gly Gln Gln Val Ala Trp Ile His Tyr Asp Glu Glu Gly	
20 25 30	
aac cag cac acc aag acc gct aag atc gca gag ctt ctg gct acc gtt	144
Asn Gln His Thr Lys Thr Ala Lys Ile Ala Glu Leu Leu Ala Thr Val	
35 40 45	
ggc gtt gcc cgc gtt cct gct acc gaa gtt gtt gca ggt gac atc gct	192
Gly Val Ala Arg Val Pro Ala Thr Glu Val Val Ala Gly Asp Ile Ala	
50 55 60	
gct atc tcc ggc atc gaa gac atc atg att ggc gat acc ctc gcg gat	240
Ala Ile Ser Gly Ile Glu Asp Ile Met Ile Gly Asp Thr Leu Ala Asp	
65 70 75 80	
cct gag aac cca gtt gca ctg cct cgc atc acc gtt gat gag cca gca	288
Pro Glu Asn Pro Val Ala Leu Pro Arg Ile Thr Val Asp Glu Pro Ala	
85 90 95	
ctg tcc atg acc atc ggt gtg aac acc tca cca atg gct ggt cgt ggc	336
Leu Ser Met Thr Ile Gly Val Asn Thr Ser Pro Met Ala Gly Arg Gly	
100 105 110	
ggc gga gac aag ctg acc gca cgt gtg gtc aag gct cgt ctt gag aac	384
Gly Gly Asp Lys Leu Thr Ala Arg Val Val Lys Ala Arg Leu Glu Asn	
115 120 125	
gaa ctg atc ggt aac gtg tcc ctg aag gtc aac cca act gag cgc cca	432
Glu Leu Ile Gly Asn Val Ser Leu Lys Val Asn Pro Thr Glu Arg Pro	
130 135 140	
gat acc tgg gaa gtt cag ggt cgt ggc gaa atg gct ctg tcc atc ctc	480
Asp Thr Trp Glu Val Gln Gly Arg Gly Glu Met Ala Leu Ser Ile Leu	
145 150 155 160	

gtt gag acc atg cgt cgc gaa ggc ttc gag ctc acc gtt ggt aag cca 528  
 Val Glu Thr Met Arg Arg Glu Gly Phe Glu Leu Thr Val Gly Lys Pro  
 165 170 175  
 cag gtt gtt acc cag acc atc gac ggc aag ctg cac gag cct tac gag 576  
 Gln Val Val Thr Gln Thr Ile Asp Gly Lys Leu His Glu Pro Tyr Glu  
 180 185 190  
 atc atc gtc atc gac gtt cct tcc gag tac cag ggc aac gtg acc cag 624  
 Ile Ile Val Ile Asp Val Pro Ser Glu Tyr Gln Gly Asn Val Thr Gln  
 195 200 205  
 ctg ctg gct acc cgc aag ggc ctc atg cag tcc atg tcc acc acc cca 672  
 Leu Leu Ala Thr Arg Lys Gly Leu Met Gln Ser Met Ser Thr Thr Pro  
 210 215 220  
 ggt tcc gac tgg atc cgc atg gaa ttc cgt att cct gct cgt ggc ctg 720  
 Gly Ser Asp Trp Ile Arg Met Glu Phe Arg Ile Pro Ala Arg Gly Leu  
 225 230 235 240  
 att ggt ttc cgt acc cag ttc atg act gaa acc cgt ggt acc ggt atc 768  
 Ile Gly Phe Arg Thr Gln Phe Met Thr Glu Thr Arg Gly Thr Gly Ile  
 245 250 255  
 gct aac tcc tac tct gac ggc atg gat gtt tgg gct ggc gaa atc aag 816  
 Ala Asn Ser Tyr Ser Asp Gly Met Asp Val Trp Ala Gly Glu Ile Lys  
 260 265 270  
 ggc cgc gca cac ggt tcc ttg gtt gct gac cgt tcc ggc cag atc acc 864  
 Gly Arg Ala His Gly Ser Leu Val Ala Asp Arg Ser Gly Gln Ile Thr  
 275 280 285  
 gct tac gct ctg acc cag ctg gca gac cgt ggt agc ttc 903  
 Ala Tyr Ala Leu Thr Gln Leu Ala Asp Arg Gly Ser Phe  
 290 295 300

&lt;210&gt; 228

&lt;211&gt; 301

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 228

Ser Ser Phe Leu Gly Arg Ile Gly Leu Val Arg Val His Ala Gly Thr  
 1 5 10 15  
 Leu Arg Lys Gly Gln Gln Val Ala Trp Ile His Tyr Asp Glu Glu Gly  
 20 25 30  
 Asn Gln His Thr Lys Thr Ala Lys Ile Ala Glu Leu Leu Ala Thr Val  
 35 40 45  
 Gly Val Ala Arg Val Pro Ala Thr Glu Val Val Ala Gly Asp Ile Ala  
 50 55 60  
 Ala Ile Ser Gly Ile Glu Asp Ile Met Ile Gly Asp Thr Leu Ala Asp  
 65 70 75 80  
 Pro Glu Asn Pro Val Ala Leu Pro Arg Ile Thr Val Asp Glu Pro Ala  
 85 90 95

Leu Ser Met Thr Ile Gly Val Asn Thr Ser Pro Met Ala Gly Arg Gly  
 100 105 110  
 Gly Gly Asp Lys Leu Thr Ala Arg Val Val Lys Ala Arg Leu Glu Asn  
 115 120 125  
 Glu Leu Ile Gly Asn Val Ser Leu Lys Val Asn Pro Thr Glu Arg Pro  
 130 135 140  
 Asp Thr Trp Glu Val Gln Gly Arg Gly Glu Met Ala Leu Ser Ile Leu  
 145 150 155 160  
 Val Glu Thr Met Arg Arg Glu Gly Phe Glu Leu Thr Val Gly Lys Pro  
 165 170 175  
 Gln Val Val Thr Gln Thr Ile Asp Gly Lys Leu His Glu Pro Tyr Glu  
 180 185 190  
 Ile Ile Val Ile Asp Val Pro Ser Glu Tyr Gln Gly Asn Val Thr Gln  
 195 200 205  
 Leu Leu Ala Thr Arg Lys Gly Leu Met Gln Ser Met Ser Thr Thr Pro  
 210 215 220  
 Gly Ser Asp Trp Ile Arg Met Glu Phe Arg Ile Pro Ala Arg Gly Leu  
 225 230 235 240  
 Ile Gly Phe Arg Thr Gln Phe Met Thr Glu Thr Arg Gly Thr Gly Ile  
 245 250 255  
 Ala Asn Ser Tyr Ser Asp Gly Met Asp Val Trp Ala Gly Glu Ile Lys  
 260 265 270  
 Gly Arg Ala His Gly Ser Leu Val Ala Asp Arg Ser Gly Gln Ile Thr  
 275 280 285  
 Ala Tyr Ala Leu Thr Gln Leu Ala Asp Arg Gly Ser Phe  
 290 295 300

&lt;210&gt; 229

&lt;211&gt; 581

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (19)..(558)

&lt;223&gt; RXA02365

&lt;400&gt; 229

gaatttgtgg gaccgaca atg gag ctg tgc cag act aag cgt ggt cag atg 51  
 Met Glu Leu Cys Gln Thr Lys Arg Gly Gln Met 10  
 1 5  
 ggt ggc atg gac tac ctt tcg gag gac cgc gtg gag ctg cgc tac acc 99  
 Gly Gly Met Asp Tyr Leu Ser Glu Asp Arg Val Glu Leu Arg Tyr Thr 15 20 25  
 atg cct ttg ggt gag atc atc ttt gac ttc ttc gat atg ttg aag tct 147  
 Met Pro Leu Gly Glu Ile Ile Phe Asp Phe Phe Asp Met Leu Lys Ser

30	35	40	
cgc acc aag ggt tac gct tgc ctg aac tac gag gaa gct ggc gag cag			195
Arg Thr Lys Gly Tyr Ala Ser Leu Asn Tyr Glu Glu Ala Gly Glu Gln			
45	50	55	
act gcc gac ctg gtc aag gta gat atc ttg ctc caa ggt gaa cct gtg			243
Thr Ala Asp Leu Val Lys Val Asp Ile Leu Leu Gln Gly Glu Pro Val			
60	65	70	75
gat gca ttc tct gcg atc gtg cac cgc gat aat gcg cag tgg tac gga			291
Asp Ala Phe Ser Ala Ile Val His Arg Asp Asn Ala Gln Trp Tyr Gly			
	80	85	90
aac aag atg act gtg aag ctg aag gaa ctg atc cct cgc cag cag ttc			339
Asn Lys Met Thr Val Lys Leu Lys Glu Leu Ile Pro Arg Gln Gln Phe			
	95	100	105
gaa gtt cct gtg cag gca gcc att ggt tcc aag gtt atc gct cgt gaa			387
Glu Val Pro Val Gln Ala Ala Ile Gly Ser Lys Val Ile Ala Arg Glu			
	110	115	120
aac att cgt gca ctg cgc aag gac gtg ttg gcg aag tgt tac ggt ggc			435
Asn Ile Arg Ala Leu Arg Lys Asp Val Leu Ala Lys Cys Tyr Gly Gly			
	125	130	135
gat att tcc cgt aag cgc aag ctt ctg gaa aag cag aag gct ggt aag			483
Asp Ile Ser Arg Lys Arg Lys Leu Leu Glu Lys Gln Lys Ala Gly Lys			
	140	145	150
aag cgc atg aag aac atc ggt tgc gtc gag gtt cct cag gaa gca ttc			531
Lys Arg Met Lys Asn Ile Gly Ser Val Glu Val Pro Gln Glu Ala Phe			
	160	165	170
gta gca gca ctg tct acc gac gag gca taaaaaactt tagcctcttt tag			581
Val Ala Ala Leu Ser Thr Asp Glu Ala			
	175	180	

&lt;210&gt; 230

&lt;211&gt; 180

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 230

Met	Glu	Leu	Cys	Gln	Thr	Lys	Arg	Gly	Gln	Met	Gly	Gly	Met	Asp	Tyr
1				5					10					15	

Leu	Ser	Glu	Asp	Arg	Val	Glu	Leu	Arg	Tyr	Thr	Met	Pro	Leu	Gly	Glu
			20					25					30		

Ile	Ile	Phe	Asp	Phe	Phe	Asp	Met	Leu	Lys	Ser	Arg	Thr	Lys	Gly	Tyr
		35					40					45			

Ala	Ser	Leu	Asn	Tyr	Glu	Glu	Ala	Gly	Glu	Gln	Thr	Ala	Asp	Leu	Val
	50					55					60				

Lys	Val	Asp	Ile	Leu	Leu	Gln	Gly	Glu	Pro	Val	Asp	Ala	Phe	Ser	Ala
65					70					75					80

<400> 231																
aaaactgctg atggttttggc agttcagggc tgtttaactg tttgggtttg ctcaggtaga																60
gtaggacacc gttattttaat tgaaggggacc cctgacgcat																115
Met Ala Glu Lys Phe																5
gca gaa aca aca ttt acg gat cca gcc agg att cgt aac ttc tgc atc																163
Ala Glu Thr Thr Phe Thr Asp Pro Ala Arg Ile Arg Asn Phe Cys Ile																20
att gcc cac att gac cac ggt aaa tct acg ctc gct gac cgt atc ctg																211
Ile Ala His Ile Asp His Gly Lys Ser Thr Leu Ala Asp Arg Ile Leu																35
cag ctg tct aac gtt gtg gat gcc cgc gat atg cgt gat cag tac ctg																259
Gln Leu Ser Asn Val Val Asp Ala Arg Asp Met Arg Asp Gln Tyr Leu																40
gac aac atg gac atc gaa cgt gaa cgt ggc att acc att aag gct cag																307
Asp Asn Met Asp Ile Glu Arg Glu Arg Gly Ile Thr Ile Lys Ala Gln																55
aac gtt cgc ctg cca tgg att cct cgc agt ggt gag tac gag ggc cag																355
Asn Val Arg Leu Pro Trp Ile Pro Arg Ser Gly Glu Tyr Glu Gly Gln																70
cag atc gtc atg cag atg atc gat acg cca ggc cac gtg gac ttc acc																403
Gln Ile Val Met Gln Met Ile Asp Thr Pro Gly His Val Asp Phe Thr																85

90							95						100					
tat	gaa	gtg	tct	cgg	gcg	ctt	gaa	gcg	tgt	gaa	ggc	gcg	att	ttg	ctt	451		
Tyr	Glu	Val	Ser	Arg	Ala	Leu	Glu	Ala	Cys	Glu	Gly	Ala	Ile	Leu	Leu			
			105				110						115					
gtt	gat	gca	gcg	cag	ggc	att	gaa	gcc	cag	acc	ttg	gca	aac	ttg	tat	499		
Val	Asp	Ala	Ala	Gln	Gly	Ile	Glu	Ala	Gln	Thr	Leu	Ala	Asn	Leu	Tyr			
			120				125						130					
ttg	gct	atg	gaa	aac	gat	ctt	gag	atc	atc	cct	gtg	ctg	aac	aag	att	547		
Leu	Ala	Met	Glu	Asn	Asp	Leu	Glu	Ile	Ile	Pro	Val	Leu	Asn	Lys	Ile			
			135				140						145					
gac	ctt	cca	gcg	gcg	gat	cca	gac	aag	tac	gcg	ttg	gag	atc	gcc	aac	595		
Asp	Leu	Pro	Ala	Ala	Asp	Pro	Asp	Lys	Tyr	Ala	Leu	Glu	Ile	Ala	Asn			
			150				155						160					
att	gtg	ggc	tgt	gaa	cct	gaa	gat	gtg	ttg	cgc	gtg	tcc	ggc	aaa	act	643		
Ile	Val	Gly	Cys	Glu	Pro	Glu	Asp	Val	Leu	Arg	Val	Ser	Gly	Lys	Thr			
			170				175						180					
ggc	atg	ggc	gtc	cct	gag	ctt	ctg	gat	aag	gtc	gtt	gaa	ctt	atc	cca	691		
Gly	Met	Gly	Val	Pro	Glu	Leu	Leu	Asp	Lys	Val	Val	Glu	Leu	Ile	Pro			
			185				190						195					
gca	cct	acc	tct	gaa	ttt	gag	gaa	gac	gcc	cca	gct	cgt	gcg	atg	att	739		
Ala	Pro	Thr	Ser	Glu	Phe	Glu	Glu	Asp	Ala	Pro	Ala	Arg	Ala	Met	Ile			
			200				205						210					
ttc	gac	tct	gtc	tat	gac	acc	tac	cgc	ggc	gtg	gtt	acc	tac	atc	cgc	787		
Phe	Asp	Ser	Val	Tyr	Asp	Thr	Tyr	Arg	Gly	Val	Val	Thr	Tyr	Ile	Arg			
			215				220						225					
atg	atg	gac	ggc	aag	ctg	aca	cct	cgc	caa	aag	atc	aag	atg	atg	tcc	835		
Met	Met	Asp	Gly	Lys	Leu	Thr	Pro	Arg	Gln	Lys	Ile	Lys	Met	Met	Ser			
			230				235						240					
acc	ggc	gcc	acc	cac	gag	ttg	ctg	gaa	atc	ggc	atc	gtg	agc	ccc	acc	883		
Thr	Gly	Ala	Thr	His	Glu	Leu	Leu	Glu	Ile	Gly	Ile	Val	Ser	Pro	Thr			
			250				255						260					
cct	aaa	aag	tgt	gtg	ggc	ctt	gga	cct	ggc	gag	gtt	ggc	tac	ctg	atc	931		
Pro	Lys	Lys	Cys	Val	Gly	Leu	Gly	Pro	Gly	Glu	Val	Gly	Tyr	Leu	Ile			
			265				270						275					
acc	ggc	gtg	aag	gac	gtg	cgc	caa	tct	aag	gtg	ggc	gat	acc	gtc	acg	979		
Thr	Gly	Val	Lys	Asp	Val	Arg	Gln	Ser	Lys	Val	Gly	Asp	Thr	Val	Thr			
			280				285						290					
tg	gca	att	cat	gga	gct	gag	cag	cca	ctg	cgc	ggc	tac	cag	gaa	cca	1027		
Trp	Ala	Ile	His	Gly	Ala	Glu	Gln	Pro	Leu	Arg	Gly	Tyr	Gln	Glu	Pro			
			295				300						305					
aca	ccg	atg	gtt	tac	tcg	ggc	ttg	ttc	ccg	att	tcc	caa	gcg	gat	ttc	1075		
Thr	Pro	Met	Val	Tyr	Ser	Gly	Leu	Phe	Pro	Ile	Ser	Gln	Ala	Asp	Phe			
			310				315						320					
ccc</																		

ctc acg tac gaa ccc gaa acg tcc gta gca ctg ggc ttt ggt ttc cga 1171  
 Leu Thr Tyr Glu Pro Glu Thr Ser Val Ala Leu Gly Phe Gly Phe Arg  
                   345                                  350                                  355

tgt ggc ttc ctc gga ctg ctg cac atg gaa atc acc cgt gac cga ctc 1219  
 Cys Gly Phe Leu Gly Leu Leu His Met Glu Ile Thr Arg Asp Arg Leu  
                   360                                  365                                  370

gaa cgt gag ttt ggc ctt gat ctg att tct acc gcg cca tct gtt aac 1267  
 Glu Arg Glu Phe Gly Leu Asp Leu Ile Ser Thr Ala Pro Ser Val Asn  
                   375                                  380                                  385

tac cgc gtt att gat gag gcg ggc aag gaa ttc cgc gtc cac aac cca 1315  
 Tyr Arg Val Ile Asp Glu Ala Gly Lys Glu Phe Arg Val His Asn Pro  
 390                                  395                                  400                                  405

tct gac tgg cct ggc gga aag ctc agt gaa gtt tac gag ccc atc 1360  
 Ser Asp Trp Pro Gly Gly Lys Leu Ser Glu Val Tyr Glu Pro Ile  
                                   410                                  415                                  420

<210> 232

<211> 420

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 232

Met Ala Glu Lys Phe Ala Glu Thr Thr Phe Thr Asp Pro Ala Arg Ile  
   1                                  5                                  10                                  15

Arg Asn Phe Cys Ile Ile Ala His Ile Asp His Gly Lys Ser Thr Leu  
                   20                                  25                                  30

Ala Asp Arg Ile Leu Gln Leu Ser Asn Val Val Asp Ala Arg Asp Met  
                   35                                  40                                  45

Arg Asp Gln Tyr Leu Asp Asn Met Asp Ile Glu Arg Glu Arg Gly Ile  
                   50                                  55                                  60

Thr Ile Lys Ala Gln Asn Val Arg Leu Pro Trp Ile Pro Arg Ser Gly  
                   65                                  70                                  75                                  80

Glu Tyr Glu Gly Gln Gln Ile Val Met Gln Met Ile Asp Thr Pro Gly  
                                   85                                  90                                  95

His Val Asp Phe Thr Tyr Glu Val Ser Arg Ala Leu Glu Ala Cys Glu  
                   100                                  105                                  110

Gly Ala Ile Leu Leu Val Asp Ala Ala Gln Gly Ile Glu Ala Gln Thr  
                   115                                  120                                  125

Leu Ala Asn Leu Tyr Leu Ala Met Glu Asn Asp Leu Glu Ile Ile Pro  
                   130                                  135                                  140

Val Leu Asn Lys Ile Asp Leu Pro Ala Ala Asp Pro Asp Lys Tyr Ala  
                   145                                  150                                  155                                  160

Leu Glu Ile Ala Asn Ile Val Gly Cys Glu Pro Glu Asp Val Leu Arg  
                                   165                                  170                                  175



Val Ser Gly Lys Thr Gly Met Gly Val Pro Glu Leu Leu Asp Lys Val  
 180 185 190  
 Val Glu Leu Ile Pro Ala Pro Thr Ser Glu Phe Glu Glu Asp Ala Pro  
 195 200 205  
 Ala Arg Ala Met Ile Phe Asp Ser Val Tyr Asp Thr Tyr Arg Gly Val  
 210 215 220  
 Val Thr Tyr Ile Arg Met Met Asp Gly Lys Leu Thr Pro Arg Gln Lys  
 225 230 235 240  
 Ile Lys Met Met Ser Thr Gly Ala Thr His Glu Leu Leu Glu Ile Gly  
 245 250 255  
 Ile Val Ser Pro Thr Pro Lys Lys Cys Val Gly Leu Gly Pro Gly Glu  
 260 265 270  
 Val Gly Tyr Leu Ile Thr Gly Val Lys Asp Val Arg Gln Ser Lys Val  
 275 280 285  
 Gly Asp Thr Val Thr Trp Ala Ile His Gly Ala Glu Gln Pro Leu Arg  
 290 295 300  
 Gly Tyr Gln Glu Pro Thr Pro Met Val Tyr Ser Gly Leu Phe Pro Ile  
 305 310 315 320  
 Ser Gln Ala Asp Phe Pro Asp Leu Arg Asp Ala Leu Glu Lys Leu Gln  
 325 330 335  
 Leu Asn Asp Ala Ser Leu Thr Tyr Glu Pro Glu Thr Ser Val Ala Leu  
 340 345 350  
 Gly Phe Gly Phe Arg Cys Gly Phe Leu Gly Leu Leu His Met Glu Ile  
 355 360 365  
 Thr Arg Asp Arg Leu Glu Arg Glu Phe Gly Leu Asp Leu Ile Ser Thr  
 370 375 380  
 Ala Pro Ser Val Asn Tyr Arg Val Ile Asp Glu Ala Gly Lys Glu Phe  
 385 390 395 400  
 Arg Val His Asn Pro Ser Asp Trp Pro Gly Gly Lys Leu Ser Glu Val  
 405 410 415  
 Tyr Glu Pro Ile  
 420

&lt;210&gt; 233

&lt;211&gt; 2205

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(2182)

&lt;223&gt; RXA01573

&lt;400&gt; 233

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aaaaaccggc gcattgccgg tattttttcca ggagaatttta	atg aag agg ctt tcc	115
	Met Lys Arg Leu Ser	
	1 5	
cgt gca gcc ctc gca gtg gtc gcc acc acc gca gtt agc ttc agc gca		163
Arg Ala Ala Leu Val Val Val Ala Thr Thr Ala Val Ser Phe Ser Ala		
	10 15 20	
ctc gca gtt cca gct ttc gca gac gaa gca agc aat gtt gag ctc aac		211
Leu Ala Val Pro Ala Phe Ala Asp Glu Ala Ser Asn Val Glu Leu Asn		
	25 30 35	
atc ctc ggt gtc acc gac ttc cac gga cac atc gag cag aag gct gtt		259
Ile Leu Gly Val Thr Asp Phe His Gly His Ile Glu Gln Lys Ala Val		
	40 45 50	
aaa gat gat aag gga gta atc acc ggt tac tca gaa atg ggt gcc agt		307
Lys Asp Asp Lys Gly Val Ile Thr Gly Tyr Ser Glu Met Gly Ala Ser		
	55 60 65	
ggc gtt gcc tgc tac gtc gac gct gaa cgc gcg gac aac cca aac acc		355
Gly Val Ala Cys Tyr Val Asp Ala Glu Arg Ala Asp Asn Pro Asn Thr		
	70 75 80 85	
cgc ttc atc acc gtt ggt gac aac att ggt gga tcc cca ttc gtg tcc		403
Arg Phe Ile Thr Val Gly Asp Asn Ile Gly Gly Ser Pro Phe Val Ser		
	90 95 100	
tcc atc ctg aag gat gag cca acc ttg caa gcc ctc agc gcc atc ggt		451
Ser Ile Leu Lys Asp Glu Pro Thr Leu Gln Ala Leu Ser Ala Ile Gly		
	105 110 115	
gtt gac gca tcc gca ctg ggc aat cac gaa ttc gac cag ggc tac tca		499
Val Asp Ala Ser Ala Leu Gly Asn His Glu Phe Asp Gln Gly Tyr Ser		
	120 125 130	
gac ctg gtg aac cgc gtt tcc ctc gac ggc tcc ggc agc gca aag ttc		547
Asp Leu Val Asn Arg Val Ser Leu Asp Gly Ser Gly Ser Ala Lys Phe		
	135 140 145	
cca tac ctc ggc gca aac gtt gaa ggt ggc acc cca gca cct gca aag		595
Pro Tyr Leu Gly Ala Asn Val Glu Gly Gly Thr Pro Ala Pro Ala Lys		
	150 155 160 165	
tct gaa atc atc gag atg gac ggc gtc aag atc gct tac gtc ggc gca		643
Ser Glu Ile Ile Glu Met Asp Gly Val Lys Ile Ala Tyr Val Gly Ala		
	170 175 180	
gta acc gag gag acc gca acc ttg gtc tcc cca gca ggc atc gaa ggc		691
Val Thr Glu Glu Thr Ala Thr Leu Val Ser Pro Ala Gly Ile Glu Gly		
	185 190 195	
atc acc ttc acc ggc gac atc gac gct atc aac gca gaa gca gat cgc		739
Ile Thr Phe Thr Gly Asp Ile Asp Ala Ile Asn Ala Glu Ala Asp Arg		
	200 205 210	
gtc att gag gca ggc gaa gca gac gta gtc atc gca ttg atc cac gct		787
Val Ile Glu Ala Gly Glu Ala Asp Val Val Ile Ala Leu Ile His Ala		
	215 220 225	

gaa gcc gct cca acc gat cta ttc tcc aac aac gtt gac gtt gta ttc	835
Glu Ala Ala Pro Thr Asp Leu Phe Ser Asn Asn Val Asp Val Val Phe	
230 235 240 245	
tcc gga cac acc cac ttc gac tac gtt gct gaa ggc gaa gca cgt ggc	883
Ser Gly His Thr His Phe Asp Tyr Val Ala Glu Gly Glu Ala Arg Gly	
250 255 260	
gac aag cag cca ctc gtt gtc atc cag ggc cac gaa tac ggc aag gtc	931
Asp Lys Gln Pro Leu Val Val Ile Gln Gly His Glu Tyr Gly Lys Val	
265 270 275	
atc tcc gac gtg gag atc tcc tac gac cgc gaa gca ggc aag atc acc	979
Ile Ser Asp Val Glu Ile Ser Tyr Asp Arg Glu Ala Gly Lys Ile Thr	
280 285 290	
aac att gag gcg aag aat gtc tct gct act gac gtt gtg gaa aac tgt	1027
Asn Ile Glu Ala Lys Asn Val Ser Ala Thr Asp Val Val Glu Asn Cys	
295 300 305	
gag act cca aac aca gca gtc gac gca atc gtt gca gct gct gtt gag	1075
Glu Thr Pro Asn Thr Ala Val Asp Ala Ile Val Ala Ala Ala Val Glu	
310 315 320 325	
gcc gct gaa gaa gca ggt aat gaa gtt gtt gca acc att gac aac ggc	1123
Ala Ala Glu Glu Ala Gly Asn Glu Val Val Ala Thr Ile Asp Asn Gly	
330 335 340	
ttc tac cgt ggg gcg gat gaa gag ggt acg acc ggc tcc aac cgt ggt	1171
Phe Tyr Arg Gly Ala Asp Glu Glu Gly Thr Thr Gly Ser Asn Arg Gly	
345 350 355	
gtt gag tct tcc ctg agc aac ctc atc gca gaa gct gga ctg tgg gca	1219
Val Glu Ser Ser Leu Ser Asn Leu Ile Ala Glu Ala Gly Leu Trp Ala	
360 365 370	
gtc aac gac gcg acc atc ctg aac gct gac atc ggc atc atg aac gca	1267
Val Asn Asp Ala Thr Ile Leu Asn Ala Asp Ile Gly Ile Met Asn Ala	
375 380 385	
ggc ggc gtg cgt gcg gac ctc gaa gca ggc gaa gtt acc ttc gca gat	1315
Gly Gly Val Arg Ala Asp Leu Glu Ala Gly Glu Val Thr Phe Ala Asp	
390 395 400 405	
gca tac gca acc cag aac ttc tcc aac acc tac ggc gta cgt gaa gtg	1363
Ala Tyr Ala Thr Gln Asn Phe Ser Asn Thr Tyr Gly Val Arg Glu Val	
410 415 420	
tct ggt gcg cag ttc aaa gaa gca ctg gaa cag cag tgg aag gaa acc	1411
Ser Gly Ala Gln Phe Lys Glu Ala Leu Glu Gln Gln Trp Lys Glu Thr	
425 430 435	
ggc gac cgc cca cgt ctg gca ttg gga ctg tcc agc aac gtc cag tac	1459
Gly Asp Arg Pro Arg Leu Ala Leu Gly Leu Ser Ser Asn Val Gln Tyr	
440 445 450	
tcc tac gac gag acc cgc gaa tac ggc gac cgc atc acc cac atc acc	1507
Ser Tyr Asp Glu Thr Arg Glu Tyr Gly Asp Arg Ile Thr His Ile Thr	
455 460 465	
ttc aac ggt gag cca atg gat atg aag gag acc tac cgc gtc aca gga	1555

Phe 470	Asn	Gly	Glu	Pro	Met 475	Asp	Met	Lys	Glu	Thr 480	Tyr	Arg	Val	Thr	Gly 485	
tca Ser	tcc Ser	ttc Phe	ctg Leu	ctc Leu 490	gca Ala	ggt Gly	ggc Gly	gac Asp 495	tcc Ser	ttc Phe	act Thr	gca Ala	ttc Phe	gct Ala 500	gaa Glu	1603
ggc Gly	ggc Gly	cca Pro	atc Ile 505	gct Ala	gaa Glu	acc Thr	ggc Gly 510	atg Met	gtt Val	gac Asp	att Ile	gac Asp	ctg Leu 515	ttc Phe	aac Asn	1651
aac Asn	tac Tyr	atc Ile 520	gca Ala	gct Ala	cac His	cca Pro	gat Asp 525	gca Ala	cca Pro	att Ile	cgt Arg	gca Ala 530	aat Asn	cag Gln	agc Ser	1699
tca Ser	gta Val 535	ggc Gly	atc Ile	gcc Ala	ctt Leu	tcc Ser 540	ggc Gly	ccg Pro	gca Ala	gtt Val 545	gca Ala	gaa Glu	gac Asp	gga Gly	act Thr	1747
ttg Leu 550	gtc Val	cct Pro	ggt Gly	gaa Glu	gag Glu 555	ctg Leu	acc Thr	gtc Val	gat Asp	ctt Leu 560	tct Ser	tcc Ser	ctc Leu	tcc Ser	tac Tyr 565	1795
acc Thr	gga Gly	cct Pro	gaa Glu	gct Ala	aag Lys 570	cca Pro	acc Thr	acc Thr	gtt Val 575	gag Glu	gtg Val	acc Thr	gtt Val	ggt Gly	act Thr 580	1843
gag Glu	aag Lys	aag Lys	act Thr 585	gcg Ala	gac Asp	gtc Val	gat Asp	aac Asn 590	acc Thr	atc Ile	gtt Val	cct Pro	cag Gln 595	ttt Phe	gac Asp	1891
agc Ser	acc Thr	ggc Gly 600	aag Lys	gca Ala	act Thr	gtc Val	acc Thr 605	ctg Leu	act Thr	gtt Val	cct Pro	gag Glu 610	gga Gly	gct Ala	acc Thr	1939
tct Ser 615	gtc Val	aag Lys	atc Ile	gca Ala	act Thr	gac Asp	aat Asn 620	ggc Gly	act Thr	acc Thr	ttt Phe 625	gaa Glu	ctg Leu	cca Pro	gta Val	1987
acc Thr 630	gta Val	aac Asn	ggt Gly	gaa Glu	ggc Gly 635	aac Asn	aat Asn	gat Asp	gac Asp 640	gat Asp	gat Asp	gat Asp	aag Lys	gag Glu	cag Gln 645	2035
cag Gln	tcc Ser	tcc Ser	gga Gly	tcc Ser 650	tcc Ser	gac Asp	gcc Ala	ggt Gly	tcc Ser 655	ctt Leu	gta Val	gca Ala	gtt Val	ctc Leu 660	ggt Gly	2083
gtt Val	ctt Leu	gga Gly	gca Ala 665	ctc Leu	ggt Gly	ggc Gly	ctg Leu 670	gtg Val	gcg Ala	ttc Phe	ttc Phe	ctg Leu	aac Asn 675	tct Ser	gcg Ala	2131
cag Gln	ggc Gly	gca Ala	cca Pro	ttc Phe	ttg Leu	gct Ala	cag Gln 685	ctt Leu	cag Gln	gct Ala	atg Met	ttt Phe 690	gcg Ala	cag Gln	ttc Phe	2179
atg Met	taataacttg	tagtaaataa	atc													2205

&lt;211&gt; 694

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 234

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Met Lys Arg Leu Ser Arg Ala Ala Leu Ala Val Val Ala Thr Thr Ala
 1           5           10           15

Val Ser Phe Ser Ala Leu Ala Val Pro Ala Phe Ala Asp Glu Ala Ser
           20           25           30

Asn Val Glu Leu Asn Ile Leu Gly Val Thr Asp Phe His Gly His Ile
 35           40           45

Glu Gln Lys Ala Val Lys Asp Asp Lys Gly Val Ile Thr Gly Tyr Ser
 50           55           60

Glu Met Gly Ala Ser Gly Val Ala Cys Tyr Val Asp Ala Glu Arg Ala
 65           70           75           80

Asp Asn Pro Asn Thr Arg Phe Ile Thr Val Gly Asp Asn Ile Gly Gly
           85           90           95

Ser Pro Phe Val Ser Ser Ile Leu Lys Asp Glu Pro Thr Leu Gln Ala
 100          105          110

Leu Ser Ala Ile Gly Val Asp Ala Ser Ala Leu Gly Asn His Glu Phe
 115          120          125

Asp Gln Gly Tyr Ser Asp Leu Val Asn Arg Val Ser Leu Asp Gly Ser
 130          135          140

Gly Ser Ala Lys Phe Pro Tyr Leu Gly Ala Asn Val Glu Gly Gly Thr
 145          150          155          160

Pro Ala Pro Ala Lys Ser Glu Ile Ile Glu Met Asp Gly Val Lys Ile
           165          170          175

Ala Tyr Val Gly Ala Val Thr Glu Glu Thr Ala Thr Leu Val Ser Pro
 180          185          190

Ala Gly Ile Glu Gly Ile Thr Phe Thr Gly Asp Ile Asp Ala Ile Asn
 195          200          205

Ala Glu Ala Asp Arg Val Ile Glu Ala Gly Glu Ala Asp Val Val Ile
 210          215          220

Ala Leu Ile His Ala Glu Ala Ala Pro Thr Asp Leu Phe Ser Asn Asn
 225          230          235          240

Val Asp Val Val Phe Ser Gly His Thr His Phe Asp Tyr Val Ala Glu
 245          250          255

Gly Glu Ala Arg Gly Asp Lys Gln Pro Leu Val Val Ile Gln Gly His
 260          265          270

Glu Tyr Gly Lys Val Ile Ser Asp Val Glu Ile Ser Tyr Asp Arg Glu
 275          280          285

Ala Gly Lys Ile Thr Asn Ile Glu Ala Lys Asn Val Ser Ala Thr Asp
 290          295          300

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Val Val Glu Asn Cys Glu Thr Pro Asn Thr Ala Val Asp Ala Ile Val  
 305 310 315 320  
 Ala Ala Ala Val Glu Ala Ala Glu Glu Ala Gly Asn Glu Val Val Ala  
 325 330 335  
 Thr Ile Asp Asn Gly Phe Tyr Arg Gly Ala Asp Glu Glu Gly Thr Thr  
 340 345 350  
 Gly Ser Asn Arg Gly Val Glu Ser Ser Leu Ser Asn Leu Ile Ala Glu  
 355 360 365  
 Ala Gly Leu Trp Ala Val Asn Asp Ala Thr Ile Leu Asn Ala Asp Ile  
 370 375 380  
 Gly Ile Met Asn Ala Gly Gly Val Arg Ala Asp Leu Glu Ala Gly Glu  
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 Val Thr Phe Ala Asp Ala Tyr Ala Thr Gln Asn Phe Ser Asn Thr Tyr  
 405 410 415  
 Gly Val Arg Glu Val Ser Gly Ala Gln Phe Lys Glu Ala Leu Glu Gln  
 420 425 430  
 Gln Trp Lys Glu Thr Gly Asp Arg Pro Arg Leu Ala Leu Gly Leu Ser  
 435 440 445  
 Ser Asn Val Gln Tyr Ser Tyr Asp Glu Thr Arg Glu Tyr Gly Asp Arg  
 450 455 460  
 Ile Thr His Ile Thr Phe Asn Gly Glu Pro Met Asp Met Lys Glu Thr  
 465 470 475 480  
 Tyr Arg Val Thr Gly Ser Ser Phe Leu Leu Ala Gly Gly Asp Ser Phe  
 485 490 495  
 Thr Ala Phe Ala Glu Gly Gly Pro Ile Ala Glu Thr Gly Met Val Asp  
 500 505 510  
 Ile Asp Leu Phe Asn Asn Tyr Ile Ala Ala His Pro Asp Ala Pro Ile  
 515 520 525  
 Arg Ala Asn Gln Ser Ser Val Gly Ile Ala Leu Ser Gly Pro Ala Val  
 530 535 540  
 Ala Glu Asp Gly Thr Leu Val Pro Gly Glu Glu Leu Thr Val Asp Leu  
 545 550 555 560  
 Ser Ser Leu Ser Tyr Thr Gly Pro Glu Ala Lys Pro Thr Thr Val Glu  
 565 570 575  
 Val Thr Val Gly Thr Glu Lys Lys Thr Ala Asp Val Asp Asn Thr Ile  
 580 585 590  
 Val Pro Gln Phe Asp Ser Thr Gly Lys Ala Thr Val Thr Leu Thr Val  
 595 600 605  
 Pro Glu Gly Ala Thr Ser Val Lys Ile Ala Thr Asp Asn Gly Thr Thr  
 610 615 620

Phe Glu Leu Pro Val Thr Val Asn Gly Glu Gly Asn Asn Asp Asp Asp  
 625 630 635 640  
 Asp Asp Lys Glu Gln Gln Ser Ser Gly Ser Ser Asp Ala Gly Ser Leu  
 645 650 655  
 Val Ala Val Leu Gly Val Leu Gly Ala Leu Gly Gly Leu Val Ala Phe  
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 675 680 685  
 Met Phe Ala Gln Phe Met  
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 <213> Corynebacterium glutamicum

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 <223> RXN01445

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 Met Ile Pro Leu Ile  
 1 5  
 aat gta cgt ttt ccc gtt gcc gcc tta cct ctc gca tta gtg gcg act 163  
 Asn Val Arg Phe Pro Val Ala Ala Leu Pro Leu Ala Leu Val Ala Thr  
 10 15 20  
 gta tgg ctt aat gct tgg gca gac cat ctt ctc cta act ggt ttt att 211  
 Val Trp Leu Asn Ala Trp Ala Asp His Leu Leu Leu Thr Gly Phe Ile  
 25 30 35  
 gtt tat ctt gct gtg gaa tac gca aca agc cgt ggg cgc ttc gct ctc 259  
 Val Tyr Leu Ala Val Glu Tyr Ala Thr Ser Arg Gly Arg Phe Ala Leu  
 40 45 50  
 gca ttg att ttg gga gtt gaa tgg atc tta att gct tat ggg gta gct 307  
 Ala Leu Ile Leu Gly Val Glu Trp Ile Leu Ile Ala Tyr Gly Val Ala  
 55 60 65  
 ttg gaa agg cct ctt gag gct aaa gac tct cca tct ctc att acc gaa 355  
 Leu Glu Arg Pro Leu Glu Ala Lys Asp Ser Pro Ser Leu Ile Thr Glu  
 70 75 80 85  
 att ttg ctc ata ctt gta gca gct ggc aca ggg gca ggt cgg tgg aaa 403  
 Ile Leu Leu Ile Leu Val Ala Ala Gly Thr Gly Ala Gly Arg Trp Lys  
 90 95 100  
 att ttg agt gaa cgc aag caa cgt gca att act cag cag gaa atc atc 451  
 Ile Leu Ser Glu Arg Lys Gln Arg Ala Ile Thr Gln Gln Glu Ile Ile  
 105 110 115

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aaa aaa atc cgt act gat ata gcg cac tat ttg cat gac agt atg gca 499
Lys Lys Ile Arg Thr Asp Ile Ala His Tyr Leu His Asp Ser Met Ala
120 125 130

aga tcg ttg gca ata atg ata gtt caa tca aag ctg act gaa cta gag 547
Arg Ser Leu Ala Ile Met Ile Val Gln Ser Lys Leu Thr Glu Leu Glu
135 140 145

cct gat cca aaa aag att caa gaa aaa cta aac agt att gcc aaa att 595
Pro Asp Pro Lys Lys Ile Gln Glu Lys Leu Asn Ser Ile Ala Lys Ile
150 155 160 165

gga caa gag gca gtg gct gat ttg cat caa tta gtt aga cac ctc gtg 643
Gly Gln Glu Ala Val Ala Asp Leu His Gln Leu Val Arg His Leu Val
170 175 180

gtc gag gag tct gct gaa aaa gcc aca gcg ttt gga gca tgg gct gca 691
Val Glu Glu Ser Ala Glu Lys Ala Thr Ala Phe Gly Ala Trp Ala Ala
185 190 195

gtt tct att cat gac acg gtt aat tct gcc att cag tta tta gta gat 739
Val Ser Ile His Asp Thr Val Asn Ser Ala Ile Gln Leu Leu Val Asp
200 205 210

gca gga cat gtc gtt tcc ttt gac agt aga aaa aag aac tat aag ctg 787
Ala Gly His Val Val Ser Phe Asp Ser Arg Lys Lys Asn Tyr Lys Leu
215 220 225

gac cat att gct gaa acg gcg ttt gct tta gcc ttc aat gag gca gtc 835
Asp His Ile Ala Glu Thr Ala Phe Ala Leu Ala Phe Asn Glu Ala Val
230 235 240 245

tgt aat gca att aaa cat tct ccg ccc aag gca aac gtt act att cgc 883
Cys Asn Ala Ile Lys His Ser Pro Pro Lys Ala Asn Val Thr Ile Arg
250 255 260

ata aca gaa aaa gca cag tct ctt cag att cta gta atg aat cct att 931
Ile Thr Glu Lys Ala Gln Ser Leu Gln Ile Leu Val Met Asn Pro Ile
265 270 275

gga gat tgg cat gca aat ggg gag tcc gca att cca ggt gtg ggc att 979
Gly Asp Trp His Ala Asn Gly Glu Ser Ala Ile Pro Gly Val Gly Ile
280 285 290

ggc gta gaa agc tta acc aga agg ata cgt aat att aaa gga cag gtc 1027
Gly Val Glu Ser Leu Thr Arg Arg Ile Arg Asn Ile Lys Gly Gln Val
295 300 305

tgt gtg act tca ctg caa gga tac tgg aaa gta gtt att tca cta cct 1075
Cys Val Thr Ser Leu Gln Gly Tyr Trp Lys Val Val Ile Ser Leu Pro
310 315 320 325

ttg aaa tgt gag gat tct taaattgtct ctatttggtg aac 1116
Leu Lys Cys Glu Asp Ser
330

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&lt;210&gt; 236

&lt;211&gt; 331

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum



&lt;400&gt; 236

Met	Ile	Pro	Leu	Ile	Asn	Val	Arg	Phe	Pro	Val	Ala	Ala	Leu	Pro	Leu
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Ala	Leu	Val	Ala	Thr	Val	Trp	Leu	Asn	Ala	Trp	Ala	Asp	His	Leu	Leu
			20					25					30		
Leu	Thr	Gly	Phe	Ile	Val	Tyr	Leu	Ala	Val	Glu	Tyr	Ala	Thr	Ser	Arg
		35					40					45			
Gly	Arg	Phe	Ala	Leu	Ala	Leu	Ile	Leu	Gly	Val	Glu	Trp	Ile	Leu	Ile
	50					55					60				
Ala	Tyr	Gly	Val	Ala	Leu	Glu	Arg	Pro	Leu	Glu	Ala	Lys	Asp	Ser	Pro
65					70					75					80
Ser	Leu	Ile	Thr	Glu	Ile	Leu	Leu	Ile	Leu	Val	Ala	Ala	Gly	Thr	Gly
				85					90					95	
Ala	Gly	Arg	Trp	Lys	Ile	Leu	Ser	Glu	Arg	Lys	Gln	Arg	Ala	Ile	Thr
			100					105					110		
Gln	Gln	Glu	Ile	Ile	Lys	Lys	Ile	Arg	Thr	Asp	Ile	Ala	His	Tyr	Leu
		115					120					125			
His	Asp	Ser	Met	Ala	Arg	Ser	Leu	Ala	Ile	Met	Ile	Val	Gln	Ser	Lys
	130					135					140				
Leu	Thr	Glu	Leu	Glu	Pro	Asp	Pro	Lys	Lys	Ile	Gln	Glu	Lys	Leu	Asn
145					150					155					160
Ser	Ile	Ala	Lys	Ile	Gly	Gln	Glu	Ala	Val	Ala	Asp	Leu	His	Gln	Leu
			165						170					175	
Val	Arg	His	Leu	Val	Val	Glu	Glu	Ser	Ala	Glu	Lys	Ala	Thr	Ala	Phe
			180					185					190		
Gly	Ala	Trp	Ala	Ala	Val	Ser	Ile	His	Asp	Thr	Val	Asn	Ser	Ala	Ile
		195					200					205			
Gln	Leu	Leu	Val	Asp	Ala	Gly	His	Val	Val	Ser	Phe	Asp	Ser	Arg	Lys
	210					215					220				
Lys	Asn	Tyr	Lys	Leu	Asp	His	Ile	Ala	Glu	Thr	Ala	Phe	Ala	Leu	Ala
225					230					235					240
Phe	Asn	Glu	Ala	Val	Cys	Asn	Ala	Ile	Lys	His	Ser	Pro	Pro	Lys	Ala
			245						250					255	
Asn	Val	Thr	Ile	Arg	Ile	Thr	Glu	Lys	Ala	Gln	Ser	Leu	Gln	Ile	Leu
			260					265					270		
Val	Met	Asn	Pro	Ile	Gly	Asp	Trp	His	Ala	Asn	Gly	Glu	Ser	Ala	Ile
		275					280					285			
Pro	Gly	Val	Gly	Ile	Gly	Val	Glu	Ser	Leu	Thr	Arg	Arg	Ile	Arg	Asn
	290					295					300				
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305					310					315					320

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Val Lys Thr Ser Gln 5																
gcg acc atc gcc cga att gag aga gtt ctc att tgg gga ttg cat tta 163																
Ala Thr Ile Ala Arg Ile Glu Arg Val Leu Ile Trp Gly Leu His Leu 20																
ctc att gcc gtt ttg ttg gtg ttg gtg tgt tgg cgt gcc agc cat tgg 211																
Leu Ile Ala Val Leu Leu Val Leu Val Cys Trp Arg Ala Ser His Trp 35																
ggt gtg tgg gtg ctc gct ttt ggc tat ggc gtg gtt tat gtg gcg ggt 259																
Gly Val Trp Val Leu Ala Phe Gly Tyr Gly Val Val Tyr Val Ala Gly 50																
gtg gtc ccg aat tcg ccg ttt aag aat cac cct atg gcg tgg ttt ctt 307																
Val Val Pro Asn Ser Pro Phe Lys Asn His Pro Met Ala Trp Phe Leu 65																
gtg ctg agt ttg ttg tgg gcg agc ctg att tgg gat gga ccg gag cct 355																
Val Leu Ser Leu Leu Trp Ala Ser Leu Ile Trp Asp Gly Pro Glu Pro 85																
gcg tat ttg gtg ttt ccg atg ttt ttc ctc gca gtg ttg atc acg aca 403																
Ala Tyr Leu Val Phe Pro Met Phe Phe Leu Ala Val Leu Ile Thr Thr 100																
ccg ctg aaa tcc gcg atc atc att gca ata ctg acg gcg atc gcg gtg 451																
Pro Leu Lys Ser Ala Ile Ile Ile Ala Ile Leu Thr Ala Ile Ala Val 115																
gtt acg ttg gct atg cac ctg ggg ttt tct gtt ggc gtt gtc acc ggt 499																
Val Thr Leu Ala Met His Leu Gly Phe Ser Val Gly Val Thr Thr Gly 130																
ccg atc ctt ggc gcg ttg gtg gcg tgg gta atg ggt acg tgt ttt cag 547																
Pro Ile Leu Gly Ala Leu Val Ala Trp Val Met Gly Thr Cys Phe Gln 145																
tta ttg gca caa gcc tta aag gag ctt gtc gac gca cgt gcg tcg gcg 595																
Leu Leu Ala Gln Ala Leu Lys Glu Leu Val Asp Ala Arg Ala Ser Ala 165																

atc cgg gcg tcg aaa agc gct ggc gag cag gca gaa cga gcc cgc ata	643
Ile Arg Ala Ser Lys Ser Ala Gly Glu Gln Ala Glu Arg Ala Arg Ile	
170 175 180	
gcg ggc gaa ata cat gac act gtg gcg cag ggg ttg tcc tcg att cag	691
Ala Gly Glu Ile His Asp Thr Val Ala Gln Gly Leu Ser Ser Ile Gln	
185 190 195	
atg ttg ttg cat gcg gcg gaa aaa cgg gtg gat gat ccg cag gcg tta	739
Met Leu Leu His Ala Ala Glu Lys Arg Val Asp Asp Pro Gln Ala Leu	
200 205 210	
agc cat ata cgg ttg gcc agg caa acg aca gct gat aat ttg gcg gag	787
Ser His Ile Arg Leu Ala Arg Gln Thr Thr Ala Asp Asn Leu Ala Glu	
215 220 225	
acc agg cag atc att gct gcg ctg caa ccg act cca ctc att ggg gcg	835
Thr Arg Gln Ile Ile Ala Ala Leu Gln Pro Thr Pro Leu Ile Gly Ala	
230 235 240 245	
gat ctg ccg gtg gcg ttg gcc aga ctg tcg tcg acc acc ccg atg gga	883
Asp Leu Pro Val Ala Leu Ala Arg Leu Ser Ser Thr Thr Pro Met Gly	
250 255 260	
cag aac atc acg ttt gaa gtc gac gga tcc cca cgg gta tta cct gat	931
Gln Asn Ile Thr Phe Glu Val Asp Gly Ser Pro Arg Val Leu Pro Asp	
265 270 275	
gcg atg gag gca gag atc gta cga att gcc caa acg ctg ctg gga aat	979
Ala Met Glu Ala Glu Ile Val Arg Ile Ala Gln Thr Leu Leu Gly Asn	
280 285 290	
gtg gtg cgg cat gca cag gca gat tct gca aaa atg acc ctg aca tat	1027
Val Val Arg His Ala Gln Ala Asp Ser Ala Lys Met Thr Leu Thr Tyr	
295 300 305	
caa gat gat caa ata ctt cta gat gtc atc gat aat ggg cag gga ttt	1075
Gln Asp Asp Gln Ile Leu Leu Asp Val Ile Asp Asn Gly Gln Gly Phe	
310 315 320 325	
gat gtg gca gaa gtg atc cgt aaa aaa tcc att gga ctg ccc aca gcg	1123
Asp Val Ala Glu Val Ile Arg Lys Lys Ser Ile Gly Leu Pro Thr Ala	
330 335 340	
caa cgc cgg gct gaa ggg ctg ggc gga aca ata att att gaa tct aca	1171
Gln Arg Arg Ala Glu Gly Leu Gly Gly Thr Ile Ile Ile Glu Ser Thr	
345 350 355	
atc gga tcg gga act gga att tcc gcc cgt ttt ccc tat cca caa aag	1219
Ile Gly Ser Gly Thr Gly Ile Ser Ala Arg Phe Pro Tyr Pro Gln Lys	
360 365 370	
gac caa gat aag tgatccgtat tctgttgget gat	1254
Asp Gln Asp Lys	
375	

&lt;210&gt; 238

&lt;211&gt; 377

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 238

Val	Lys	Thr	Ser	Gln	Ala	Thr	Ile	Ala	Arg	Ile	Glu	Arg	Val	Leu	Ile	1	5	10	15
Trp	Gly	Leu	His	Leu	Leu	Ile	Ala	Val	Leu	Leu	Val	Leu	Val	Cys	Trp	20	25	30	
Arg	Ala	Ser	His	Trp	Gly	Val	Trp	Val	Leu	Ala	Phe	Gly	Tyr	Gly	Val	35	40	45	
Val	Tyr	Val	Ala	Gly	Val	Val	Pro	Asn	Ser	Pro	Phe	Lys	Asn	His	Pro	50	55	60	
Met	Ala	Trp	Phe	Leu	Val	Leu	Ser	Leu	Leu	Trp	Ala	Ser	Leu	Ile	Trp	65	70	75	80
Asp	Gly	Pro	Glu	Pro	Ala	Tyr	Leu	Val	Phe	Pro	Met	Phe	Phe	Leu	Ala	85	90	95	
Val	Leu	Ile	Thr	Thr	Pro	Leu	Lys	Ser	Ala	Ile	Ile	Ile	Ala	Ile	Leu	100	105	110	
Thr	Ala	Ile	Ala	Val	Val	Thr	Leu	Ala	Met	His	Leu	Gly	Phe	Ser	Val	115	120	125	
Gly	Val	Val	Thr	Gly	Pro	Ile	Leu	Gly	Ala	Leu	Val	Ala	Trp	Val	Met	130	135	140	
Gly	Thr	Cys	Phe	Gln	Leu	Ala	Gln	Ala	Leu	Lys	Glu	Leu	Val	Asp		145	150	155	160
Ala	Arg	Ala	Ser	Ala	Ile	Arg	Ala	Ser	Lys	Ser	Ala	Gly	Glu	Gln	Ala	165	170	175	
Glu	Arg	Ala	Arg	Ile	Ala	Gly	Glu	Ile	His	Asp	Thr	Val	Ala	Gln	Gly	180	185	190	
Leu	Ser	Ser	Ile	Gln	Met	Leu	Leu	His	Ala	Ala	Glu	Lys	Arg	Val	Asp	195	200	205	
Asp	Pro	Gln	Ala	Leu	Ser	His	Ile	Arg	Leu	Ala	Arg	Gln	Thr	Thr	Ala	210	215	220	
Asp	Asn	Leu	Ala	Glu	Thr	Arg	Gln	Ile	Ile	Ala	Ala	Leu	Gln	Pro	Thr	225	230	235	240
Pro	Leu	Ile	Gly	Ala	Asp	Leu	Pro	Val	Ala	Leu	Ala	Arg	Leu	Ser	Ser	245	250	255	
Thr	Thr	Pro	Met	Gly	Gln	Asn	Ile	Thr	Phe	Glu	Val	Asp	Gly	Ser	Pro	260	265	270	
Arg	Val	Leu	Pro	Asp	Ala	Met	Glu	Ala	Glu	Ile	Val	Arg	Ile	Ala	Gln	275	280	285	
Thr	Leu	Leu	Gly	Asn	Val	Val	Arg	His	Ala	Gln	Ala	Asp	Ser	Ala	Lys	290	295	300	
Met	Thr	Leu	Thr	Tyr	Gln	Asp	Asp	Gln	Ile	Leu	Leu	Asp	Val	Ile	Asp				

305                      310                      315                      320  
 Asn Gly Gln Gly Phe Asp Val Ala Glu Val Ile Arg Lys Lys Ser Ile  
                                  325                                   330                                   335  
 Gly Leu Pro Thr Ala Gln Arg Arg Ala Glu Gly Leu Gly Gly Thr Ile  
                                  340                                   345                                   350  
 Ile Ile Glu Ser Thr Ile Gly Ser Gly Thr Gly Ile Ser Ala Arg Phe  
                                  355                                   360                                   365  
 Pro Tyr Pro Gln Lys Asp Gln Asp Lys  
                  370                                   375

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 <213> Corynebacterium glutamicum

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 <223> RXN03071

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   1                                  5                                  10                                  15  
  
 aac gag cag atc acc gaa gcc ttc gag cgc gac gtc gtc cca tac gcg    96  
 Asn Glu Gln Ile Thr Glu Ala Phe Glu Arg Asp Val Val Pro Tyr Ala  
                                   20                                  25                                  30  
  
 gag ctt ttc gac gcc tcc ggc cag att cct tca tcg cag gag ttc ttc    144  
 Glu Leu Phe Asp Ala Ser Gly Gln Ile Pro Ser Ser Gln Glu Phe Phe  
                                   35                                  40                                  45  
  
 cgc gtg tca ctc acc gga cag tat ctt cca gac agt gag gtt ttg ctg    192  
 Arg Val Ser Leu Thr Gly Gln Tyr Leu Pro Asp Ser Glu Val Leu Leu  
                                   50                                  55                                  60  
  
 cgc ctt cgc ccc gtc gac tcc ggc cca gca ttc caa tcg tta acc ccc    240  
 Arg Leu Arg Pro Val Asp Ser Gly Pro Ala Phe Gln Ser Leu Thr Pro  
                                   65                                  70                                  75                                  80  
  
 ttc gaa ctt gaa aac gga cag att gtc ctc gtc aac cgt ggt tac gaa    288  
 Phe Glu Leu Glu Asn Gly Gln Ile Val Leu Val Asn Arg Gly Tyr Glu  
                                   85                                  90                                  95  
  
 tca tca gag ggc aca atc gtc cca gag atc gag cct gct cct tca cac    336  
 Ser Ser Glu Gly Thr Ile Val Pro Glu Ile Glu Pro Ala Pro Ser His  
                                   100                                  105                                  110  
  
 cag taaccatcac cggattcgcc gca    362  
 Gln

<210> 240  
 <211> 113

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 240

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 1 5 10 15

Asn Glu Gln Ile Thr Glu Ala Phe Glu Arg Asp Val Val Pro Tyr Ala  
 20 25 30

Glu Leu Phe Asp Ala Ser Gly Gln Ile Pro Ser Ser Gln Glu Phe Phe  
 35 40 45

Arg Val Ser Leu Thr Gly Gln Tyr Leu Pro Asp Ser Glu Val Leu Leu  
 50 55 60

Arg Leu Arg Pro Val Asp Ser Gly Pro Ala Phe Gln Ser Leu Thr Pro  
 65 70 75 80

Phe Glu Leu Glu Asn Gly Gln Ile Val Leu Val Asn Arg Gly Tyr Glu  
 85 90 95

Ser Ser Glu Gly Thr Ile Val Pro Glu Ile Glu Pro Ala Pro Ser His  
 100 105 110

Gln

&lt;210&gt; 241

&lt;211&gt; 558

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(535)

&lt;223&gt; RXN03072

&lt;400&gt; 241

atcagagggc acaatcgctc cagagatcga gcctgctcct tcacaccagt aaccatcacc 60

ggattcgccg caagaacgag ggcctccagg ttctgcacct atg gaa gac agc ggc 115  
 Met Glu Asp Ser Gly  
 1 5

tac acc cag gtc tac gga att aac acc gaa cag atc agt gac gtc acc 163  
 Tyr Thr Gln Val Tyr Gly Ile Asn Thr Glu Gln Ile Ser Asp Val Thr  
 10 15 20

ggc ctt gat ctt ggc acc gac tac gtc cag gtc gca gaa ggc gaa cct 211  
 Gly Leu Asp Leu Gly Thr Asp Tyr Val Gln Val Ala Glu Gly Glu Pro  
 25 30 35

ggt gtt ttg aac cca atg cca ctg cct caa atg gac cgc ggt aac cac 259  
 Gly Val Leu Asn Pro Met Pro Leu Pro Gln Met Asp Arg Gly Asn His  
 40 45 50

ctc tca tac ggc ttc cag tgg atc gcc ttc ggc atc atg gca cct tta 307  
 Leu Ser Tyr Gly Phe Gln Trp Ile Ala Phe Gly Ile Met Ala Pro Leu  
 55 60 65

ggg ctt gga tac ttc atc tgg gct gaa atg cgc gaa cga cgc cgc gac 355  
 Gly Leu Gly Tyr Phe Ile Trp Ala Glu Met Arg Glu Arg Arg Arg Asp  
 70 75 80 85

aaa gca gaa cgc gaa cag atg gcc gag cta aac act ctt gaa cca gtg 403  
 Lys Ala Glu Arg Glu Gln Met Ala Glu Leu Asn Thr Leu Glu Pro Val  
 90 95 100

gtg gaa acc cct gaa gtt gtt gaa act gca gaa cca acc atc acc ccg 451  
 Val Glu Thr Pro Glu Val Val Glu Thr Ala Glu Pro Thr Ile Thr Pro  
 105 110 115

gct gca tcc aaa cga cgt tca cgc tac ggc gat caa cac cgc aat cac 499  
 Ala Ala Ser Lys Arg Arg Ser Arg Tyr Gly Asp Gln His Arg Asn His  
 120 125 130

tac gag aag atc tcc aaa cga gac caa gag cgc ttc taagcccgtc 545  
 Tyr Glu Lys Ile Ser Lys Arg Asp Gln Glu Arg Phe  
 135 140 145

tcatttttgc acc 558

<210> 242

<211> 145

<212> PRT

<213> Corynebacterium glutamicum

<400> 242

Met Glu Asp Ser Gly Tyr Thr Gln Val Tyr Gly Ile Asn Thr Glu Gln  
 1 5 10 15

Ile Ser Asp Val Thr Gly Leu Asp Leu Gly Thr Asp Tyr Val Gln Val  
 20 25 30

Ala Glu Gly Glu Pro Gly Val Leu Asn Pro Met Pro Leu Pro Gln Met  
 35 40 45

Asp Arg Gly Asn His Leu Ser Tyr Gly Phe Gln Trp Ile Ala Phe Gly  
 50 55 60

Ile Met Ala Pro Leu Gly Leu Gly Tyr Phe Ile Trp Ala Glu Met Arg  
 65 70 75 80

Glu Arg Arg Arg Asp Lys Ala Glu Arg Glu Gln Met Ala Glu Leu Asn  
 85 90 95

Thr Leu Glu Pro Val Val Glu Thr Pro Glu Val Val Glu Thr Ala Glu  
 100 105 110

Pro Thr Ile Thr Pro Ala Ala Ser Lys Arg Arg Ser Arg Tyr Gly Asp  
 115 120 125

Gln His Arg Asn His Tyr Glu Lys Ile Ser Lys Arg Asp Gln Glu Arg  
 130 135 140

Phe

145

$\langle 210 \rangle$	244
$\langle 211 \rangle$	159



&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 244

```

Met Thr Val Asp Leu Tyr Gln Ala Arg Ile Pro Phe Gln Arg Asp Gly
 1           5           10           15
Val Arg Phe Asp His Thr Met Ile Thr His Ile Gln Ala Gly Leu His
          20           25           30
Leu Gly Gly Cys Arg Ala Ala Gly Leu Leu Pro Ile Pro Ala His Ile
          35           40           45
Asp His Ile Val Arg Leu Thr Ala Ala Asp Phe Tyr Asp Thr Gln Ser
          50           55           60
Ala Pro Gln Leu Leu Ser Asn Thr Val Leu Asp Val Leu Asp Thr Thr
          65           70           75           80
Thr Gln Asp Leu Lys Ala Leu Trp Pro Val Ala Glu His Ile Ala Thr
          85           90           95
Thr Ile Pro Glu Ser Glu Asn Val Leu Ile His Cys Gln Met Gly Ile
          100          105          110
Asn Arg Ser Ala Ala Leu Met Thr Arg Val Leu Met Leu Arg Asn Asp
          115          120          125
Cys Thr Ala Asp Glu Ala Ile Ala Leu Leu Arg Asp Arg Arg Ser Pro
          130          135          140
Phe Val Leu Phe Asn Glu His Phe Val Glu Gln Leu Arg Ala Leu
          145          150          155

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&lt;210&gt; 245

&lt;211&gt; 1344

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1321)

&lt;223&gt; RXN03090

&lt;400&gt; 245

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tcaattatca gtactatgac gatgactggg acgacgacga tgatgacttc gacgacgact 60
gggacgacga ctaactaacc cctgaggcac tttctatttc atg gct aaa tca act 115
                                   Met Ala Lys Ser Thr
                                   1           5
cct ttg att gca tcg cta cgc tgg cga att gtc ctg tgg atg aca gcg 163
Pro Leu Ile Ala Ser Leu Arg Trp Arg Ile Val Leu Trp Met Thr Ala
          10           15           20
gtt gtt ttc ttg acc cta gcc agc gtt gtg atc att acc cgt tcg gtg 211
Val Val Phe Leu Thr Leu Ala Ser Val Val Ile Ile Thr Arg Ser Val
          25           30           35
ctg ctt tca gag gta acc aac acc gcg aac tcg gca gtt gag cag gaa 259

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Leu	Leu	Ser	Glu	Val	Thr	Asn	Thr	Ala	Asn	Ser	Ala	Val	Glu	Gln	Glu		
		40					45					50					
att	gag	gag	ttt	cgt	cgc	ttt	gca	gcc	gaa	gga	att	gat	cca	aca	act	307	
Ile	Glu	Glu	Phe	Arg	Arg	Phe	Ala	Ala	Glu	Gly	Ile	Asp	Pro	Thr	Thr		
	55					60					65						
gcg	cag	cct	ttt	gag	tca	ggt	cat	cgc	ctg	atg	gag	gtt	tac	ctg	tcg	355	
Ala	Gln	Pro	Phe	Glu	Ser	Gly	His	Arg	Leu	Met	Glu	Val	Tyr	Leu	Ser		
	70				75					80					85		
agg	cag	att	ccg	gat	gaa	aat	gaa	gcc	att	gtc	ggc	att	ttc	ccc	gga	403	
Arg	Gln	Ile	Pro	Asp	Glu	Asn	Glu	Ala	Ile	Val	Gly	Ile	Phe	Pro	Gly		
				90					95					100			
gag	ctc	att	cag	gtt	gat	tac	tcc	cag	ctc	agt	ggc	gcc	cat	ccg	ctt	451	
Glu	Leu	Ile	Gln	Val	Asp	Tyr	Ser	Gln	Leu	Ser	Gly	Ala	His	Pro	Leu		
			105					110					115				
cct	ttg	gaa	cac	tcc	gat	ccg	ttg	att	tcg	gaa	atc	cga	cag	acc	acg	499	
Pro	Leu	Glu	His	Ser	Asp	Pro	Leu	Ile	Ser	Glu	Ile	Arg	Gln	Thr	Thr		
		120					125					130					
ctg	aat	tct	gga	gtt	ttc	agc	gat	ctt	gaa	cgc	gga	acc	act	cac	tgg	547	
Leu	Asn	Ser	Gly	Val	Phe	Ser	Asp	Leu	Glu	Arg	Gly	Thr	Thr	His	Trp		
	135					140					145						
gga	aag	gtg	aat	ttc	caa	act	gct	tcc	ggt	gag	gcc	gat	ggt	gag	ttc	595	
Gly	Lys	Val	Asn	Phe	Gln	Thr	Ala	Ser	Gly	Glu	Ala	Asp	Gly	Glu	Phe		
	150			155					160						165		
gtt	gtc	gca	ttc	ttc	gct	gat	aat	ctt	aaa	gac	cag	gtc	aac	ggc	cag	643	
Val	Val	Ala	Phe	Phe	Ala	Asp	Asn	Leu	Lys	Asp	Gln	Val	Asn	Gly	Gln		
			170					175						180			
atc	cag	att	ctt	att	ttg	atc	ggc	aca	ggg	ggt	ttg	att	gcc	tca	att	691	
Ile	Gln	Ile	Leu	Ile	Leu	Ile	Gly	Thr	Gly	Gly	Leu	Ile	Ala	Ser	Ile		
			185					190					195				
ctg	att	gct	tgg	ttg	att	gcg	ggc	cag	atc	att	gcc	ccg	atc	cgc	aaa	739	
Leu	Ile	Ala	Trp	Leu	Ile	Ala	Gly	Gln	Ile	Ile	Ala	Pro	Ile	Arg	Lys		
		200					205					210					
ttg	agt	tcc	gtg	tcc	gca	aag	atc	agt	aat	tcg	gat	ctc	acc	tgg	cgc	787	
Leu	Ser	Ser	Val	Ser	Ala	Lys	Ile	Ser	Asn	Ser	Asp	Leu	Thr	Trp	Arg		
	215					220					225						
gtc	cct	gtg	gag	ggt	cgt	gat	gag	att	gcg	cag	ctg	gcc	agg	act	ttt	835	
Val	Pro	Val	Glu	Gly	Arg	Asp	Glu	Ile	Ala	Gln	Leu	Ala	Arg	Thr	Phe		
	230				235					240					245		
aat	gcc	atg	ttg	gat	cgc	atc	gaa	atc	gcg	tat	aac	gat	cag	cgc	cag	883	
Asn	Ala	Met	Leu	Asp	Arg	Ile	Glu	Ile	Ala	Tyr	Asn	Asp	Gln	Arg	Gln		
				250					255					260			
ttc	gtt	gat	gat	gcc	ggc	cac	gag	ctg	cgc	acc	ccg	atc	aca	gtg	gtg	931	
Phe	Val	Asp	Asp	Ala	Gly	His	Glu	Leu	Arg	Thr	Pro	Ile	Thr	Val	Val		
			265					270					275				
cgt	ggc	cag	tta	gag	ctt	ctc	gcc	acc	acc	ccg	ccg	gag	gaa	caa	gcg	979	
Arg	Gly	Gln	Leu	Glu	Leu	Leu	Ala	Thr	Thr	Pro	Pro	Glu	Glu	Gln	Ala		

280	285	290	
cgg tcg att gag ctg gcc acc act gag ttg gat	cga atg tcg cga atg	1027	
Arg Ser Ile Glu Leu Ala Thr Thr Glu Leu Asp	Arg Met Ser Arg Met		
295	300 305		
gtc aat gat ctg ctc acc ctc gca gtc gcc gat tct ggc acc ttc atc		1075	
Val Asn Asp Leu Leu Thr Leu Ala Val Ala Asp Ser Gly Thr Phe Ile			
310	315 320 325		
cac gcc cac ccc acg gat gtc acg gat tta aca atc gat atc gaa gac		1123	
His Ala His Pro Thr Asp Val Thr Asp Leu Thr Ile Asp Ile Glu Asp			
	330 335 340		
aaa gcc cgc acc atc agc gac cga att ttg ctt gtc gac gcc cgc ccg		1171	
Lys Ala Arg Thr Ile Ser Asp Arg Ile Leu Leu Val Asp Ala Arg Pro			
	345 350 355		
agg gcc tcg tca gcc tcg acg agc agc ggg tca ccg agg cag tgc ttg		1219	
Arg Ala Ser Ser Ala Ser Thr Ser Ser Gly Ser Pro Arg Gln Cys Leu			
	360 365 370		
gag ttg ttc ggc aat gcg ttg cgc tac agc gat gat gtg gtg gag ttg		1267	
Glu Leu Phe Gly Asn Ala Leu Arg Tyr Ser Asp Val Val Glu Leu			
	375 380 385		
ggt tca gga ttt caa ggg gtc tgg ccc cca ccg cat ttt tcg cat ttg		1315	
Gly Ser Gly Phe Gln Gly Val Trp Pro Pro Pro His Phe Ser His Leu			
	390 395 400 405		
ggt tcg tgacaaagga aacggtgttg ata		1344	
Gly Ser			

&lt;210&gt; 246

&lt;211&gt; 407

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 246

Met Ala Lys Ser Thr Pro Leu Ile Ala Ser Leu Arg Trp Arg Ile Val	
1 5 10 15	
Leu Trp Met Thr Ala Val Val Phe Leu Thr Leu Ala Ser Val Val Ile	
20 25 30	
Ile Thr Arg Ser Val Leu Leu Ser Glu Val Thr Asn Thr Ala Asn Ser	
35 40 45	
Ala Val Glu Gln Glu Ile Glu Glu Phe Arg Arg Phe Ala Ala Glu Gly	
50 55 60	
Ile Asp Pro Thr Thr Ala Gln Pro Phe Glu Ser Gly His Arg Leu Met	
65 70 75 80	
Glu Val Tyr Leu Ser Arg Gln Ile Pro Asp Glu Asn Glu Ala Ile Val	
85 90 95	
Gly Ile Phe Pro Gly Glu Leu Ile Gln Val Asp Tyr Ser Gln Leu Ser	
100 105 110	

Gly Ala His Pro Leu Pro Leu Glu His Ser Asp Pro Leu Ile Ser Glu  
 115 120 125  
 Ile Arg Gln Thr Thr Leu Asn Ser Gly Val Phe Ser Asp Leu Glu Arg  
 130 135 140  
 Gly Thr Thr His Trp Gly Lys Val Asn Phe Gln Thr Ala Ser Gly Glu  
 145 150 155 160  
 Ala Asp Gly Glu Phe Val Val Ala Phe Phe Ala Asp Asn Leu Lys Asp  
 165 170 175  
 Gln Val Asn Gly Gln Ile Gln Ile Leu Ile Leu Ile Gly Thr Gly Gly  
 180 185 190  
 Leu Ile Ala Ser Ile Leu Ile Ala Trp Leu Ile Ala Gly Gln Ile Ile  
 195 200 205  
 Ala Pro Ile Arg Lys Leu Ser Ser Val Ser Ala Lys Ile Ser Asn Ser  
 210 215 220  
 Asp Leu Thr Trp Arg Val Pro Val Glu Gly Arg Asp Glu Ile Ala Gln  
 225 230 235 240  
 Leu Ala Arg Thr Phe Asn Ala Met Leu Asp Arg Ile Glu Ile Ala Tyr  
 245 250 255  
 Asn Asp Gln Arg Gln Phe Val Asp Asp Ala Gly His Glu Leu Arg Thr  
 260 265 270  
 Pro Ile Thr Val Val Arg Gly Gln Leu Glu Leu Leu Ala Thr Thr Pro  
 275 280 285  
 Pro Glu Glu Gln Ala Arg Ser Ile Glu Leu Ala Thr Thr Glu Leu Asp  
 290 295 300  
 Arg Met Ser Arg Met Val Asn Asp Leu Leu Thr Leu Ala Val Ala Asp  
 305 310 315 320  
 Ser Gly Thr Phe Ile His Ala His Pro Thr Asp Val Thr Asp Leu Thr  
 325 330 335  
 Ile Asp Ile Glu Asp Lys Ala Arg Thr Ile Ser Asp Arg Ile Leu Leu  
 340 345 350  
 Val Asp Ala Arg Pro Arg Ala Ser Ser Ala Ser Thr Ser Ser Gly Ser  
 355 360 365  
 Pro Arg Gln Cys Leu Glu Leu Phe Gly Asn Ala Leu Arg Tyr Ser Asp  
 370 375 380  
 Asp Val Val Glu Leu Gly Ser Gly Phe Gln Gly Val Trp Pro Pro Pro  
 385 390 395 400  
 His Phe Ser His Leu Gly Ser  
 405

&lt;210&gt; 247

&lt;211&gt; 351

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(328)

&lt;223&gt; RXN00617

&lt;400&gt; 247

tacagcgatg atgtggtgga gttgggttca ggatttcaag gggctctggcc cccaccgcat 60

ttttcgcatt tgggttcgtg acaaaggaaa cgggtgttgat atg gat gaa caa gaa 115  
 Met Asp Glu Gln Glu  
 1 5

gcc ctg ttc gat cgc ttc tcc aga ggc tcc caa aaa aat tca cgg cgt 163  
 Ala Leu Phe Asp Arg Phe Ser Arg Gly Ser Gln Lys Asn Ser Arg Arg  
 10 15 20

ccc ggt ggc gct ggc ctg gga tta tcc att gtc aag gcg atc ggc gaa 211  
 Pro Gly Gly Ala Gly Leu Gly Leu Ser Ile Val Lys Ala Ile Gly Glu  
 25 30 35

gcc cac gtc ggc cga gct ttc gtc aat tcc aca cca ggt cta gga tcc 259  
 Ala His Val Gly Arg Ala Phe Val Asn Ser Thr Pro Gly Leu Gly Ser  
 40 45 50

att ttc ggc ctg gaa atc ccc gca cca gaa caa tca aag gaa tac acc 307  
 Ile Phe Gly Leu Glu Ile Pro Ala Pro Glu Gln Ser Lys Glu Tyr Thr  
 55 60 65

cat gag caa gat cct gct cgc tgaagatgac gccggcatcg cag 351  
 His Glu Gln Asp Pro Ala Arg  
 70 75

&lt;210&gt; 248

&lt;211&gt; 76

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 248

Met Asp Glu Gln Glu Ala Leu Phe Asp Arg Phe Ser Arg Gly Ser Gln  
 1 5 10 15

Lys Asn Ser Arg Arg Pro Gly Gly Ala Gly Leu Gly Leu Ser Ile Val  
 20 25 30

Lys Ala Ile Gly Glu Ala His Val Gly Arg Ala Phe Val Asn Ser Thr  
 35 40 45

Pro Gly Leu Gly Ser Ile Phe Gly Leu Glu Ile Pro Ala Pro Glu Gln  
 50 55 60

Ser Lys Glu Tyr Thr His Glu Gln Asp Pro Ala Arg  
 65 70 75

&lt;210&gt; 249

&lt;211&gt; 720

&lt;212&gt; DNA

$\langle 220 \rangle$ 

<221> CDS

<222> (101) . . (697)

<223> RXN02990

<400> 249

gaagactaag caccagtttt aacaaagcag ggacaatcca cacacttaaa ccatgatgtg															60
gcttggttcct gcttttttcgt caacgaaggg caacaacgcg atg gat atc caa gcc															115
Met Asp Ile Gln Ala															5
gaa aag att gaa aag ctc aga aaa gca ctc gac aac ttt gaa cgc gct															163
Glu Lys Ile Glu Lys Leu Arg Lys Ala Leu Asp Asn Phe Glu Arg Ala															20
cat gcg cga ggc gaa tca gac ttc ttt gac cat gaa aaa gaa gaa aag															211
His Ala Arg Gly Glu Ser Asp Phe Phe Asp His Glu Lys Glu Glu Lys															35
aaa gcc aac gta cgc aga cgt gcc ctg ctg ctg ctt aac caa cgc gca															259
Lys Ala Asn Val Arg Arg Arg Ala Leu Leu Leu Leu Asn Gln Arg Ala															50
cga tca gtc aac gaa cta agc acc aga ctt aaa gca ctg gag ttt gag															307
Arg Ser Val Asn Glu Leu Ser Thr Arg Leu Lys Ala Leu Glu Phe Glu															65
gaa gac atc atc aat gag gtc att ggc gat ctc acc aga tcc aaa ctg															355
Glu Asp Ile Ile Asn Glu Val Ile Gly Asp Leu Thr Arg Ser Lys Leu															85
ctt gat gat gaa gtt ttt gcc act gag tgg gtt cgg caa cgt gct gcc															403
Leu Asp Asp Glu Val Phe Ala Thr Glu Trp Val Arg Gln Arg Ala Ala															100
agg cga gga aaa tct tcg cgt gcg ctg gac cgc gaa ctg cag gaa aaa															451
Arg Arg Gly Lys Ser Ser Arg Ala Leu Asp Arg Glu Leu Gln Glu Lys															115
ggc gtc gac aag caa acg cgt gct gcg gcg ctt gag caa atc gac cag															499
Gly Val Asp Lys Gln Thr Arg Ala Ala Ala Leu Glu Gln Ile Asp Gln															130
gcc gat gag cgg gac acg gcg cgg gcg gtg gcc gtg aaa aag gcg cgc															547
Ala Asp Glu Arg Asp Thr Ala Arg Ala Val Ala Val Lys Lys Ala Arg															145
tca gag acc aag att ccg cag gac cgc gcc gac tac gac aaa gcg ctt															595
Ser Glu Thr Lys Ile Pro Gln Asp Arg Ala Asp Tyr Asp Lys Ala Leu															165
cgg cgc gtg gtt ggt gcg ctg gca cgg cgg gga ttt ccg gct gga atg															643
Arg Arg Val Val Gly Ala Leu Ala Arg Arg Gly Phe Pro Ala Gly Met															180
tcc atg gac ctt gcg cgg gaa gcg cta gac gcg cga atc gag gat ttg															691
Ser Met Asp Leu Ala Arg Glu Ala Leu Asp Ala Arg Ile Glu Asp Leu															195

aaa aac taaaccccg atgggaatca tcc  
Lys Asn

720

<210> 250  
<211> 199  
<212> PRT  
<213> Corynebacterium glutamicum

<400> 250  
Met Asp Ile Gln Ala Glu Lys Ile Glu Lys Leu Arg Lys Ala Leu Asp  
1 5 10 15  
Asn Phe Glu Arg Ala His Ala Arg Gly Glu Ser Asp Phe Phe Asp His  
20 25 30  
Glu Lys Glu Glu Lys Lys Ala Asn Val Arg Arg Arg Ala Leu Leu Leu  
35 40 45  
Leu Asn Gln Arg Ala Arg Ser Val Asn Glu Leu Ser Thr Arg Leu Lys  
50 55 60  
Ala Leu Glu Phe Glu Glu Asp Ile Ile Asn Glu Val Ile Gly Asp Leu  
65 70 75 80  
Thr Arg Ser Lys Leu Leu Asp Asp Glu Val Phe Ala Thr Glu Trp Val  
85 90 95  
Arg Gln Arg Ala Ala Arg Arg Gly Lys Ser Ser Arg Ala Leu Asp Arg  
100 105 110  
Glu Leu Gln Glu Lys Gly Val Asp Lys Gln Thr Arg Ala Ala Ala Leu  
115 120 125  
Glu Gln Ile Asp Gln Ala Asp Glu Arg Asp Thr Ala Arg Ala Val Ala  
130 135 140  
Val Lys Lys Ala Arg Ser Glu Thr Lys Ile Pro Gln Asp Arg Ala Asp  
145 150 155 160  
Tyr Asp Lys Ala Leu Arg Arg Val Val Gly Ala Leu Ala Arg Arg Gly  
165 170 175  
Phe Pro Ala Gly Met Ser Met Asp Leu Ala Arg Glu Ala Leu Asp Ala  
180 185 190  
Arg Ile Glu Asp Leu Lys Asn  
195

<210> 251  
<211> 341  
<212> DNA  
<213> Corynebacterium glutamicum  
  
<220>  
<221> CDS  
<222> (1)..(318)  
<223> RXN03100

&lt;400&gt; 251

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     1                    5                    10                    15

act agc ctc tac ctc tgg aaa gaa atg gta gag aag gcc gat tcc ttt 96  
 Thr Ser Leu Tyr Leu Trp Lys Glu Met Val Glu Lys Ala Asp Ser Phe  
                     20                    25                    30

gat gtc gcc gca att caa gca gcc gcc gac gga acc act ttt gat gca 144  
 Asp Val Ala Ala Ile Gln Ala Ala Ala Asp Gly Thr Thr Phe Asp Ala  
                     35                    40                    45

cca gaa gga acc gtg gtg gtt ggc ggc gat aac cac cac atc tcc aaa 192  
 Pro Glu Gly Thr Val Val Val Gly Gly Asp Asn His His Ile Ser Lys  
                     50                    55                    60

aca ccg cgc atc ggt cga atc cgc ccg gat gga ttg atc gac acc att 240  
 Thr Pro Arg Ile Gly Arg Ile Arg Pro Asp Gly Leu Ile Asp Thr Ile  
                     65                    70                    75                    80

tgg gaa acc gat tcc cca gtt gat ccg gac cca tac ttg tct tcc tat 288  
 Trp Glu Thr Asp Ser Pro Val Asp Pro Asp Pro Tyr Leu Ser Ser Tyr  
                     85                    90                    95

gac tgg gcc aag acc acc gct gcg act tcc taagagataa aaatcatgga cat 341  
 Asp Trp Ala Lys Thr Thr Ala Ala Thr Ser  
                     100                    105

&lt;210&gt; 252

&lt;211&gt; 106

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 252

Leu Tyr Gly Gln Asp Lys Val Thr Ser Asp Pro Met Glu Ala Ala Tyr  
     1                    5                    10                    15

Thr Ser Leu Tyr Leu Trp Lys Glu Met Val Glu Lys Ala Asp Ser Phe  
                     20                    25                    30

Asp Val Ala Ala Ile Gln Ala Ala Ala Asp Gly Thr Thr Phe Asp Ala  
                     35                    40                    45

Pro Glu Gly Thr Val Val Val Gly Gly Asp Asn His His Ile Ser Lys  
                     50                    55                    60

Thr Pro Arg Ile Gly Arg Ile Arg Pro Asp Gly Leu Ile Asp Thr Ile  
                     65                    70                    75                    80

Trp Glu Thr Asp Ser Pro Val Asp Pro Asp Pro Tyr Leu Ser Ser Tyr  
                     85                    90                    95

Asp Trp Ala Lys Thr Thr Ala Ala Thr Ser  
                     100                    105

&lt;210&gt; 253



<211> 525  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(502)  
 <223> RXN00031

<400> 253  
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 ccataaacgc ccacttaatc aacgtgggct tcgcgatggc gtg gca gct ggc caa 115  
 Val Ala Ala Gly Gln  
 1 5  
 tgg cta gct ggc aac atc ggc gaa att gat cat gtg ctg tgt tca gat 163  
 Trp Leu Ala Gly Asn Ile Gly Glu Ile Asp His Val Leu Cys Ser Asp  
 10 15 20  
 gcc acc cgc aca caa tta acg tgg gaa cgc gtc cag ctt ggt ggc gca 211  
 Ala Thr Arg Thr Gln Leu Thr Trp Glu Arg Val Gln Leu Gly Gly Ala  
 25 30 35  
 acc gcc aaa ggc tct agc ttc cac aat gac atc tat gaa aac caa gtg 259  
 Thr Ala Lys Gly Ser Ser Phe His Asn Asp Ile Tyr Glu Asn Gln Val  
 40 45 50  
 tct gaa ttt aaa cat tta ata aca ggg ctc cca gat gta gtt ggt acc 307  
 Ser Glu Phe Lys His Leu Ile Thr Gly Leu Pro Asp Val Val Gly Thr  
 55 60 65  
 gcc cta ctc atc ggg cac tgg cca ggc gtg gaa gaa cta gcc cat tat 355  
 Ala Leu Leu Ile Gly His Trp Pro Gly Val Glu Glu Leu Ala His Tyr  
 70 75 80 85  
 ttt ggc atc cgc gat gaa cat ccc ggt tgg gat cag atg gaa gaa aag 403  
 Phe Gly Ile Arg Asp Glu His Pro Gly Trp Asp Gln Met Glu Glu Lys  
 90 95 100  
 ttt ccc acc agc gcc att gcg gtg ttg gaa ttt aac acc cct tgg tca 451  
 Phe Pro Thr Ser Ala Ile Ala Val Leu Glu Phe Asn Thr Pro Trp Ser  
 105 110 115  
 aaa ctt gag aga aac tct gct cgg ttg aca gat ttt gtc att cca cgg 499  
 Lys Leu Glu Arg Asn Ser Ala Arg Leu Thr Asp Phe Val Ile Pro Arg  
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 Gly

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 <213> Corynebacterium glutamicum

<400> 254  
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 20 25 30

Gln Leu Gly Gly Ala Thr Ala Lys Gly Ser Ser Phe His Asn Asp Ile  
 35 40 45

Tyr Glu Asn Gln Val Ser Glu Phe Lys His Leu Ile Thr Gly Leu Pro  
 50 55 60

Asp Val Val Gly Thr Ala Leu Leu Ile Gly His Trp Pro Gly Val Glu  
 65 70 75 80

Glu Leu Ala His Tyr Phe Gly Ile Arg Asp Glu His Pro Gly Trp Asp  
 85 90 95

Gln Met Glu Glu Lys Phe Pro Thr Ser Ala Ile Ala Val Leu Glu Phe  
 100 105 110

Asn Thr Pro Trp Ser Lys Leu Glu Arg Asn Ser Ala Arg Leu Thr Asp  
 115 120 125

Phe Val Ile Pro Arg Gly  
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<220>  
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 Val Thr Glu Leu Ile  
 1 5

cag aat gaa tcc caa gaa atc gct gag ctg gaa gcc ggc cag cag gtt 163  
 Gln Asn Glu Ser Gln Glu Ile Ala Glu Leu Glu Ala Gly Gln Gln Val  
 10 15 20

gca ttg cgt gaa ggt tat ctt cct gcg gtg atc aca gtg agc ggt aaa 211  
 Ala Leu Arg Glu Gly Tyr Leu Pro Ala Val Ile Thr Val Ser Gly Lys  
 25 30 35

gac cgc cca ggt gtg act gcc gcg ttc ttt agg gtc ttg tcc gct aat 259  
 Asp Arg Pro Gly Val Thr Ala Ala Phe Phe Arg Val Leu Ser Ala Asn  
 40 45 50

cag gtt cag gtc ttg gac gtt gag cag tca atg ttc cgt ggc ttt ttg 307  
 Gln Val Gln Val Leu Asp Val Glu Gln Ser Met Phe Arg Gly Phe Leu  
 55 60 65

aac ttg gcg gcg ttt gtg ggt atc gca cct gag cgt gtc gag acc gtc 355  
 Asn Leu Ala Ala Phe Val Gly Ile Ala Pro Glu Arg Val Glu Thr Val

70	75					80					85					
acc aca ggc ctg act gac acc ctc aag gtg cat gga cag tcc gtg gtg	Thr Thr Gly Leu Thr Asp Thr Leu Lys Val His Gly Gln Ser Val Val															403
	90					95					100					
gtg gag ctg cag gaa act gtg cag tcg tcc cgt cct cgt tct tcc cat	Val Glu Leu Gln Glu Thr Val Gln Ser Ser Arg Pro Arg Ser Ser His					110					115					451
	105															
gtt gtt gtg gtg ttg ggt gat ccg gtt gat gcg ttg gat att tcc cgc	Val Val Val Val Leu Gly Asp Pro Val Asp Ala Leu Asp Ile Ser Arg					125					130					499
	120															
att ggt cag acc ctg gcg gat tac gat gcc aac att gac acc att cgt	Ile Gly Gln Thr Leu Ala Asp Tyr Asp Ala Asn Ile Asp Thr Ile Arg					140					145					547
	135															
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	150										165					
ccg gat gtc agc cct ggt ggt ggt gaa gcg atg cgt aag gcg ctt gct	Pro Asp Val Ser Pro Gly Gly Gly Glu Ala Met Arg Lys Ala Leu Ala					170					175					643
											180					
gct ctt acc tct gag ctg aat gtg gat att gcg att gag cgt tct ggt	Ala Leu Thr Ser Glu Leu Asn Val Asp Ile Ala Ile Glu Arg Ser Gly					185					190					691
											195					
ttg ctg cgt cgt tct aag cgt ctg gtg tgc ttc gat tgt gat tcc acg	Leu Leu Arg Arg Ser Lys Arg Leu Val Cys Phe Asp Cys Asp Ser Thr					200					205					739
											210					
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											225					
gaa gct gaa gtt gcg gca gtt act gag cgt gcg atg cgc ggt gag ctc	Glu Ala Glu Val Ala Ala Val Thr Glu Arg Ala Met Arg Gly Glu Leu					230					235					835
											240					245
gat ttc gag gag tct ctg cgt gag cgt gtg aag gcg ttg gct ggt ttg	Asp Phe Glu Glu Ser Leu Arg Glu Arg Val Lys Ala Leu Ala Gly Leu					250					255					883
											260					
gat gcg tcg gtg atc gat gag gtc gct gcc gct att gag ctg acc cct	Asp Ala Ser Val Ile Asp Glu Val Ala Ala Ala Ile Glu Leu Thr Pro					265					270					931
											275					
ggg gcg cgc acc acg atc cgt acg ctg aac cgc atg ggt tac cag acc	Gly Ala Arg Thr Thr Ile Arg Thr Leu Asn Arg Met Gly Tyr Gln Thr					280					285					979
											290					
gct gtt gtt tcc ggt ggt ttc atc cag gtg ttg gaa ggt ttg gct gag	Ala Val Val Ser Gly Gly Phe Ile Gln Val Leu Glu Gly Leu Ala Glu					295					300					1027
											305					
gag ttg gag ttg gat tat gtc cgc gcc aac act ttg gaa atc gtt gat	Glu Leu Glu Leu Asp Tyr Val Arg Ala Asn Thr Leu Glu Ile Val Asp					310					315					1075
											320					325

ggc aag ctg acc ggc aac gtc acc gga aag atc gtt gac cgc gct gcg 1123  
 Gly Lys Leu Thr Gly Asn Val Thr Gly Lys Ile Val Asp Arg Ala Ala  
 330 335 340  
 aag gct gag ttc ctc cgt gag ttc gct gcg gat tct ggc ctg aag atg 1171  
 Lys Ala Glu Phe Leu Arg Glu Phe Ala Ala Asp Ser Gly Leu Lys Met  
 345 350 355  
 tac cag act gtc gct gtc ggt gat ggc gct aat gac atc gat atg ctc 1219  
 Tyr Gln Thr Val Ala Val Gly Asp Gly Ala Asn Asp Ile Asp Met Leu  
 360 365 370  
 tcc gct gcg ggt ctg ggt gtt gct ttc aac gcg aag cct gcg ctg aag 1267  
 Ser Ala Ala Gly Leu Gly Val Ala Phe Asn Ala Lys Pro Ala Leu Lys  
 375 380 385  
 gag att gcg gat act tcc gtg aac cac cca ttc ctc gac gag gtt ttg 1315  
 Glu Ile Ala Asp Thr Ser Val Asn His Pro Phe Leu Asp Glu Val Leu  
 390 395 400 405  
 cac atc atg ggc att tcc cgc gac gag atc gat ctg gcg gat cag gaa 1363  
 His Ile Met Gly Ile Ser Arg Asp Glu Ile Asp Leu Ala Asp Gln Glu  
 410 415 420  
 gac ggc act ttc cac cgc gtt cca ttg acc aat gcc taaagattcg 1409  
 Asp Gly Thr Phe His Arg Val Pro Leu Thr Asn Ala  
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<210> 256  
 <211> 433  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 256  
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 Thr Val Ser Gly Lys Asp Arg Pro Gly Val Thr Ala Ala Phe Phe Arg  
 35 40 45  
 Val Leu Ser Ala Asn Gln Val Gln Val Leu Asp Val Glu Gln Ser Met  
 50 55 60  
 Phe Arg Gly Phe Leu Asn Leu Ala Ala Phe Val Gly Ile Ala Pro Glu  
 65 70 75 80  
 Arg Val Glu Thr Val Thr Th Gly Leu Thr Asp Thr Leu Lys Val His  
 85 90 95  
 Gly Gln Ser Val Val Val Glu Leu Gln Glu Thr Val Gln Ser Ser Arg  
 100 105 110  
 Pro Arg Ser Ser His Val Val Val Val Leu Gly Asp Pro Val Asp Ala  
 115 120 125

Leu Asp Ile Ser Arg Ile Gly Gln Thr Leu Ala Asp Tyr Asp Ala Asn  
 130 135 140  
 Ile Asp Thr Ile Arg Gly Ile Ser Asp Tyr Pro Val Thr Gly Leu Glu  
 145 150 155 160  
 Leu Lys Val Thr Val Pro Asp Val Ser Pro Gly Gly Gly Glu Ala Met  
 165 170 175  
 Arg Lys Ala Leu Ala Ala Leu Thr Ser Glu Leu Asn Val Asp Ile Ala  
 180 185 190  
 Ile Glu Arg Ser Gly Leu Leu Arg Arg Ser Lys Arg Leu Val Cys Phe  
 195 200 205  
 Asp Cys Asp Ser Thr Leu Ile Thr Gly Glu Val Ile Glu Met Leu Ala  
 210 215 220  
 Ala His Ala Gly Lys Glu Ala Glu Val Ala Ala Val Thr Glu Arg Ala  
 225 230 235 240  
 Met Arg Gly Glu Leu Asp Phe Glu Glu Ser Leu Arg Glu Arg Val Lys  
 245 250 255  
 Ala Leu Ala Gly Leu Asp Ala Ser Val Ile Asp Glu Val Ala Ala Ala  
 260 265 270  
 Ile Glu Leu Thr Pro Gly Ala Arg Thr Thr Ile Arg Thr Leu Asn Arg  
 275 280 285  
 Met Gly Tyr Gln Thr Ala Val Val Ser Gly Gly Phe Ile Gln Val Leu  
 290 295 300  
 Glu Gly Leu Ala Glu Glu Leu Glu Leu Asp Tyr Val Arg Ala Asn Thr  
 305 310 315 320  
 Leu Glu Ile Val Asp Gly Lys Leu Thr Gly Asn Val Thr Gly Lys Ile  
 325 330 335  
 Val Asp Arg Ala Ala Lys Ala Glu Phe Leu Arg Glu Phe Ala Ala Asp  
 340 345 350  
 Ser Gly Leu Lys Met Tyr Gln Thr Val Ala Val Gly Asp Gly Ala Asn  
 355 360 365  
 Asp Ile Asp Met Leu Ser Ala Ala Gly Leu Gly Val Ala Phe Asn Ala  
 370 375 380  
 Lys Pro Ala Leu Lys Glu Ile Ala Asp Thr Ser Val Asn His Pro Phe  
 385 390 395 400  
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 Leu Ala Asp Gln Glu Asp Gly Thr Phe His Arg Val Pro Leu Thr Asn  
 420 425 430

Ala

<400> 257																
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Met Ser Arg Ser Pro 5																
ctt act aaa ggt cta aat caa ctt gaa cac ctc gag tta gat aag tca 163																
Leu Thr Lys Gly Leu Asn Gln Leu Glu His Leu Glu Leu Asp Lys Ser 20																
cta act gcg tgg tgg tgg gca gaa gat gat cct ttg tac ctc gca ggt 211																
Leu Thr Ala Trp Ser Trp Ala Glu Asp Asp Pro Leu Tyr Leu Ala Gly 35																
gag aac tta aac ggc agt tac ctc att gtc gca gga cga gtg cgg gtc 259																
Glu Asn Leu Asn Gly Ser Tyr Leu Ile Val Ala Gly Arg Val Arg Val 50																
tct cgc gac acc atc gac ggg aaa gaa ctc acc gtt gat att gca acg 307																
Ser Arg Asp Thr Ile Asp Gly Lys Glu Leu Thr Val Asp Ile Ala Thr 65																
ccc ggc gat gtt att ggt gcg ata gat aca gaa cct cag ccg gca gta 355																
Pro Gly Asp Val Ile Gly Ala Ile Asp Thr Glu Pro Gln Pro Ala Val 85																
gat tcc gct tgg gca ata gaa acc acc tgt gcg ctg ttt ctt cca gca 403																
Asp Ser Ala Trp Ala Ile Glu Thr Thr Cys Ala Leu Phe Leu Pro Ala 100																
acc gcg ttg gca act gtg att gaa cag cat cca agt ttt gct ttg gcg 451																
Thr Ala Leu Ala Thr Val Ile Glu Gln His Pro Ser Phe Ala Leu Ala 115																
atg att cgg atg cag cag caa cgt ttg gct aca gcc aga gat cat gaa 499																
Met Ile Arg Met Gln Gln Gln Arg Leu Ala Thr Ala Arg Asp His Glu 130																
att aac ctg act acg acc aca gtt gag caa cga gta gct att gca gtg 547																
Ile Asn Leu Thr Thr Thr Val Glu Gln Arg Val Ala Ile Ala Val 145																
aga act ctg gga cga aaa atc ggg caa cga cga ccc gat gga atc ttg 595																
Arg Thr Leu Gly Arg Lys Ile Gly Gln Arg Arg Pro Asp Gly Ile Leu 165																
ctc att caa gtt cga atc cgg cgg gaa gat gtt gcg ggt tta gca ggc 643																
Leu Ile Gln Val Arg Ile Arg Arg Glu Asp Val Ala Gly Leu Ala Gly 180																

acc acc gtg gaa tct act tct aga gtt ttg gcg cga tta cgt aaa gaa 691  
 Thr Thr Val Glu Ser Thr Ser Arg Val Leu Ala Arg Leu Arg Lys Glu  
 185 190 195

ggg gtc att gat agc ggt agg gaa tgattgccgt ggtcgatgaa cgg 738  
 Gly Val Ile Asp Ser Gly Arg Glu  
 200 205

<210> 258

<211> 205

<212> PRT

<213> Corynebacterium glutamicum

<400> 258

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Glu Leu Asp Lys Ser Leu Thr Ala Trp Ser Trp Ala Glu Asp Asp Pro  
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Leu Tyr Leu Ala Gly Glu Asn Leu Asn Gly Ser Tyr Leu Ile Val Ala  
 35 40 45

Gly Arg Val Arg Val Ser Arg Asp Thr Ile Asp Gly Lys Glu Leu Thr  
 50 55 60

Val Asp Ile Ala Thr Pro Gly Asp Val Ile Gly Ala Ile Asp Thr Glu  
 65 70 75 80

Pro Gln Pro Ala Val Asp Ser Ala Trp Ala Ile Glu Thr Thr Cys Ala  
 85 90 95

Leu Phe Leu Pro Ala Thr Ala Leu Ala Thr Val Ile Glu Gln His Pro  
 100 105 110

Ser Phe Ala Leu Ala Met Ile Arg Met Gln Gln Gln Arg Leu Ala Thr  
 115 120 125

Ala Arg Asp His Glu Ile Asn Leu Thr Thr Thr Thr Val Glu Gln Arg  
 130 135 140

Val Ala Ile Ala Val Arg Thr Leu Gly Arg Lys Ile Gly Gln Arg Arg  
 145 150 155 160

Pro Asp Gly Ile Leu Leu Ile Gln Val Arg Ile Arg Arg Glu Asp Val  
 165 170 175

Ala Gly Leu Ala Gly Thr Thr Val Glu Ser Thr Ser Arg Val Leu Ala  
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Arg Leu Arg Lys Glu Gly Val Ile Asp Ser Gly Arg Glu  
 195 200 205

<210> 259

<211> 900

<212> DNA

<213> Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(877)

&lt;223&gt; RXN01349

&lt;400&gt; 259

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aattcacggtt ttctcgttac ccgaaaggaa ttgatcgatt atg gcg aca tca cgt 115
                                         Met Ala Thr Ser Arg
                                         1 5

cga gat gcc gaa aac ata gac cag gcc ggt agc gaa ttc att gaa tct 163
Arg Asp Ala Glu Asn Ile Asp Gln Ala Gly Ser Glu Phe Ile Glu Ser
                        10 15 20

gat tca gga cac acc gca acc cct gaa gag gta gta gcc acc gct ctg 211
Asp Ser Gly His Thr Ala Thr Pro Glu Glu Val Val Ala Thr Ala Leu
                        25 30 35

aca ttt ttt gca gag gat ggt ttt agc gaa acc aaa ttg gag aaa atc 259
Thr Phe Phe Ala Glu Asp Gly Phe Ser Glu Thr Lys Leu Glu Lys Ile
                        40 45 50

gcg aag gca tct ggc atg tcc aag cgc atg atc cac tat cac ttt ggc 307
Ala Lys Ala Ser Gly Met Ser Lys Arg Met Ile His Tyr His Phe Gly
                        55 60 65

gat aag aaa ggc ctg tac atc aag gct gtt tcc tac gcg ttg cga ttg 355
Asp Lys Lys Gly Leu Tyr Ile Lys Ala Val Ser Tyr Ala Leu Arg Leu
                        70 75 80 85

ctg cgc cca gag gct gaa gcg atg caa ctt gat tcc gcg gta cca gtt 403
Leu Arg Pro Glu Ala Glu Ala Met Gln Leu Asp Ser Ala Val Pro Val
                        90 95 100

gat ggt gtc cgc aaa atc gtc gag gct tta tat acc tgc atc acc aag 451
Asp Gly Val Arg Lys Ile Val Glu Ala Leu Tyr Thr Cys Ile Thr Lys
                        105 110 115

cac cca gaa gca gtg cgc ctg cta ttg atg gaa aac ctg cat agc caa 499
His Pro Glu Ala Val Arg Leu Leu Met Glu Asn Leu His Ser Gln
                        120 125 130

gac agc gtg gat tcc acc gcg gca tat tcc gat gaa tcc aat gtg ctg 547
Asp Ser Val Asp Ser Thr Ala Ala Tyr Ser Asp Glu Ser Asn Val Leu
                        135 140 145

ctc aac ctg gat aag ctg ctc atg ctt ggc cag gat gcc ggc gcc ttc 595
Leu Asn Leu Asp Lys Leu Leu Met Leu Gly Gln Asp Ala Gly Ala Phe
                        150 155 160 165

cgt cct gga atc tcc gca gaa gac gta ctg gtt ctt att agc tcc ctg 643
Arg Pro Gly Ile Ser Ala Glu Asp Val Leu Val Leu Ile Ser Ser Leu
                        170 175 180

gcc tac ttc cgc gta tcc aac aag gtc acg ttg aag aac ctc tac tcc 691
Ala Tyr Phe Arg Val Ser Asn Lys Val Thr Leu Lys Asn Leu Tyr Ser
                        185 190 195

ctt gat ttg gaa tca gag gcc aat att gaa ggc atg aag cgc atc gtc 739

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Leu Asp Leu Glu Ser Glu Ala Asn Ile Glu Gly Met Lys Arg Ile Val  
 200 205 210  
 gtt gac acg gtg ctg gca ttc ttg acc tca aat att caa aat tct ggc 787  
 Val Asp Thr Val Leu Ala Phe Leu Thr Ser Asn Ile Gln Asn Ser Gly  
 215 220 225  
 aac tcc agc tac ctg gtt gtt ggt ggc aag act gca gaa cca gaa act 835  
 Asn Ser Ser Tyr Leu Val Val Gly Gly Lys Thr Ala Glu Pro Glu Thr  
 230 235 240 245  
 gat gac agc gtc tac agc ttt gat acg gac gtg ttc gaa aac 877  
 Asp Asp Ser Val Tyr Ser Phe Asp Thr Asp Val Phe Glu Asn  
 250 255  
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<210> 260  
 <211> 259  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 260  
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 Glu Phe Ile Glu Ser Asp Ser Gly His Thr Ala Thr Pro Glu Glu Val  
 20 25 30  
 Val Ala Thr Ala Leu Thr Phe Phe Ala Glu Asp Gly Phe Ser Glu Thr  
 35 40 45  
 Lys Leu Glu Lys Ile Ala Lys Ala Ser Gly Met Ser Lys Arg Met Ile  
 50 55 60  
 His Tyr His Phe Gly Asp Lys Lys Gly Leu Tyr Ile Lys Ala Val Ser  
 65 70 75 80  
 Tyr Ala Leu Arg Leu Leu Arg Pro Glu Ala Glu Ala Met Gln Leu Asp  
 85 90 95  
 Ser Ala Val Pro Val Asp Gly Val Arg Lys Ile Val Glu Ala Leu Tyr  
 100 105 110  
 Thr Cys Ile Thr Lys His Pro Glu Ala Val Arg Leu Leu Leu Met Glu  
 115 120 125  
 Asn Leu His Ser Gln Asp Ser Val Asp Ser Thr Ala Ala Tyr Ser Asp  
 130 135 140  
 Glu Ser Asn Val Leu Leu Asn Leu Asp Lys Leu Leu Met Leu Gly Gln  
 145 150 155 160  
 Asp Ala Gly Ala Phe Arg Pro Gly Ile Ser Ala Glu Asp Val Leu Val  
 165 170 175  
 Leu Ile Ser Ser Leu Ala Tyr Phe Arg Val Ser Asn Lys Val Thr Leu  
 180 185 190  
 Lys Asn Leu Tyr Ser Leu Asp Leu Glu Ser Glu Ala Asn Ile Glu Gly

195	200	205
Met Lys Arg Ile Val Val Asp Thr Val Leu Ala Phe Leu Thr Ser Asn		
210	215	220
Ile Gln Asn Ser Gly Asn Ser Ser Tyr Leu Val Val Gly Gly Lys Thr		
225	230	235 240
Ala Glu Pro Glu Thr Asp Asp Ser Val Tyr Ser Phe Asp Thr Asp Val		
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Phe Glu Asn		

<210> 261  
 <211> 792  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(769)  
 <223> RXN00467

<400> 261  
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 Met His Ile Ser Asp  
 1 5  
 ctt ccc gat agg tcc cag gac tac ctg aag aca atc tgg gac atc aca 163  
 Leu Pro Asp Arg Ser Gln Asp Tyr Leu Lys Thr Ile Trp Asp Ile Thr  
 10 15 20  
 gaa ctc ctt gat gat caa cca gca gca ctc ggc gat atc gcc gaa aaa 211  
 Glu Leu Leu Asp Asp Gln Pro Ala Ala Leu Gly Asp Ile Ala Glu Lys  
 25 30 35  
 atg aac cag aaa act cct acc gcc tcc gaa gca atc aaa aag ctg gcg 259  
 Met Asn Gln Lys Thr Pro Thr Ala Ser Glu Ala Ile Lys Lys Leu Ala  
 40 45 50  
 gca agg ggc ctg gtc aac cat gaa aaa tat gct ggt gtc acc ctc act 307  
 Ala Arg Gly Leu Val Asn His Glu Lys Tyr Ala Gly Val Thr Leu Thr  
 55 60 65  
 gaa cag ggc aaa acg cta gcc atc gac atg gtg cga cgc cac cgc ctg 355  
 Glu Gln Gly Lys Thr Leu Ala Ile Asp Met Val Arg Arg His Arg Leu  
 70 75 80 85  
 ctg gaa acc ttc ctc cac gat gtt ttg gga tac acc tgg gac gaa gtc 403  
 Leu Glu Thr Phe Leu His Asp Val Leu Gly Tyr Thr Trp Asp Glu Val  
 90 95 100  
 cac gcc gat gca gac ctg ttg gaa cat gca gcc tct gat cag ctc atc 451  
 His Ala Asp Ala Asp Leu Leu Glu His Ala Ala Ser Asp Gln Leu Ile  
 105 110 115  
 gaa cgc atc gat gct cac ttg ggt cgt cca cgc aaa gat ccc cac ggc 499

Glu Arg Ile Asp Ala His Leu Gly Arg Pro Arg Lys Asp Pro His Gly  
 120 125 130  
 gat ccc ata cca act gcc gaa ggc gtt att gaa gag tct ccc cga acc 547  
 Asp Pro Ile Pro Thr Ala Glu Gly Val Ile Glu Glu Ser Pro Arg Thr  
 135 140 145  
 acc ctc gag gca gtt cag cca ggg gag act gtc acg att tcc agg gtc 595  
 Thr Leu Glu Ala Val Gln Pro Gly Glu Thr Val Thr Ile Ser Arg Val  
 150 155 160 165  
 aaa gac att gat cct gaa ttg ctg cgc tac ctc gcg caa tac aac gtc 643  
 Lys Asp Ile Asp Pro Glu Leu Leu Arg Tyr Leu Ala Gln Tyr Asn Val  
 170 175 180  
 tca cca gga tgc cgg atc acc gtt gcg tcc ggc cca cta gct ggc atg 691  
 Ser Pro Gly Cys Arg Ile Thr Val Ala Ser Gly Pro Leu Ala Gly Met  
 185 190 195  
 gtg cat gtc gtt gta gaa ggc acc gac acc agc ttc ccc ctg gcc gaa 739  
 Val His Val Val Val Glu Gly Thr Asp Thr Ser Phe Pro Leu Ala Glu  
 200 205 210  
 acg caa ctg cca tta att aca gtg cag gac taagcagatt catcataatg gtg 792  
 Thr Gln Leu Pro Leu Ile Thr Val Gln Asp  
 215 220

&lt;210&gt; 262

&lt;211&gt; 223

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 262

Met His Ile Ser Asp Leu Pro Asp Arg Ser Gln Asp Tyr Leu Lys Thr  
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 Ile Trp Asp Ile Thr Glu Leu Leu Asp Asp Gln Pro Ala Ala Leu Gly  
 20 25 30  
 Asp Ile Ala Glu Lys Met Asn Gln Lys Thr Pro Thr Ala Ser Glu Ala  
 35 40 45  
 Ile Lys Lys Leu Ala Ala Arg Gly Leu Val Asn His Glu Lys Tyr Ala  
 50 55 60  
 Gly Val Thr Leu Thr Glu Gln Gly Lys Thr Leu Ala Ile Asp Met Val  
 65 70 75 80  
 Arg Arg His Arg Leu Leu Glu Thr Phe Leu His Asp Val Leu Gly Tyr  
 85 90 95  
 Thr Trp Asp Glu Val His Ala Asp Ala Asp Leu Leu Glu His Ala Ala  
 100 105 110  
 Ser Asp Gln Leu Ile Glu Arg Ile Asp Ala His Leu Gly Arg Pro Arg  
 115 120 125  
 Lys Asp Pro His Gly Asp Pro Ile Pro Thr Ala Glu Gly Val Ile Glu  
 130 135 140

Glu Ser Pro Arg Thr Thr Leu Glu Ala Val Gln Pro Gly Glu Thr Val  
 145 150 155 160  
 Thr Ile Ser Arg Val Lys Asp Ile Asp Pro Glu Leu Leu Arg Tyr Leu  
 165 170 175  
 Ala Gln Tyr Asn Val Ser Pro Gly Cys Arg Ile Thr Val Ala Ser Gly  
 180 185 190  
 Pro Leu Ala Gly Met Val His Val Val Val Glu Gly Thr Asp Thr Ser  
 195 200 205  
 Phe Pro Leu Ala Glu Thr Gln Leu Pro Leu Ile Thr Val Gln Asp  
 210 215 220

&lt;210&gt; 263

&lt;211&gt; 861

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(838)

&lt;223&gt; RXN02954

&lt;400&gt; 263

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aagcttcata tcacttttcc acagcctgaa agaacatact atg tcc gca gct tta 115  
 Met Ser Ala Ala Leu  
 1 5

cct cac aca gca gca gat ccc gta cac acc acc cca gcg aaa ccg ctg 163  
 Pro His Thr Ala Ala Asp Pro Val His Thr Thr Pro Ala Lys Pro Leu  
 10 15 20

ctc gat cat gtc tta gat tca cta gga cgc agc atc atc agt ggt gaa 211  
 Leu Asp His Val Leu Asp Ser Leu Gly Arg Ser Ile Ile Ser Gly Glu  
 25 30 35

atg gaa gcc ggt agc aca ttc aaa ctg caa gac atc ggt gaa aaa ttc 259  
 Met Glu Ala Gly Ser Thr Phe Lys Leu Gln Asp Ile Gly Glu Lys Phe  
 40 45 50

ggt atc tcc cgc acc gtc gcc aga gaa gcc atg cgt gcc tta gag caa 307  
 Gly Ile Ser Arg Thr Val Ala Arg Glu Ala Met Arg Ala Leu Glu Gln  
 55 60 65

ctt ggg ttg gtg gcc tca tcg aga cga att ggt att aca gtg ctc tcg 355  
 Leu Gly Leu Val Ala Ser Ser Arg Arg Ile Gly Ile Thr Val Leu Ser  
 70 75 80 85

cac gag cac tgg gct gtc ttt gac aaa gcc att att cgc tgg cgc ctc 403  
 His Glu His Trp Ala Val Phe Asp Lys Ala Ile Ile Arg Trp Arg Leu  
 90 95 100

gaa gat gag cgt caa cgt gaa cag caa ctg cag tca ctc acc gaa ctt 451  
 Glu Asp Glu Arg Gln Arg Glu Gln Leu Gln Ser Leu Thr Glu Leu  
 105 110 115

cgt att gcc att gaa cca att gct gca cgc agt gtt gcc ctt cat gca 499  
 Arg Ile Ala Ile Glu Pro Ile Ala Ala Arg Ser Val Ala Leu His Ala  
 120 125 130

tcg agc gca gag att gct atc atc ggt gat ctt gct gca cga atg cgt 547  
 Ser Ser Ala Glu Ile Ala Ile Ile Gly Asp Leu Ala Ala Arg Met Arg  
 135 140 145

aac ctc ggt gaa gct ggt cgt ggc gca tca caa gaa ttc cta gac gca 595  
 Asn Leu Gly Glu Ala Gly Arg Gly Ala Ser Gln Glu Phe Leu Asp Ala  
 150 155 160 165

gat gtg aaa ttt cat gag ctt att ttg cag tat tgc cat aat gag atg 643  
 Asp Val Lys Phe His Glu Leu Ile Leu Gln Tyr Cys His Asn Glu Met  
 170 175 180

ttc gct gcc atg gca cca ccc ata aaa gct gta cta gtc ggg cgc acc 691  
 Phe Ala Ala Met Ala Pro Pro Ile Lys Ala Val Leu Val Gly Arg Thr  
 185 190 195

aca ctt ggc ctt caa ccc gat cga cct gcc gaa gaa gtc ttg gac aat 739  
 Thr Leu Gly Leu Gln Pro Asp Arg Pro Ala Glu Glu Val Leu Asp Asn  
 200 205 210

cat gat gct ctc gca cac gca cta agt gtt cgt aat gca gac ctc gcc 787  
 His Asp Ala Leu Ala His Ala Leu Ser Val Arg Asn Ala Asp Leu Ala  
 215 220 225

gaa aaa gca tcc agg agc att ctg aat gag gtg cgc gac gca ctg acc 835  
 Glu Lys Ala Ser Arg Ser Ile Leu Asn Glu Val Arg Asp Ala Leu Thr  
 230 235 240 245

tcg taattgccac taaacgagtc act 861  
 Ser

<210> 264  
 <211> 246  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 264  
 Met Ser Ala Ala Leu Pro His Thr Ala Ala Asp Pro Val His Thr Thr  
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Pro Ala Lys Pro Leu Leu Asp His Val Leu Asp Ser Leu Gly Arg Ser  
 20 25 30

Ile Ile Ser Gly Glu Met Glu Ala Gly Ser Thr Phe Lys Leu Gln Asp  
 35 40 45

Ile Gly Glu Lys Phe Gly Ile Ser Arg Thr Val Ala Arg Glu Ala Met  
 50 55 60

Arg Ala Leu Glu Gln Leu Gly Leu Val Ala Ser Ser Arg Arg Ile Gly  
 65 70 75 80

Ile Thr Val Leu Ser His Glu His Trp Ala Val Phe Asp Lys Ala Ile  
 85 90 95

Ile Arg Trp Arg Leu Glu Asp Glu Arg Gln Arg Glu Gln Gln Leu Gln  
 100 105 110  
 Ser Leu Thr Glu Leu Arg Ile Ala Ile Glu Pro Ile Ala Ala Arg Ser  
 115 120 125  
 Val Ala Leu His Ala Ser Ser Ala Glu Ile Ala Ile Ile Gly Asp Leu  
 130 135 140  
 Ala Ala Arg Met Arg Asn Leu Gly Glu Ala Gly Arg Gly Ala Ser Gln  
 145 150 155 160  
 Glu Phe Leu Asp Ala Asp Val Lys Phe His Glu Leu Ile Leu Gln Tyr  
 165 170 175  
 Cys His Asn Glu Met Phe Ala Ala Met Ala Pro Pro Ile Lys Ala Val  
 180 185 190  
 Leu Val Gly Arg Thr Thr Leu Gly Leu Gln Pro Asp Arg Pro Ala Glu  
 195 200 205  
 Glu Val Leu Asp Asn His Asp Ala Leu Ala His Ala Leu Ser Val Arg  
 210 215 220  
 Asn Ala Asp Leu Ala Glu Lys Ala Ser Arg Ser Ile Leu Asn Glu Val  
 225 230 235 240  
 Arg Asp Ala Leu Thr Ser  
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<210> 265  
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 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(457)  
 <223> RXN03023

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 Val Pro Leu Tyr Lys  
 1 5  
 cag atc gct tct ttg att gag gac tcc atc gtt gac gga acc ttg agc 163  
 Gln Ile Ala Ser Leu Ile Glu Asp Ser Ile Val Asp Gly Thr Leu Ser  
 10 15 20  
 att gat caa cgc gtg cct tct act aat gaa cta gcc gcg ttc cat cgc 211  
 Ile Asp Gln Arg Val Pro Ser Thr Asn Glu Leu Ala Ala Phe His Arg  
 25 30 35  
 att aat ccc gcc acc gca cgc aac ggc ctg acc ctc ctt gtc gaa gcc 259  
 Ile Asn Pro Ala Thr Ala Arg Asn Gly Leu Thr Leu Leu Val Glu Ala  
 40 45 50

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ggc atc ctc tat aag aag cgt ggc att ggc atg ttc gtc agc gcc cag 307
Gly Ile Leu Tyr Lys Lys Arg Gly Ile Gly Met Phe Val Ser Ala Gln
   55                                60                                65

gcc cca gca ctc atc cga gag cgg cga gat gcc gcc ttc gcg gct act 355
Ala Pro Ala Leu Ile Arg Glu Arg Arg Asp Ala Ala Phe Ala Ala Thr
   70                                75                                80                                85

tat gta gca ccg ctt atc gac gaa tcc atc cac ctt ggt ttc act cgt 403
Tyr Val Ala Pro Leu Ile Asp Glu Ser Ile His Leu Gly Phe Thr Arg
                   90                                95                                100

gcg cgc att cac gcc ctt tta gac cag gtc gct gaa agt agg gcc ctg 451
Ala Arg Ile His Ala Leu Leu Asp Gln Val Ala Glu Ser Arg Gly Leu
                   105                                110                                115

tac aag tagcgcttaa accctcttga cct 480
Tyr Lys

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<210> 266
<211> 119
<212> PRT
<213> Corynebacterium glutamicum

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<400> 266
Val Pro Leu Tyr Lys Gln Ile Ala Ser Leu Ile Glu Asp Ser Ile Val
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Asp Gly Thr Leu Ser Ile Asp Gln Arg Val Pro Ser Thr Asn Glu Leu
   20                                25                                30

Ala Ala Phe His Arg Ile Asn Pro Ala Thr Ala Arg Asn Gly Leu Thr
   35                                40                                45

Leu Leu Val Glu Ala Gly Ile Leu Tyr Lys Lys Arg Gly Ile Gly Met
   50                                55                                60

Phe Val Ser Ala Gln Ala Pro Ala Leu Ile Arg Glu Arg Arg Asp Ala
   65                                70                                75                                80

Ala Phe Ala Ala Thr Tyr Val Ala Pro Leu Ile Asp Glu Ser Ile His
   85                                90                                95

Leu Gly Phe Thr Arg Ala Arg Ile His Ala Leu Leu Asp Gln Val Ala
  100                                105                                110

Glu Ser Arg Gly Leu Tyr Lys
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<210> 267
<211> 843
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(820)
<223> RXN03127

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&lt;400&gt; 267

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gatatgatca gaaccatctc cagattagga agtgaacaca atg gaa agc tcc aaa 115
                                         Met Glu Ser Ser Lys
                                         1      5

aag act tcg cga tca agg tcc act act caa gaa gca gtg cgc gac att 163
Lys Thr Ser Arg Ser Arg Ser Thr Thr Gln Glu Ala Val Arg Asp Ile
              10              15              20

aaa aaa tac att cgg gac aac cgg ctg cgt acg gga gac ctt ctt cct 211
Lys Lys Tyr Ile Arg Asp Asn Arg Leu Arg Thr Gly Asp Leu Leu Pro
              25              30              35

tcc gaa gcg ttc tta tgt gag gaa ttg ggt tgt tcc cgt tct gcg atc 259
Ser Glu Ala Phe Leu Cys Glu Glu Leu Gly Cys Ser Arg Ser Ala Ile
              40              45              50

agg gag gcg atc cgc gcg ctc gtg acc ttg gac atc gtc gag gtt cgc 307
Arg Glu Ala Ile Arg Ala Leu Val Thr Leu Asp Ile Val Glu Val Arg
              55              60              65

cac ggc tac ggc act ttc gtg tcc agg atg tcc ctc gag ccc ctg atc 355
His Gly Tyr Gly Thr Phe Val Ser Arg Met Ser Leu Glu Pro Leu Ile
              70              75              80              85

aac ggg atg gtg ttc cgc acg gtg ttg gac aat gac acc tcg gtg gaa 403
Asn Gly Met Val Phe Arg Thr Val Leu Asp Asn Asp Thr Ser Val Glu
              90              95              100

aac ctt ttc tac gtg gtg gat acc cgc gaa atc ctt gac ctt tca ctt 451
Asn Leu Phe Tyr Val Val Asp Thr Arg Glu Ile Leu Asp Leu Ser Leu
              105              110              115

ggc gaa gag ctg atc gag gtg ttc acc gac gat gac cgc gag cta ctc 499
Gly Glu Glu Leu Ile Glu Val Phe Thr Asp Asp Asp Arg Glu Leu Leu
              120              125              130

ctt gat ctg gtg gac aag atg cgc gag cac aac gat cag ggc gaa tcc 547
Leu Asp Leu Val Asp Lys Met Arg Glu His Asn Asp Gln Gly Glu Ser
              135              140              145

ttt gtg gtg gag gat caa aaa ttc cac cga gca ctc cta gcg cga acg 595
Phe Val Val Glu Asp Gln Lys Phe His Arg Ala Leu Leu Ala Arg Thr
              150              155              160              165

aaa aac ccg ctg att aga gag ctc aac gat gcg ttt tgg cag atc caa 643
Lys Asn Pro Leu Ile Arg Glu Leu Asn Asp Ala Phe Trp Gln Ile Gln
              170              175              180

acc gag gcg cag ccc atg ctc aat ctg gct atg ccc gca gac atc gac 691
Thr Glu Ala Gln Pro Met Leu Asn Leu Ala Met Pro Ala Asp Ile Asp
              185              190              195

gaa acc atc aaa gct cac agc gac atc gtc gaa gcg ctc tcc agc ggc 739
Glu Thr Ile Lys Ala His Ser Asp Ile Val Glu Ala Leu Ser Ser Gly
              200              205              210

aac atc gac gat tat cgc agc gcc gtg ctc gct cac tac gcg ccg ttt 787

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Asn Ile Asp Asp Tyr Arg Ser Ala Val Leu Ala His Tyr Ala Pro Phe  
 215 220 225

cgc cgc atg att tcc aac atg ctc gat gcg cac tagcctcatt gcgcgcgggt 840  
 Arg Arg Met Ile Ser Asn Met Leu Asp Ala His  
 230 235 240

tgt 843

<210> 268

<211> 240

<212> PRT

<213> Corynebacterium glutamicum

<400> 268

Met Glu Ser Ser Lys Lys Thr Ser Arg Ser Arg Ser Thr Thr Gln Glu  
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Ala Val Arg Asp Ile Lys Lys Tyr Ile Arg Asp Asn Arg Leu Arg Thr  
 20 25 30

Gly Asp Leu Leu Pro Ser Glu Ala Phe Leu Cys Glu Glu Leu Gly Cys  
 35 40 45

Ser Arg Ser Ala Ile Arg Glu Ala Ile Arg Ala Leu Val Thr Leu Asp  
 50 55 60

Ile Val Glu Val Arg His Gly Tyr Gly Thr Phe Val Ser Arg Met Ser  
 65 70 75 80

Leu Glu Pro Leu Ile Asn Gly Met Val Phe Arg Thr Val Leu Asp Asn  
 85 90 95

Asp Thr Ser Val Glu Asn Leu Phe Tyr Val Val Asp Thr Arg Glu Ile  
 100 105 110

Leu Asp Leu Ser Leu Gly Glu Glu Leu Ile Glu Val Phe Thr Asp Asp  
 115 120 125

Asp Arg Glu Leu Leu Leu Asp Leu Val Asp Lys Met Arg Glu His Asn  
 130 135 140

Asp Gln Gly Glu Ser Phe Val Val Glu Asp Gln Lys Phe His Arg Ala  
 145 150 155 160

Leu Leu Ala Arg Thr Lys Asn Pro Leu Ile Arg Glu Leu Asn Asp Ala  
 165 170 175

Phe Trp Gln Ile Gln Thr Glu Ala Gln Pro Met Leu Asn Leu Ala Met  
 180 185 190

Pro Ala Asp Ile Asp Glu Thr Ile Lys Ala His Ser Asp Ile Val Glu  
 195 200 205

Ala Leu Ser Ser Gly Asn Ile Asp Asp Tyr Arg Ser Ala Val Leu Ala  
 210 215 220

His Tyr Ala Pro Phe Arg Arg Met Ile Ser Asn Met Leu Asp Ala His  
 225 230 235 240

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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <223> RXN03155

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 Gly Tyr Pro Pro Pro Thr Ala Ser Lys Asp Ala Ala Gly Gly Leu  
 1 5 10 15

cca caa ctg atc aga gag ctt ctc gac gcg acc ccc atc gat cat tgg 96  
 Pro Gln Leu Ile Arg Glu Leu Leu Asp Ala Thr Pro Ile Asp His Trp  
 20 25 30

tcc aac gat cgg cct act ctc acg ctg cca gag cat tgg gtg aca gac 144  
 Ser Asn Asp Arg Pro Thr Leu Thr Leu Pro Glu His Trp Val Thr Asp  
 35 40 45

atc gac att aag aac cct gtg ctt cgg gaa gtc gcc tcc cat ccc ttc 192  
 Ile Asp Ile Lys Asn Pro Val Leu Arg Glu Val Ala Ser His Pro Phe  
 50 55 60

ttc gat ggc tgc ccg atc gga gat tta gat gcc gat gcc ttt gtg gag 240  
 Phe Asp Gly Cys Pro Ile Gly Asp Leu Asp Ala Asp Ala Phe Val Glu  
 65 70 75 80

gat ggc acc ctc att cac gaa aac ggg act tta aga ttc cgc agc cct 288  
 Asp Gly Thr Leu Ile His Glu Asn Gly Thr Leu Arg Phe Arg Ser Pro  
 85 90 95

gag gaa cgc acc ttg gtt cgg gct tct act ccc cca tcg atg gca aga 336  
 Glu Glu Arg Thr Leu Val Arg Ala Ser Thr Pro Pro Ser Met Ala Arg  
 100 105 110

agc ccg cgg gag tgg gaa tcg acg gag gga ggc gtc gat aag cta att 384  
 Ser Pro Arg Glu Trp Glu Ser Thr Glu Gly Gly Val Asp Lys Leu Ile  
 115 120 125

gcc gca gga aac ctg ccc ctg gcc cga ctg cat gta gag gaa cta ccc 432  
 Ala Ala Gly Asn Leu Pro Leu Ala Arg Leu His Val Glu Glu Leu Pro  
 130 135 140

cgt gcc gat gag cag cgc gca ttt ttg gcg ctg tac ggc ggg cag tcg 480  
 Arg Ala Asp Glu Gln Arg Ala Phe Leu Ala Leu Tyr Gly Gly Gln Ser  
 145 150 155 160

ttt gag gcg gcc tcg gcg tcg ccg ttt tat gcg ctg gcc acc tgg aat 528  
 Phe Glu Ala Ala Ser Ala Ser Pro Phe Tyr Ala Leu Ala Thr Trp Asn  
 165 170 175

ccg gag gcg ttg cgg ggc gat ccg acc ttc gat atg ttc gcc gat gcg 576  
 Pro Glu Ala Leu Arg Gly Asp Pro Thr Phe Asp Met Phe Ala Asp Ala

180						185						190						
cta	gac	act	ggg	cat	tac	agg	gaa	gtc	ccg	cgt	ccg	gat	gcc	cct	gaa	624		
Leu	Asp	Thr	Gly	His	Tyr	Arg	Glu	Val	Pro	Arg	Pro	Asp	Ala	Pro	Glu			
		195					200					205						
gaa	agc	cag	atc	cac	gat	ttc	atc	agt	ggc	tgg	ctg	gcg	ttg	gtt	tac	672		
Glu	Ser	Gln	Ile	His	Asp	Phe	Ile	Ser	Gly	Trp	Leu	Ala	Leu	Val	Tyr			
	210					215					220							
gat	gat	ccc	ctc	acc	gcc	cgc	cgt	ctg	ctc	tcc	agt	agg	ggc	ccc	tcc	720		
Asp	Asp	Pro	Leu	Thr	Ala	Arg	Arg	Leu	Leu	Ser	Ser	Arg	Gly	Pro	Ser			
225					230					235					240			
gat	ttg	gtg	gga	ctg	tgg	cag	tcg	gcg	ttt	ttg	gcg	cga	gcg	cac	tac	768		
Asp	Leu	Val	Gly	Leu	Trp	Gln	Ser	Ala	Phe	Leu	Ala	Arg	Ala	His	Tyr			
				245					250					255				
gtg	ctg	gga	gaa	ttc	caa	gaa	gcc	tcc	gcc	gtt	gtc	gaa	cgc	ggc	cta	816		
Val	Leu	Gly	Glu	Phe	Gln	Glu	Ala	Ser	Ala	Val	Val	Glu	Arg	Gly	Leu			
			260					265					270					
gcc	acc	ggc	gac	cgc	acc	gga	gcc	tcc	cta	ctc	gaa	ccc	gtg	cac	ctg	864		
Ala	Thr	Gly	Asp	Arg	Thr	Gly	Ala	Ser	Leu	Leu	Glu	Pro	Val	His	Leu			
		275					280					285						
tgg	acc	ggc	gcc	caa	gtc	gca	gcc	atg	act	ggg	cgc	acc	gaa	ttg	gcc	912		
Trp	Thr	Gly	Ala	Gln	Val	Ala	Ala	Met	Thr	Gly	Arg	Thr	Glu	Leu	Ala			
	290					295					300							
aac	cac	tat	tta	cag	cgc	ctg	acc	gtg	ccc	gac	gat	gcg	ttc	ctc	atc	960		
Asn	His	Tyr	Leu	Gln	Arg	Leu	Thr	Val	Pro	Asp	Asp	Ala	Phe	Leu	Ile			
305					310					315					320			
caa	aaa	ctc	agc	gca	tcc	atg	ggc	aaa	ttg	atc	acc	gca	tcc	atg	acc	1008		
Gln	Lys	Leu	Ser	Ala	Ser	Met	Gly	Lys	Leu	Ile	Thr	Ala	Ser	Met	Thr			
				325					330					335				
tca	gac	acc	cgc	gca	gca	acc	ttg	gcc	ggc	gac	cgc	atg	gcg	tcg	gtc	1056		
Ser	Asp	Thr	Arg	Ala	Ala	Thr	Leu	Ala	Gly	Asp	Arg	Met	Ala	Ser	Val			
			340					345					350					
gta	tac	acc	acc	aat	acc	cag	cag	ccc	gga	ttt	tgg	gcc	tgg	gaa	gac	1104		
Val	Tyr	Thr	Thr	Asn	Thr	Gln	Gln	Pro	Gly	Phe	Trp	Ala	Trp	Glu	Asp			
		355					360					365						
atg	tat	gcg	atc	tca	ttg	atc	cga	acg	gga	cgc	atc	gac	gcc	gca	gcc	1152		
Met	Tyr	Ala	Ile	Ser	Leu	Ile	Arg	Thr	Gly	Arg	Ile	Asp	Ala	Ala	Ala			
	370					375					380							
gcc	gtc	atg	gat	ggc	atc	cct	gac	tcc	acc	atc	ccc	tcg	ctg	cgt	gcc	1200		
Ala	Val	Met	Asp	Gly	Ile	Pro	Asp	Ser	Thr	Ile	Pro	Ser	Leu	Arg	Ala			
385					390					395					400			
cga	aat	ttg	gtg	ccc	caa	gca	aac	atc	gaa	atc	caa	cga	ggc	tcc	aca	1248		
Arg	Asn	Leu	Val	Pro	Gln	Ala	Asn	Ile	Glu	Ile	Gln	Arg	Gly	Ser	Thr			
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gca	cga	ggc	gta	aaa	atg	ctc	tcc	gaa	gcc	gtc	gac	ctc	att	tcc	tcc	1296		
Ala	Arg	Gly	Val	Lys	Met	Leu	Ser	Glu	Ala	Val	Asp	Leu	Ile	Ser	Ser			
			420					425					430					

gtc aac atg cca gca tat gaa gcc cgc atc ctc ttc gaa tac ggg ctg 1344  
 Val Asn Met Pro Ala Tyr Glu Ala Arg Ile Leu Phe Glu Tyr Gly Leu  
 435 440 445  
 gtt cta cga cgc atg ggc agg cgc agc caa gca gcc gaa atg ttc acc 1392  
 Val Leu Arg Arg Met Gly Arg Arg Ser Gln Ala Ala Glu Met Phe Thr  
 450 455 460  
 cac gcc gaa gaa gtc ttc acc gcc atg ggt gcg gtc act ctg gct gcc 1440  
 His Ala Glu Glu Val Phe Thr Ala Met Gly Ala Val Thr Leu Ala Ala  
 465 470 475 480  
 cgc tgc cac ggc gaa cga cga gtc gca ggc gtt ggg cca cgc aga tca 1488  
 Arg Cys His Gly Glu Arg Arg Val Ala Gly Val Gly Pro Arg Arg Ser  
 485 490 495  
 gcg cag gga ctc acc cct caa gag gaa caa atc act gcg ctg gtt gtc 1536  
 Ala Gln Gly Leu Thr Pro Gln Glu Glu Gln Ile Thr Ala Leu Val Val  
 500 505 510  
 gac ggc tgc tcc aac caa gaa gtc gcc cgt gag ctt tcc ctc tcc gcc 1584  
 Asp Gly Cys Ser Asn Gln Glu Val Ala Arg Glu Leu Ser Leu Ser Ala  
 515 520 525  
 aaa acg gtg gaa tat cac ctc acg agg gtg tac aaa aag ctc ggg gtg 1632  
 Lys Thr Val Glu Tyr His Leu Thr Arg Val Tyr Lys Lys Leu Gly Val  
 530 535 540  
 agc tcc cgt gga gag ctt cga gaa tta ctg aag gtc tgacacagcg 1678  
 Ser Ser Arg Gly Glu Leu Arg Glu Leu Leu Lys Val  
 545 550 555  
 ttgttcagca gct 1691

&lt;210&gt; 270

&lt;211&gt; 556

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 270

Gly Tyr Pro Pro Pro Pro Thr Ala Ser Lys Asp Ala Ala Gly Gly Leu  
 1 5 10 15  
 Pro Gln Leu Ile Arg Glu Leu Leu Asp Ala Thr Pro Ile Asp His Trp  
 20 25 30  
 Ser Asn Asp Arg Pro Thr Leu Thr Leu Pro Glu His Trp Val Thr Asp  
 35 40 45  
 Ile Asp Ile Lys Asn Pro Val Leu Arg Glu Val Ala Ser His Pro Phe  
 50 55 60  
 Phe Asp Gly Cys Pro Ile Gly Asp Leu Asp Ala Asp Ala Phe Val Glu  
 65 70 75 80  
 Asp Gly Thr Leu Ile His Glu Asn Gly Thr Leu Arg Phe Arg Ser Pro  
 85 90 95  
 Glu Glu Arg Thr Leu Val Arg Ala Ser Thr Pro Pro Ser Met Ala Arg

100					105					110					
Ser	Pro	Arg	Glu	Trp	Glu	Ser	Thr	Glu	Gly	Gly	Val	Asp	Lys	Leu	Ile
		115					120					125			
Ala	Ala	Gly	Asn	Leu	Pro	Leu	Ala	Arg	Leu	His	Val	Glu	Glu	Leu	Pro
		130				135					140				
Arg	Ala	Asp	Glu	Gln	Arg	Ala	Phe	Leu	Ala	Leu	Tyr	Gly	Gly	Gln	Ser
145					150					155					160
Phe	Glu	Ala	Ala	Ser	Ala	Ser	Pro	Phe	Tyr	Ala	Leu	Ala	Thr	Trp	Asn
				165					170					175	
Pro	Glu	Ala	Leu	Arg	Gly	Asp	Pro	Thr	Phe	Asp	Met	Phe	Ala	Asp	Ala
			180					185					190		
Leu	Asp	Thr	Gly	His	Tyr	Arg	Glu	Val	Pro	Arg	Pro	Asp	Ala	Pro	Glu
		195					200					205			
Glu	Ser	Gln	Ile	His	Asp	Phe	Ile	Ser	Gly	Trp	Leu	Ala	Leu	Val	Tyr
		210					215				220				
Asp	Asp	Pro	Leu	Thr	Ala	Arg	Arg	Leu	Leu	Ser	Ser	Arg	Gly	Pro	Ser
225					230					235					240
Asp	Leu	Val	Gly	Leu	Trp	Gln	Ser	Ala	Phe	Leu	Ala	Arg	Ala	His	Tyr
				245					250					255	
Val	Leu	Gly	Glu	Phe	Gln	Glu	Ala	Ser	Ala	Val	Val	Glu	Arg	Gly	Leu
			260					265					270		
Ala	Thr	Gly	Asp	Arg	Thr	Gly	Ala	Ser	Leu	Leu	Glu	Pro	Val	His	Leu
		275					280					285			
Trp	Thr	Gly	Ala	Gln	Val	Ala	Ala	Met	Thr	Gly	Arg	Thr	Glu	Leu	Ala
		290				295					300				
Asn	His	Tyr	Leu	Gln	Arg	Leu	Thr	Val	Pro	Asp	Asp	Ala	Phe	Leu	Ile
305					310					315					320
Gln	Lys	Leu	Ser	Ala	Ser	Met	Gly	Lys	Leu	Ile	Thr	Ala	Ser	Met	Thr
				325					330					335	
Ser	Asp	Thr	Arg	Ala	Ala	Thr	Leu	Ala	Gly	Asp	Arg	Met	Ala	Ser	Val
			340				345						350		
Val	Tyr	Thr	Thr	Asn	Thr	Gln	Gln	Pro	Gly	Phe	Trp	Ala	Trp	Glu	Asp
			355				360					365			
Met	Tyr	Ala	Ile	Ser	Leu	Ile	Arg	Thr	Gly	Arg	Ile	Asp	Ala	Ala	Ala
		370				375					380				
Ala	Val	Met	Asp	Gly	Ile	Pro	Asp	Ser	Thr	Ile	Pro	Ser	Leu	Arg	Ala
385					390					395					400
Arg	Asn	Leu	Val	Pro	Gln	Ala	Asn	Ile	Glu	Ile	Gln	Arg	Gly	Ser	Thr
				405					410					415	
Ala	Arg	Gly	Val	Lys	Met	Leu	Ser	Glu	Ala	Val	Asp	Leu	Ile	Ser	Ser
			420					425					430		

Val Asn Met Pro Ala Tyr Glu Ala Arg Ile Leu Phe Glu Tyr Gly Leu  
 435 440 445

Val Leu Arg Arg Met Gly Arg Arg Ser Gln Ala Ala Glu Met Phe Thr  
 450 455 460

His Ala Glu Glu Val Phe Thr Ala Met Gly Ala Val Thr Leu Ala Ala  
 465 470 475 480

Arg Cys His Gly Glu Arg Arg Val Ala Gly Val Gly Pro Arg Arg Ser  
 485 490 495

Ala Gln Gly Leu Thr Pro Gln Glu Glu Gln Ile Thr Ala Leu Val Val  
 500 505 510

Asp Gly Cys Ser Asn Gln Glu Val Ala Arg Glu Leu Ser Leu Ser Ala  
 515 520 525

Lys Thr Val Glu Tyr His Leu Thr Arg Val Tyr Lys Lys Leu Gly Val  
 530 535 540

Ser Ser Arg Gly Glu Leu Arg Glu Leu Leu Lys Val  
 545 550 555

<210> 271  
 <211> 774  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(751)  
 <223> RXN01315

<400> 271  
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aatattgcac tgagtgcgaag ttacactag gtttacttca gtg gat att gaa gag 115  
 Val Asp Ile Glu Glu  
 1 5

cag ccc tcg tta aga gaa atc aag cgc caa atg acc ctg gaa gcg ata 163  
 Gln Pro Ser Leu Arg Glu Ile Lys Arg Gln Met Thr Leu Glu Ala Ile  
 10 15 20

gaa gat aac gca acc agg ctc att ctg gag cgt ggc ttc gac aat gtc 211  
 Glu Asp Asn Ala Thr Arg Leu Ile Leu Glu Arg Gly Phe Asp Asn Val  
 25 30 35

aca atc gaa gac atc tgc gca gag gca ggg ata tcc aag cgc aca ttc 259  
 Thr Ile Glu Asp Ile Cys Ala Glu Ala Gly Ile Ser Lys Arg Thr Phe  
 40 45 50

ttt aac tac gtg gag tcc aaa gag tct gtg gcc atc ggg cac aca gcc 307  
 Phe Asn Tyr Val Glu Ser Lys Glu Ser Val Ala Ile Gly His Thr Ala  
 55 60 65

aag ctc cca acg gat gaa gaa cgt gaa gca ttc ctg gct acg cgt cat 355  
 Lys Leu Pro Thr Asp Glu Glu Arg Glu Ala Phe Leu Ala Thr Arg His

70	75	80	85	
gaa aat att atc gat act gta ttt gac ctg gta atc aac ctc ttt ggc				403
Glu Asn Ile Ile Asp Thr Val Phe Asp Leu Val Ile Asn Leu Phe Gly	90	95	100	
aac cac gac aac tcc aag tct gga gtt gca ggc gac att atg cgt cga				451
Asn His Asp Asn Ser Lys Ser Gly Val Ala Gly Asp Ile Met Arg Arg	105	110	115	
cgc aaa gag atc cgg gtg aag cat cca gaa ctg gca gtg caa cat ttc				499
Arg Lys Glu Ile Arg Val Lys His Pro Glu Leu Ala Val Gln His Phe	120	125	130	
gcc agg ttc cac caa gca cgc gaa ggg cta gaa cac cta att gtt gag				547
Ala Arg Phe His Gln Ala Arg Glu Gly Leu Glu His Leu Ile Val Glu	135	140	145	
tac ttc gaa aaa tgg cca ggc tcc caa cat cta gat gag cct gca gat				595
Tyr Phe Glu Lys Trp Pro Gly Ser Gln His Leu Asp Glu Pro Ala Asp	150	155	160	165
cga gaa gca atc gcc ata gtt ggc ctg ctg atc tcg gtc atg ctt caa				643
Arg Glu Ala Ile Ala Ile Val Gly Leu Leu Ile Ser Val Met Leu Gln	170	175	180	
ggt tct cgt gaa tgg cac gac atg cca caa ggc acg caa gct gat ttc				691
Gly Ser Arg Glu Trp His Asp Met Pro Gln Gly Thr Gln Ala Asp Phe	185	190	195	
caa gcc tgc tgt cgc aaa gca att aaa aat act ttt ctt ctt aga ggt				739
Gln Ala Cys Cys Arg Lys Ala Ile Lys Asn Thr Phe Leu Leu Arg Gly	200	205	210	
gga ttt tca gaa tgacatcaca ggtcaagccg gac				774
Gly Phe Ser Glu	215			

&lt;210&gt; 272

&lt;211&gt; 217

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 272

Val Asp Ile Glu Glu Gln Pro Ser Leu Arg Glu Ile Lys Arg Gln Met			
1	5	10	15

Thr Leu Glu Ala Ile Glu Asp Asn Ala Thr Arg Leu Ile Leu Glu Arg			
20	25	30	

Gly Phe Asp Asn Val Thr Ile Glu Asp Ile Cys Ala Glu Ala Gly Ile			
35	40	45	

Ser Lys Arg Thr Phe Phe Asn Tyr Val Glu Ser Lys Glu Ser Val Ala			
50	55	60	

Ile Gly His Thr Ala Lys Leu Pro Thr Asp Glu Glu Arg Glu Ala Phe			
65	70	75	80

Leu Ala Thr Arg His Glu Asn Ile Ile Asp Thr Val Phe Asp Leu Val			
---	--	--	--

	85	90	95
Ile Asn Leu Phe Gly Asn His Asp Asn Ser Lys Ser Gly Val Ala Gly			
100		105	110
Asp Ile Met Arg Arg Arg Lys Glu Ile Arg Val Lys His Pro Glu Leu			
115		120	125
Ala Val Gln His Phe Ala Arg Phe His Gln Ala Arg Glu Gly Leu Glu			
130		135	140
His Leu Ile Val Glu Tyr Phe Glu Lys Trp Pro Gly Ser Gln His Leu			
145		150	155
Asp Glu Pro Ala Asp Arg Glu Ala Ile Ala Ile Val Gly Leu Leu Ile			
	165	170	175
Ser Val Met Leu Gln Gly Ser Arg Glu Trp His Asp Met Pro Gln Gly			
	180	185	190
Thr Gln Ala Asp Phe Gln Ala Cys Cys Arg Lys Ala Ile Lys Asn Thr			
	195	200	205
Phe Leu Leu Arg Gly Gly Phe Ser Glu			
210		215	

<210> 273  
 <211> 480  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <223> RXN00035

<400> 273  
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 ttagttatat gagtaaccaa ccatcgggat cgtcgcgacc gtg cct ctg tat aaa 115  
 Val Pro Leu Tyr Lys  
 1 5  
 cag atc gct tct ttg att gag gac tcc atc gtt gac gga acc ttg agc 163  
 Gln Ile Ala Ser Leu Ile Glu Asp Ser Ile Val Asp Gly Thr Leu Ser  
 10 15 20  
 att gat caa cgc gtg cct tct act aat gaa cta gcc gcg ttc cat cgc 211  
 Ile Asp Gln Arg Val Pro Ser Thr Asn Glu Leu Ala Ala Phe His Arg  
 25 30 35  
 att aat ccc gcc acc gca cgc aac ggc ctg acc ctc ctt gtc gaa gcc 259  
 Ile Asn Pro Ala Thr Ala Arg Asn Gly Leu Thr Leu Leu Val Glu Ala  
 40 45 50  
 ggc atc ctc tat aag aag cgt ggc att ggc atg ttc gtc agc gcc cag 307  
 Gly Ile Leu Tyr Lys Lys Arg Gly Ile Gly Met Phe Val Ser Ala Gln  
 55 60 65  
 gcc cca gca ctc atc cga gag cgg cga gat gcc gcc ttc gcg gct act 355



Ala Pro Ala Leu Ile Arg Glu Arg Arg Asp Ala Ala Phe Ala Ala Thr  
 70 75 80 85  
 tat gta gca ccg ctt atc gac gaa tcc atc cac ctt ggt ttc act cgt 403  
 Tyr Val Ala Pro Leu Ile Asp Glu Ser Ile His Leu Gly Phe Thr Arg  
 90 95 100  
 gcg cgc att cac gcc ctt tta gac cag gtc gct gaa agt agg ggc ctg 451  
 Ala Arg Ile His Ala Leu Leu Asp Gln Val Ala Glu Ser Arg Gly Leu  
 105 110 115  
 tac aag tagcgccttaa accctcttga cct 480  
 Tyr Lys

<210> 274  
 <211> 119  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 274  
 Val Pro Leu Tyr Lys Gln Ile Ala Ser Leu Ile Glu Asp Ser Ile Val  
 1 5 10 15  
 Asp Gly Thr Leu Ser Ile Asp Gln Arg Val Pro Ser Thr Asn Glu Leu  
 20 25 30  
 Ala Ala Phe His Arg Ile Asn Pro Ala Thr Ala Arg Asn Gly Leu Thr  
 35 40 45  
 Leu Leu Val Glu Ala Gly Ile Leu Tyr Lys Lys Arg Gly Ile Gly Met  
 50 55 60  
 Phe Val Ser Ala Gln Ala Pro Ala Leu Ile Arg Glu Arg Arg Asp Ala  
 65 70 75 80  
 Ala Phe Ala Ala Thr Tyr Val Ala Pro Leu Ile Asp Glu Ser Ile His  
 85 90 95  
 Leu Gly Phe Thr Arg Ala Arg Ile His Ala Leu Leu Asp Gln Val Ala  
 100 105 110  
 Glu Ser Arg Gly Leu Tyr Lys  
 115

<210> 275  
 <211> 810  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(787)  
 <223> RXN00049

<400> 275  
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 cttatatttta agtcaccgca gatcagctaa gggtttccct atg ccc acg cct tcg 115

Met   Pro   Thr   Pro   Ser  
1                      5

<210> 276  
 <211> 229  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 276  
 Met Pro Thr Pro Ser Gln His Lys Asp Ala Ser Thr Ala Gln Thr Asp  
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 Asn Gln Val Pro Thr Gly Arg Arg Ala Gln Lys Arg Glu Gln Thr Arg  
                   20                  25                  30  
 Ala Arg Leu Ile Thr Ser Ala Arg Thr Leu Met Ala Glu Arg Gly Val  
           35                  40                  45  
 Asp Asn Val Gly Ile Ala Glu Ile Thr Glu Gly Ala Asn Ile Gly Thr  
       50                  55                  60  
 Gly Thr Phe Tyr Asn Tyr Phe Pro Asp Arg Glu Gln Leu Leu Gln Ala  
   65                  70                  75                  80  
 Val Ala Glu Asp Ala Phe Glu Ser Val Gly Ile Ala Leu Asp Gln Val  
                   85                  90                  95  
 Leu Thr Lys Leu Asp Asp Pro Ala Glu Val Phe Ala Gly Ser Leu Arg  
           100                  105                  110  
 His Leu Val Arg His Ser Leu Glu Asp Arg Ile Trp Gly Gly Phe Phe  
       115                  120                  125  
 Ile Gln Met Gly Ala Ala His Pro Val Leu Met Arg Ile Leu Gly Pro  
       130                  135                  140  
 Arg Ala Arg Arg Asp Leu Leu His Gly Leu Glu Thr Gly Arg Phe Thr  
   145                  150                  155                  160  
 Ile Glu Asp Leu Asp Leu Ala Thr Thr Cys Thr Phe Gly Ser Leu Ile  
                   165                  170                  175  
 Ala Ala Ile Gln Met Ala Leu Ser Ala Asp Gln Asp Ser Asn Asp Asp  
           180                  185                  190  
 Lys Asp Gln Ile Phe Ala Ala Ala Met Leu Arg Met Val Gly Val Gln  
       195                  200                  205  
 Ala Ala Glu Ala Arg Glu Ile Ala Ser Arg Pro Leu Pro Glu Ile Ser  
       210                  215                  220  
 Pro Val Lys Pro Gln  
 225

<210> 277  
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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(1009)

<400> 277

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Val Leu Asn Leu Asn  
1 5

cgc tta cac atc ctg cag gaa ttc cac cgc ctg gga acg att aca gca 163  
 Arg Leu His Ile Leu Gln Glu Phe His Arg Leu Gly Thr Ile Thr Ala  
 10 15 20

gtg	gcg	gaa	tcc	atg	aac	tac	agc	cgc	tct	gcc	atc	tcc	caa	caa	atg	211
Val	Ala	Glu	Ser	Met	Asn	Tyr	Ser	Arg	Ser	Ala	Ile	Ser	Gln	Gln	Met	
			25					30					35			

gcg ctg ctg gaa aaa gaa att ggt gtg aaa ctc ttt gaa aaa agc ggc 259  
Ala Leu Leu Glu Lys Glu Ile Gly Val Lys Leu Phe Glu Lys Ser Gly  
40 45 50

cga aac ctc tac ttc aca gaa caa ggc gaa gtg ttg gcc tca gaa aca 307  
Arg Asn Leu Tyr Phe Thr Glu Gln Gly Glu Val Leu Ala Ser Glu Thr  
55 60 65

cat gcg atc atg gca gca gtc gac cat gcc cgc gca gcc gtt cta gat ...355  
His Ala Ile Met Ala Ala Val Asp His Ala Arg Ala Ala Val Leu Asp ...  
70 75 80 85

tcg	ctg	tct	gaa	gtg	tcc	gga	acg	ctg	aaa	gtc	acc	tcc	ttc	caa	tcc	403
Ser	Leu	Ser	Glu	Val	Ser	Gly	Thr	Leu	Lys	Val	Thr	Ser	Phe	Gln	Ser	
				90					95					100		

ctg ctg ttc acc ctt gcc ccg aaa gcc atc gcg cgc ctg acc gag aaa 451  
Leu Leu Phe Thr Leu Ala Pro Lys Ala Ile Ala Arg Leu Thr Glu Lys  
105 110 115

tac	cca	cac	ctg	caa	gta	gaa	atc	tcc	caa	cta	gaa	gtc	acc	gca	gcg	499
Tyr	Pro	His	Leu	Gln	Val	Glu	Ile	Ser	Gln	Leu	Glu	Val	Thr	Ala	Ala	
		120					125					130				

ctc gaa gaa ctc cgc gcc cgc cgc gtc gac gtc gca ctc ggc gag gaa 547  
Leu Glu Glu Leu Arg Ala Arg Arg Val Asp Val Ala Leu Gly Glu Glu  
135 140 145

tac	ccc	gtg	gaa	gtc	ccc	ctt	gtt	gag	gcc	agc	att	cac	cgc	gaa	gtc	595
Tyr	Pro	Val	Glu	Val	Pro	Leu	Val	Glu	Ala	Ser	Ile	His	Arg	Glu	Val	
150					155				160						165	

ctc	ttc	gaa	gac	ccc	atg	ctg	ctc	gtc	acc	cca	gca	agc	ggc	cca	tac	643
Leu	Phe	Glu	Asp	Pro	Met	Leu	Leu	Val	Thr	Pro	Ala	Ser	Gly	Pro	Tyr	
				170					175					180		

tct ggc ctc acc ctg cca gaa ctc cgc gac atc ccc atc gcc atc gat 691  
Ser Gly Leu Thr Leu Pro Glu Leu Arg Asp Ile Pro Ile Ala Ile Asp  
185 190 195

cca ccc gac ctt ccc gcg ggc gaa tgg gtc cat agg ctc tgc cgg cgc 739  
Pro Pro Asp Leu Pro Ala Gly Glu Trp Val His Arg Leu Cys Arg Arg  
200 205 210

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gcc ggg ttt gag ccc cgc gtg acc ttt gaa acc agc gat ccc atg ctc 787
Ala Gly Phe Glu Pro Arg Val Thr Phe Glu Thr Ser Asp Pro Met Leu
215 220 225

caa gca cac ctc gtg cgt agc ggc ttg gcc gtg aca ttt tcc ccc aca 835
Gln Ala His Leu Val Arg Ser Gly Leu Ala Val Thr Phe Ser Pro Thr
230 235 240 245

ctg ctc acc ccg atg ctg gaa agc gtg cac atc cag ccg ctg ccc ggc 883
Leu Leu Thr Pro Met Leu Glu Ser Val His Ile Gln Pro Leu Pro Gly
250 255 260

aac ccc acg cgc acg ctc tac acc gcg gtc agg gaa ggg cgc cag ggg 931
Asn Pro Thr Arg Thr Leu Tyr Thr Ala Val Arg Glu Gly Arg Gln Gly
265 270 275

cat cca gcc att aaa gct ttt cga cga gcc ctc gcc cat gtg gcc aaa 979
His Pro Ala Ile Lys Ala Phe Arg Arg Ala Leu Ala His Val Ala Lys
280 285 290

gaa tct tat ttg gag gct cgt cta gta gag tgagttcttg tgagccttca gac 1032
Glu Ser Tyr Leu Glu Ala Arg Leu Val Glu
295 300

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<210> 278
<211> 303
<212> PRT
<213> Corynebacterium glutamicum

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<400> 278
Val Leu Asn Leu Asn Arg Leu His Ile Leu Gln Glu Phe His Arg Leu
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Gly Thr Ile Thr Ala Val Ala Glu Ser Met Asn Tyr Ser Arg Ser Ala
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Ile Ser Gln Gln Met Ala Leu Leu Glu Lys Glu Ile Gly Val Lys Leu
35 40 45

Phe Glu Lys Ser Gly Arg Asn Leu Tyr Phe Thr Glu Gln Gly Glu Val
50 55 60

Leu Ala Ser Glu Thr His Ala Ile Met Ala Ala Val Asp His Ala Arg
65 70 75 80

Ala Ala Val Leu Asp Ser Leu Ser Glu Val Ser Gly Thr Leu Lys Val
85 90 95

Thr Ser Phe Gln Ser Leu Leu Phe Thr Leu Ala Pro Lys Ala Ile Ala
100 105 110

Arg Leu Thr Glu Lys Tyr Pro His Leu Gln Val Glu Ile Ser Gln Leu
115 120 125

Glu Val Thr Ala Ala Leu Glu Glu Leu Arg Ala Arg Arg Val Asp Val
130 135 140

Ala Leu Gly Glu Glu Tyr Pro Val Glu Val Pro Leu Val Glu Ala Ser
145 150 155 160

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Ile His Arg Glu Val Leu Phe Glu Asp Pro Met Leu Leu Val Thr Pro  
 165 170 175  
 Ala Ser Gly Pro Tyr Ser Gly Leu Thr Leu Pro Glu Leu Arg Asp Ile  
 180 185 190  
 Pro Ile Ala Ile Asp Pro Pro Asp Leu Pro Ala Gly Glu Trp Val His  
 195 200 205  
 Arg Leu Cys Arg Arg Ala Gly Phe Glu Pro Arg Val Thr Phe Glu Thr  
 210 215 220  
 Ser Asp Pro Met Leu Gln Ala His Leu Val Arg Ser Gly Leu Ala Val  
 225 230 235 240  
 Thr Phe Ser Pro Thr Leu Leu Thr Pro Met Leu Glu Ser Val His Ile  
 245 250 255  
 Gln Pro Leu Pro Gly Asn Pro Thr Arg Thr Leu Tyr Thr Ala Val Arg  
 260 265 270  
 Glu Gly Arg Gln Gly His Pro Ala Ile Lys Ala Phe Arg Arg Ala Leu  
 275 280 285  
 Ala His Val Ala Lys Glu Ser Tyr Leu Glu Ala Arg Leu Val Glu  
 290 295 300

<210> 279  
 <211> 873  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(850)  
 <223> RXN01081

<400> 279  
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 tattaagtaa gcaagtacac cggcccatta aagaggcacc atg acc cca gca aac 115  
 Met Thr Pro Ala Asn  
 1 5  
 gaa agt cct atg act aat cca tta ggt tct gcc ccc acc cca gcc aag 163  
 Glu Ser Pro Met Thr Asn Pro Leu Gly Ser Ala Pro Thr Pro Ala Lys  
 10 15 20  
 cca ctt ctt gac agt gtt ctt gat gag ctc ggt caa gat atc atc agt 211  
 Pro Leu Leu Asp Ser Val Leu Asp Glu Leu Gly Gln Asp Ile Ile Ser  
 25 30 35  
 ggc aag gtt gct gtc gga gat acc ttc aag ctg atg gac atc ggc gag 259  
 Gly Lys Val Ala Val Gly Asp Thr Phe Lys Leu Met Asp Ile Gly Glu  
 40 45 50  
 cgt ttt ggc att tcc cgc aca gtg gca cgc gaa gcg atg cgc gct ttg 307  
 Arg Phe Gly Ile Ser Arg Thr Val Ala Arg Glu Ala Met Arg Ala Leu  
 55 60 65

gag cag ctc ggt ctt gtc gct tct tca cgt cgc att ggc att act gtt 355  
 Glu Gln Leu Gly Leu Val Ala Ser Ser Arg Arg Ile Gly Ile Thr Val  
 70 75 80 85  
 ttg cca cag gaa gag tgg gct gtt ttt gat aag tcc atc att cgc tgg 403  
 Leu Pro Gln Glu Glu Trp Ala Val Phe Asp Lys Ser Ile Ile Arg Trp  
 90 95 100  
 cgt ctc aat gac gaa ggt cag cgt gaa ggc cag ctt cag tct ctt acc 451  
 Arg Leu Asn Asp Glu Gly Gln Arg Glu Gly Gln Leu Gln Ser Leu Thr  
 105 110 115  
 gag ctt cgt att gct att gaa ccg att gcc gcg cgc agc gtt gct ctt 499  
 Glu Leu Arg Ile Ala Ile Glu Pro Ile Ala Ala Arg Ser Val Ala Leu  
 120 125 130  
 cac gcg tca acc gcc gag ctc gag aaa atc cgc gcg ctc gca aca gag 547  
 His Ala Ser Thr Ala Glu Leu Glu Lys Ile Arg Ala Leu Ala Thr Glu  
 135 140 145  
 atg cgt cag ttg ggt gaa tct ggt cag ggt gcg tcc cag cgc ttc ctc 595  
 Met Arg Gln Leu Gly Glu Ser Gly Gln Gly Ala Ser Gln Arg Phe Leu  
 150 155 160 165  
 gaa gcg gac gtc act ttc cac gag ctc atc ttg cgt tat tgc cac aat 643  
 Glu Ala Asp Val Thr Phe His Glu Leu Ile Leu Arg Tyr Cys His Asn  
 170 175 180  
 gag atg ttc gct gca ctg att ccg tcg att agc gcg gtt ctt gtc ggc 691  
 Glu Met Phe Ala Ala Leu Ile Pro Ser Ile Ser Ala Val Leu Val Gly  
 185 190 195  
 cgc acc gag ctc ggc ctg cag cct gat ctg ccg gcg cac gag gcg cta 739  
 Arg Thr Glu Leu Gly Leu Gln Pro Asp Leu Pro Ala His Glu Ala Leu  
 200 205 210  
 gac aac cac gat aag ctt gcc gac gcc ctc ctt aac cgc gac gcc gac 787  
 Asp Asn His Asp Lys Leu Ala Asp Ala Leu Leu Asn Arg Asp Ala Asp  
 215 220 225  
 gcc gca gaa act gcg tcc cga aac atc ctc aat gag gtg cgc agc gcg 835  
 Ala Ala Glu Thr Ala Ser Arg Asn Ile Leu Asn Glu Val Arg Ser Ala  
 230 235 240 245  
 ctg ggc acg ctg aac taacgtgata cgcgcactgc gtt 873  
 Leu Gly Thr Leu Asn  
 250

&lt;210&gt; 280

&lt;211&gt; 250

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 280

Met Thr Pro Ala Asn Glu Ser Pro Met Thr Asn Pro Leu Gly Ser Ala  
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Pro Thr Pro Ala Lys Pro Leu Leu Asp Ser Val Leu Asp Glu Leu Gly  
 20 25 30

Gln Asp Ile Ile Ser Gly Lys Val Ala Val Gly Asp Thr Phe Lys Leu  
           35                          40                          45  
 Met Asp Ile Gly Glu Arg Phe Gly Ile Ser Arg Thr Val Ala Arg Glu  
       50                          55                          60  
 Ala Met Arg Ala Leu Glu Gln Leu Gly Leu Val Ala Ser Ser Arg Arg  
       65                          70                          75                          80  
 Ile Gly Ile Thr Val Leu Pro Gln Glu Glu Trp Ala Val Phe Asp Lys  
                           85                          90                          95  
 Ser Ile Ile Arg Trp Arg Leu Asn Asp Glu Gly Gln Arg Glu Gly Gln  
                           100                          105                          110  
 Leu Gln Ser Leu Thr Glu Leu Arg Ile Ala Ile Glu Pro Ile Ala Ala  
           115                          120                          125  
 Arg Ser Val Ala Leu His Ala Ser Thr Ala Glu Leu Glu Lys Ile Arg  
       130                          135                          140  
 Ala Leu Ala Thr Glu Met Arg Gln Leu Gly Glu Ser Gly Gln Gly Ala  
       145                          150                          155                          160  
 Ser Gln Arg Phe Leu Glu Ala Asp Val Thr Phe His Glu Leu Ile Leu  
                           165                          170                          175  
 Arg Tyr Cys His Asn Glu Met Phe Ala Ala Leu Ile Pro Ser Ile Ser  
                           180                          185                          190  
 Ala Val Leu Val Gly Arg Thr Glu Leu Gly Leu Gln Pro Asp Leu Pro  
           195                          200                          205  
 Ala His Glu Ala Leu Asp Asn His Asp Lys Leu Ala Asp Ala Leu Leu  
       210                          215                          220  
 Asn Arg Asp Ala Asp Ala Ala Glu Thr Ala Ser Arg Asn Ile Leu Asn  
       225                          230                          235                          240  
 Glu Val Arg Ser Ala Leu Gly Thr Leu Asn  
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&lt;210&gt; 281

&lt;211&gt; 998

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(975)

&lt;223&gt; RXN01160

&lt;400&gt; 281

aaa tca tcc aac aaa atc agc gac ctt gcc cgc cag ctt aat ctg ttg 48  
 Lys Ser Ser Asn Lys Ile Ser Asp Leu Ala Arg Gln Leu Asn Leu Leu  
       1                          5                          10                          15

ccg tat ttc acc agg tat aaa ggc cgt acc gtc atg gaa gca gcg cgc 96  
 Pro Tyr Phe Thr Arg Tyr Lys Gly Arg Thr Val Met Glu Ala Ala Arg



				20				25				30							
gat	ctt	ggc	caa	ccc	tcc	tcc	caa	atc	atg	gaa	gac	ctc	aac	aga	tta	144			
Asp	Leu	Gly	Gln	Pro	Ser	Ser	Gln	Ile	Met	Glu	Asp	Leu	Asn	Arg	Leu				
				35				40				45							
tgg	atg	tgt	ggg	ctg	cca	gga	ctt	ctt	cca	ggg	gac	ttg	gtg	gag	ctt	192			
Trp	Met	Cys	Gly	Leu	Pro	Gly	Leu	Leu	Pro	Gly	Asp	Leu	Val	Glu	Leu				
				50				55				60							
gat	cat	tcc	ttt	aag	gaa	gta	aaa	atc	cac	aat	gct	caa	ggc	atg	gat	240			
Asp	His	Ser	Phe	Lys	Glu	Val	Lys	Ile	His	Asn	Ala	Gln	Gly	Met	Asp				
				70				75				80							
aaa	ccc	ttg	cgc	ctc	aca	cca	act	gaa	gcc	ggg	gtt	ttg	ctg	ctg	aca	288			
Lys	Pro	Leu	Arg	Leu	Thr	Pro	Thr	Glu	Ala	Gly	Val	Leu	Leu	Leu	Thr				
				85				90				95							
ctt	gaa	tcc	ctg	gaa	tcc	ctc	ccc	ggg	att	gcg	aaa	cag	gaa	gcg	gtc	336			
Leu	Glu	Ser	Leu	Glu	Ser	Leu	Pro	Gly	Ile	Ala	Lys	Gln	Glu	Ala	Val				
				100				105				110							
gta	tct	gct	gcg	aac	aag	cta	cgc	gcc	atc	atg	ggg	gag	tat	tcc	tcg	384			
Val	Ser	Ala	Ala	Asn	Lys	Leu	Arg	Ala	Ile	Met	Gly	Glu	Tyr	Ser	Ser				
				115				120				125							
act	gtt	ttc	gac	tcc	act	gga	gaa	gac	ctc	gat	gct	gaa	gtt	cta	gag	432			
Thr	Val	Phe	Asp	Ser	Thr	Gly	Glu	Asp	Leu	Asp	Ala	Glu	Val	Leu	Glu				
				130				135				140							
atc	atc	cgc	gac	gcc	atg	gat	tta	cac	cag	cag	gtc	agt	ttt	gaa	tac	480			
Ile	Ile	Arg	Asp	Ala	Met	Asp	Leu	His	Gln	Gln	Val	Ser	Phe	Glu	Tyr				
				150				155				160							
cac	tcg	cac	aga	tca	gac	aac	acc	agc	ctg	agg	caa	gtc	agc	cct	gct	528			
His	Ser	His	Arg	Ser	Asp	Asn	Thr	Ser	Leu	Arg	Gln	Val	Ser	Pro	Ala				
				165				170				175							
cat	atc	ttc	acc	cat	gaa	ggc	gaa	acc	tac	atc	aaa	gcc	tgg	gaa	gaa	576			
His	Ile	Phe	Thr	His	Glu	Gly	Glu	Thr	Tyr	Ile	Lys	Ala	Trp	Glu	Glu				
				180				185				190							
gct	gtg	aac	caa	tgg	cgg	acg	ttt	agg	ctt	gat	cgc	atc	cga	agc	att	624			
Ala	Val	Asn	Gln	Trp	Arg	Thr	Phe	Arg	Leu	Asp	Arg	Ile	Arg	Ser	Ile				
				195				200				205							
gtg	ctt	ctt	gac	agc	aaa	gca	gtg	cac	ccg	gcg	cga	ggg	gtt	tca	gta	672			
Val	Leu	Leu	Asp	Ser	Lys	Ala	Val	His	Pro	Ala	Arg	Gly	Val	Ser	Val				
				210				215				220							
tcc	acg	gac	gat	cct	ttt	gag	ttc	gca	aaa	tct	tcc	gat	att	gcc	acg	720			
Ser	Thr	Asp	Asp	Pro	Phe	Glu	Phe	Ala	Lys	Ser	Ser	Asp	Ile	Ala	Thr				
				230				235				240							
tta	ttg	ctg	cgt	gag	gac	gca	atg	tgg	tta	ggc	aat	tac	atg	gcc	atg	768			
Leu	Leu	Leu	Arg	Glu	Asp	Ala	Met	Trp	Leu	Gly	Asn	Tyr	Met	Ala	Met				
				245				250				255							
gag	gtg	gat	gaa	acg	gtg	gaa	ccg	att	cgc	gat	agc	gac	gga	ttc	agc	816			
Glu	Val	Asp	Glu	Thr	Val	Glu	Pro	Ile	Arg										

tgg cac aca gtc cac ttt ccg ctg ctt tct agg gat tgg ttc gtc cga 864  
 Trp His Thr Val His Phe Pro Leu Leu Ser Arg Asp Trp Phe Val Arg  
 275 280 285  
 ttc gcg att ggc cat gct gag cat ttg aaa gta act agt ccc gaa gat 912  
 Phe Ala Ile Gly His Ala Glu His Leu Lys Val Thr Ser Pro Glu Asp  
 290 295 300  
 ctt cgg aaa tgc ata aag caa aag gct ttt agt ggt ttg tca gcg tat 960  
 Leu Arg Lys Cys Ile Lys Gln Lys Ala Phe Ser Gly Leu Ser Ala Tyr  
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 Asp His His Val Glu  
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 Pro Tyr Phe Thr Arg Tyr Lys Gly Arg Thr Val Met Glu Ala Ala Arg  
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 Asp Leu Gly Gln Pro Ser Ser Gln Ile Met Glu Asp Leu Asn Arg Leu  
 35 40 45  
 Trp Met Cys Gly Leu Pro Gly Leu Leu Pro Gly Asp Leu Val Glu Leu  
 50 55 60  
 Asp His Ser Phe Lys Glu Val Lys Ile His Asn Ala Gln Gly Met Asp  
 65 70 75 80  
 Lys Pro Leu Arg Leu Thr Pro Thr Glu Ala Gly Val Leu Leu Leu Thr  
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 Leu Glu Ser Leu Glu Ser Leu Pro Gly Ile Ala Lys Gln Glu Ala Val  
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 Val Ser Ala Ala Asn Lys Leu Arg Ala Ile Met Gly Glu Tyr Ser Ser  
 115 120 125  
 Thr Val Phe Asp Ser Thr Gly Glu Asp Leu Asp Ala Glu Val Leu Glu  
 130 135 140  
 Ile Ile Arg Asp Ala Met Asp Leu His Gln Gln Val Ser Phe Glu Tyr  
 145 150 155 160  
 His Ser His Arg Ser Asp Asn Thr Ser Leu Arg Gln Val Ser Pro Ala  
 165 170 175  
 His Ile Phe Thr His Glu Gly Glu Thr Tyr Ile Lys Ala Trp Glu Glu  
 180 185 190  
 Ala Val Asn Gln Trp Arg Thr Phe Arg Leu Asp Arg Ile Arg Ser Ile

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Val Leu Leu Asp Ser Lys Ala Val His Pro Ala Arg Gly Val Ser Val		
210	215	220
Ser Thr Asp Asp Pro Phe Glu Phe Ala Lys Ser Ser Asp Ile Ala Thr		
225	230	235 240
Leu Leu Leu Arg Glu Asp Ala Met Trp Leu Gly Asn Tyr Met Ala Met		
	245	250 255
Glu Val Asp Glu Thr Val Glu Pro Ile Arg Asp Ser Asp Gly Phe Ser		
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Trp His Thr Val His Phe Pro Leu Leu Ser Arg Asp Trp Phe Val Arg		
	275	280 285
Phe Ala Ile Gly His Ala Glu His Leu Lys Val Thr Ser Pro Glu Asp		
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Leu Arg Lys Cys Ile Lys Gln Lys Ala Phe Ser Gly Leu Ser Ala Tyr		
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Asp His His Val Glu		
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 Met Pro Ala Gly Ile  
 1 5  
 gca gac atg aca gat tca ttg ctc gga tgg gca tca caa act gag ctg 163  
 Ala Asp Met Thr Asp Ser Leu Leu Gly Trp Ala Ser Gln Thr Glu Leu  
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 Asp Leu Asn Gln Arg Leu Ala Gly Val Glu Tyr Phe Pro Gln Ile Gln  
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 Leu Arg His Asp Glu Leu Glu Arg Ile His Arg Phe Tyr Gly Thr Phe  
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 Leu Ser Arg Gln Val Gly Ala Gly Ala Ser Leu Gly Asp Leu Phe Glu  
 55 60 65  
 atg acc cca tgc ctg aca gtc acc acc ttg gtg tct cgg gcg tca cgg 355

Met 70	Thr	Pro	Cys	Leu	Thr 75	Val	Thr	Thr	Leu	Val 80	Ser	Arg	Ala	Ser	Arg 85	
atc	agc	gat	cca	gca	gat	ttc	ttc	ggt	gaa	tac	atc	gga	gga	ctg	gga	403
Ile	Ser	Asp	Pro	Ala	Asp	Phe	Phe	Gly	Glu	Tyr	Ile	Gly	Gly	Leu	Gly	
				90					95					100		
ctt	agc	gca	gaa	cac	gca	gca	gtt	gtt	gaa	ggg	ttg	acc	gaa	aag	ctc	451
Leu	Ser	Ala	Glu	His	Ala	Ala	Val	Val	Glu	Gly	Leu	Thr	Glu	Lys	Leu	
			105					110					115			
ttc	gca	cag	gct	ggc	ctg	ctc	gtt	cct	gag	gga	att	gca	tct	cca	ttg	499
Phe	Ala	Gln	Ala	Gly	Leu	Leu	Val	Pro	Glu	Gly	Ile	Ala	Ser	Pro	Leu	
		120					125					130				
gag	ttg	tta	tcc	atc	cac	gca	ggc	att	agt	aac	cac	gaa	gtg	gcc	gca	547
Glu	Leu	Leu	Ser	Ile	His	Ala	Gly	Ile	Ser	Asn	His	Glu	Val	Ala	Ala	
	135					140					145					
gtg	ctg	acc	gaa	gtg	gaa	aac	ggc	acc	acc	gaa	tat	cca	ttc	atg	ttc	595
Val	Leu	Thr	Glu	Val	Glu	Asn	Gly	Thr	Thr	Glu	Tyr	Pro	Phe	Met	Phe	
	150				155					160					165	
gac	gct	gtc	ctg	cgc	cta	acc	cct	gag	tgg	gca	cag	acc	ctt	atc	ggc	643
Asp	Ala	Val	Leu	Arg	Leu	Thr	Pro	Glu	Trp	Ala	Gln	Thr	Leu	Ile	Gly	
				170					175					180		
gga	gtt	caa	gaa	ctc	att	gaa	ttt	gcc	acc	acc	cac	cga	act	tct	tgg	691
Gly	Val	Gln	Glu	Leu	Ile	Glu	Phe	Ala	Thr	Thr	His	Arg	Thr	Ser	Trp	
			185					190					195			
tca	gac	cgc	cag	cgc	gaa	tcc	tca	ctg	cca	gcc	atg	atc	gat	gag	atc	739
Ser	Asp	Arg	Gln	Arg	Glu	Ser	Ser	Leu	Pro	Ala	Met	Ile	Asp	Glu	Ile	
		200					205					210				
gtt	gtg	gcg	gaa	ctt	cgg	gaa	cgc	cca	gtt	ggt	act	gcc	gac	cgt	gaa	787
Val	Val	Ala	Glu	Leu	Arg	Glu	Arg	Pro	Val	Gly	Thr	Ala	Asp	Arg	Glu	
	215					220					225					
aac	tcc	gtt	ggt	gtg	gca	ctt	cgt	gag	ctt	cgc	cca	cgc	ctc	atc	ctg	835
Asn	Ser	Val	Gly	Val	Ala	Leu	Arg	Glu	Leu	Arg	Pro	Arg	Leu	Ile	Leu	
	230				235					240					245	
gat	gca	gaa	cgc	cgc	aaa	gtc	tgc	ctg	cgt	cta	cct	gaa	cag	cgc	gtc	883
Asp	Ala	Glu	Arg	Arg	Lys	Val	Cys	Leu	Arg	Leu	Pro	Glu	Gln	Arg	Val	
				250					255					260		
agc	gac	gat	gaa	atc	aac	tgg	cga	gtc	agc	cta	gaa	ggc	acc	acc	cgg	931
Ser	Asp	Asp	Glu	Ile	Asn	Trp	Arg	Val	Ser	Leu	Glu	Gly	Thr	Thr	Arg	
			265					270					275			
att	ttc	tcc	acc	cgc	cga	gca	tgg	ggc	gat	act	tct	gga	tac	tcc	gaa	979
Ile	Phe	Ser	Thr	Arg	Arg	Ala	Trp	Gly	Asp	Thr	Ser	Gly	Tyr	Ser	Glu	
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gcc	ctc	gac	atc	act	gtc	gag	cgt	caa	atc	cgc	gaa	acc	acc	gtc	acc	1027
Ala	Leu	Asp	Ile	Thr	Val	Glu	Arg	Gln	Ile	Arg	Glu	Thr	Thr	Val	Thr	
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gac	acc	tca	aac	caa	atc	acc	tgg	gtt	gtc	cca	gtc	gtg	gac	ttc	aac	1075
Asp	Thr	Ser	Asn	Gln	Ile	Thr	Trp	Val	Val	Pro	Val	Val	Asp	Phe	Asn	

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gac cca gtg ctg gtg ttt tcc gcg cgc ggt gaa aac ctc acc gac aag				1123
Asp Pro Val Leu Val Phe Ser Ala Arg Gly Glu Asn Leu Thr Asp Lys				
	330	335	340	
gtc tcc ctg cac cat caa gag att tac gtt ctc gcg cca gcg gaa gca				1171
Val Ser Leu His His Gln Glu Ile Tyr Val Leu Ala Pro Ala Glu Ala				
	345	350	355	
aaa ctc gaa gac atg gtc act ggc cag cca gta cca gtt att gag caa				1219
Lys Leu Glu Asp Met Val Thr Gly Gln Pro Val Pro Val Ile Glu Gln				
	360	365	370	
ttc ctc gta gag ggc tgg aac tca tgg gtg tgc tcc cgc gtg gac gcc				1267
Phe Leu Val Glu Gly Trp Asn Ser Trp Val Cys Ser Arg Val Asp Ala				
	375	380	385	
cgt ggc ctg tcc tct ctg aag gtc aac aaa gaa gtc cga tgc att gac				1315
Arg Gly Leu Ser Ser Leu Lys Val Asn Lys Glu Val Arg Cys Ile Asp				
	395	400	405	
cca cgt cga cgc gtt gcc ttc cac cac cca gcc gaa ttg gtc cct cac				1363
Pro Arg Arg Arg Val Ala Phe His His Pro Ala Glu Leu Val Pro His				
	410	415	420	
gta cga tcc att tcc gga ctc ccc gta cac gcg cag tcc ctg atc gcc				1411
Val Arg Ser Ile Ser Gly Leu Pro Val His Ala Gln Ser Leu Ile Ala				
	425	430	435	
gag ttc cca cca acc ctg agc gga caa gac gaa acc tgg atg ctc tcc				1459
Glu Phe Pro Pro Thr Leu Ser Gly Gln Asp Glu Thr Trp Met Leu Ser				
	440	445	450	
atc tcg gct ttc gca ggt gta ggc gct gct ggt gaa gaa atc gcc gag				1507
Ile Ser Ala Phe Ala Gly Val Gly Ala Ala Gly Glu Glu Ile Ala Glu				
	455	460	465	
cca gag cct ttg gaa gtc cct gcc gac ggt ggc ctt ttc gcc atc ttc				1555
Pro Glu Pro Leu Glu Val Pro Ala Asp Gly Gly Leu Phe Ala Ile Phe				
	475	480	485	
gac cca gaa ata tac gac gcc cca tgg gtg ggt gaa tac ctg gtc cga				1603
Asp Pro Glu Ile Tyr Asp Ala Pro Trp Val Gly Glu Tyr Leu Val Arg				
	490	495	500	
ctc cgc ggc cca cgc aat gaa tcc ttc cga ccc gaa ttc gcc atc gtc				1651
Leu Arg Gly Pro Arg Asn Glu Ser Phe Arg Pro Glu Phe Ala Ile Val				
	505	510	515	
gaa gac atg acc acc gaa ttc gaa gtc gcc tca ggt gca tca ttt cga				1699
Glu Asp Met Thr Thr Glu Phe Glu Val Ala Ser Gly Ala Ser Phe Arg				
	520	525	530	
atc cca acc acc act ggt ctc agc gaa gcc agc cta cgc gtg cgt tcc				1747
Ile Pro Thr Thr Thr Gly Leu Ser Glu Ala Ser Leu Arg Val Arg Ser				
	535	540	545	
ggt gaa aag cac ttc acc gca gag cca cgc ctg gtc acc gtt gaa gca				1795
Gly Glu Lys His Phe Thr Ala Glu Pro Arg Leu Val Thr Val Glu Ala				
	555	560	565	

acc gac ccc aac gca tca ttc gtg gtc acc acc gat gaa ggc gat caa	1843
Thr Asp Pro Asn Ala Ser Phe Val Val Thr Thr Asp Glu Gly Asp Gln	
570 575 580	
atg cca ttg cga ttt gtg cca cca caa atc gcc atc gaa ctt cca ctg	1891
Met Pro Leu Arg Phe Val Pro Pro Gln Ile Ala Ile Glu Leu Pro Leu	
585 590 595	
acc acc gag cca cca acc tgg cgc gtc acc cgt act gtc tgt gga cca	1939
Thr Thr Glu Pro Pro Thr Trp Arg Val Thr Arg Thr Val Cys Gly Pro	
600 605 610	
cgc gac ctc gac ggt gca ggc gaa ctc cgc atc cgc acc ggt gtc gat	1987
Arg Asp Leu Asp Gly Ala Gly Glu Leu Arg Ile Arg Thr Gly Val Asp	
615 620 625	
gtc ggc gat cca aag gtc agt gtg cgc aac cac cac ggt tca cca ctg	2035
Val Gly Asp Pro Lys Val Ser Val Arg Asn His His Gly Ser Pro Leu	
630 635 640 645	
cga acc gtg aaa atg gtc acc cct gac aac ggc cgt acc tgg att gcc	2083
Arg Thr Val Lys Met Val Thr Pro Asp Asn Gly Arg Thr Trp Ile Ala	
650 655 660	
agc atg aag gaa atc gca gcc agt acc ttt gtg atg cca cgc gga tcc	2131
Ser Met Lys Glu Ile Ala Ala Ser Thr Phe Val Met Pro Arg Gly Ser	
665 670 675	
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Ile Glu Phe Glu Trp Thr Asp Arg Lys Val Asp Arg Arg Val Ser Val	
680 685 690	
acg att gct gtc att gac aaa act gag aac ttt act ggc atc acc atc	2227
Thr Ile Ala Val Ile Asp Lys Thr Glu Asn Phe Thr Gly Ile Thr Ile	
695 700 705	
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Glu Asp Gly Lys Leu Val Phe Glu Glu Leu Ala Ala Gly Arg Gln Leu	
710 715 720 725	
gct gca tgg gtg tgg cca caa acc gca ccg tgg gta agc gca gtg gaa	2323
Ala Ala Trp Val Trp Pro Gln Thr Ala Pro Trp Val Ser Ala Val Glu	
730 735 740	
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Leu Ala Val Thr Gly Pro Glu Leu Glu Leu Pro Glu Val Leu Val Gly	
745 750 755	
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Ala Gly Asn Leu Ile Val Gln Leu His Thr Ala Asp Pro Phe Thr Thr	
760 765 770	
tcc gtg acc cca ctg tca cca gga aaa gct gcg gtc acc gtt gag caa	2467
Ser Val Thr Pro Leu Ser Pro Gly Lys Ala Ala Val Thr Val Glu Gln	
775 780 785	
gaa ggc tac tac tca gca caa acc gaa gaa tat gca cag ctt tca gca	2515
Glu Gly Tyr Tyr Ser Ala Gln Thr Glu Glu Tyr Ala Gln Leu Ser Ala	
790 795 800 805	

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Phe Phe Gly Gly Glu Val Glu Glu Pro Pro Ile Ser Asp Ala Val Val	
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ccc gca ctt tgg gat gtt tcc cat atc tgg acc gaa cag gga aac acc	2611
Pro Ala Leu Trp Asp Val Ser His Ile Trp Thr Glu Gln Gly Asn Thr	
825 830 835	
gag cat ctt cca gta gtc cat gcc gcc ctg cgc tcc tca cca gcc gca	2659
Glu His Leu Pro Val Val His Ala Ala Leu Arg Ser Ser Pro Ala Ala	
840 845 850	
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Gly Lys Val Ile Ser Ser Gly Leu Ala Ala Ser Pro Phe Thr Thr Glu	
870 875 880 885	
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Ser Pro Ala Thr Glu Val His Arg Thr Ala Trp Ile Gly Thr Leu Gln	
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Leu Leu Gly Ala Leu Pro Ser Ala Phe Lys Glu Ala Glu Glu Leu Gly	
905 910 915	
aac cgc aca cca ctg ctg cca atc ctc gga caa ctt gag gaa gtc gcc	2899
Asn Arg Thr Pro Leu Leu Pro Ile Leu Gly Gln Leu Glu Glu Val Ala	
920 925 930	
ggc aag aac atc ctg tcc acc ctt gca act ggc cgt gac tcc act ttg	2947
Gly Lys Asn Ile Leu Ser Thr Leu Ala Thr Gly Arg Asp Ser Thr Leu	
935 940 945	
gac acc gca tgc atc gac caa tcc acc gtt gcg att gcc ggc atg aac	2995
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950 955 960 965	
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Ile Val Pro Gly Pro Leu Met Glu Asp Asn Thr Arg Leu Met Ala Val	
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 1080 1085 1090  
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 His Glu Val Ala Ala Val Leu Thr Glu Val Glu Asn Gly Thr Thr Glu  
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 Tyr Pro Phe Met Phe Asp Ala Val Leu Arg Leu Thr Pro Glu Trp Ala  
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Gln Thr Leu Ile Gly Gly Val Gln Glu Leu Ile Glu Phe Ala Thr Thr  
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 His Arg Thr Ser Trp Ser Asp Arg Gln Arg Glu Ser Ser Leu Pro Ala  
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 Met Ile Asp Glu Ile Val Val Ala Glu Leu Arg Glu Arg Pro Val Gly  
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 305 310 315 320  
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 325 330 335  
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 Ala Pro Ala Glu Ala Lys Leu Glu Asp Met Val Thr Gly Gln Pro Val  
 355 360 365  
 Pro Val Ile Glu Gln Phe Leu Val Glu Gly Trp Asn Ser Trp Val Cys  
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 Ser Arg Val Asp Ala Arg Gly Leu Ser Ser Leu Lys Val Asn Lys Glu  
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 Val Arg Cys Ile Asp Pro Arg Arg Arg Val Ala Phe His His Pro Ala  
 405 410 415  
 Glu Leu Val Pro His Val Arg Ser Ile Ser Gly Leu Pro Val His Ala  
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 435 440 445  
 Thr Trp Met Leu Ser Ile Ser Ala Phe Ala Gly Val Gly Ala Ala Gly  
 450 455 460  
 Glu Glu Ile Ala Glu Pro Glu Pro Leu Glu Val Pro Ala Asp Gly Gly  
 465 470 475 480  
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 485 490 495  
 Glu Tyr Leu Val Arg Leu Arg Gly Pro Arg Asn Glu Ser Phe Arg Pro

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Gly	Ala	Ser	Phe	Arg	Ile	Pro	Thr	Thr	Thr	Gly	Leu	Ser	Glu	Ala	Ser
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	610					615					620				
Arg	Thr	Gly	Val	Asp	Val	Gly	Asp	Pro	Lys	Val	Ser	Val	Arg	Asn	His
625				630						635					640
His	Gly	Ser	Pro	Leu	Arg	Thr	Val	Lys	Met	Val	Thr	Pro	Asp	Asn	Gly
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Asp	Pro	Phe	Thr	Thr	Ser	Val	Thr	Pro	Leu	Ser	Pro	Gly	Lys	Ala	Ala
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 Gly Asp Leu Ile Ser Ala Glu Ala Met Val Leu Gly Ala Arg Asn Pro  
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&lt;210&gt; 285

&lt;211&gt; 636

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(613)

&lt;223&gt; RXN02266

&lt;400&gt; 285

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His	Pro	Arg	Gln	Ala	Asp	Ser	His	Phe	Asn	Met	Leu	Leu	Pro	Asp	Gly	
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Asn	Glu	Asn	Ala	His	Gln	Leu	Ser	Val	Ala	Leu	Asn	Gln	Val	Ala	His	
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Ile	Ser	Asn	Leu	Leu	Lys	Pro	Leu	Leu	Ala	Glu	Ser	Leu	Ile	Val	Gln	
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gaa	tcc	gag	tgg	ttt	ggc	acc	ctg	acc	gac	atc	gag	cag	gat	tta	ttg	547
Glu	Ser	Glu	Trp	Phe	Gly	Thr	Leu	Thr	Asp	Ile	Glu	Gln	Asp	Leu	Leu	
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&lt;210&gt; 286

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 <213> Corynebacterium glutamicum

<400> 286

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Asn Gln Val Ala His Leu Leu Ala Tyr Asp Ala Asp Ser Ser Ile His
          35          40          45
Arg Pro Asp Gly Leu Ser Leu Ala Ser Tyr Arg Ile Leu Phe Ser Leu
          50          55          60
Trp Thr Asp Gly Pro Met Ser Pro Leu Gln Val Thr Asp Lys Thr Gly
          65          70          75          80
Met Lys Lys Ser Ala Ile Ser Asn Leu Leu Lys Pro Leu Leu Ala Glu
          85          90          95
Ser Leu Ile Val Gln Val Thr Ala Glu Asn Asp Arg Arg Ser Lys Val
          100          105          110
Leu Ser Leu Ser Glu Lys Gly Thr Thr Tyr Ile Gln Lys Thr Ala Thr
          115          120          125
Arg Gln Asn Ala Leu Glu Ser Glu Trp Phe Gly Thr Leu Thr Asp Ile
          130          135          140
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<220>

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<222> (101)..(3799)

<223> RXN02362

<400> 287

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                                   Val Thr Ile Ser Arg
                                   1          5
cga ctc aaa caa gag cgc agt ttc gct gac gat ctt caa gat ctc aaa 163
Arg Leu Lys Gln Glu Arg Ser Phe Ala Asp Asp Leu Gln Asp Leu Lys
          10          15          20
act ctc aat gat caa ctg cgg ttt aca aac gcc aaa ttg caa gct cgc 211
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Phe	Ser	Leu	Ala	Asp	Leu	Asn	Arg	Arg	Glu	Tyr	Val	Gly	Leu	Ile	Gln		
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Thr	Thr	Glu	Ser	Leu	Lys	Gln	Leu	Val	Thr	His	Ile	Pro	Ala	Arg	Ser		
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Phe	Pro	Thr	Ser	Gly	Ser	Asn	Trp	Val	Ile	Gln	Tyr	Ser	Gln	Ile	Leu			
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Gln Trp Gln Pro Lys Val Pro Ser Val Lys Ala Val Val Ala Asn Asp	
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Pro Ser Phe Glu Leu Asp Pro Gln Phe Asp Pro Phe Leu Thr His Arg	
890 895 900	
tgg atg ttc gct cca cga agt ggg aag gtc tta ctc cca caa gaa atc	2851
Trp Met Phe Ala Pro Arg Ser Gly Lys Val Leu Leu Pro Gln Glu Ile	
905 910 915	
cgc aca gtg tgg gac gcc cga ttc aat atg cgc cat gtc tta gcg cag	2899
Arg Thr Val Trp Asp Ala Arg Phe Asn Met Arg His Val Leu Ala Gln	
920 925 930	
cgt gaa aac ctt cat gtg aaa tcg att caa gat ttt gac gat gcc acc	2947
Arg Glu Asn Leu His Val Lys Ser Ile Gln Asp Phe Asp Asp Ala Thr	
935 940 945	
agt acc tat ctc acc agt gat cct cgg gtg gca tta gat gaa ttg gat	2995
Ser Thr Tyr Leu Thr Ser Asp Pro Arg Val Ala Leu Asp Glu Leu Asp	
950 955 960 965	
aag agc tca att ccg tct aat tcc cac ttt gaa tca ttc atc cga tcc	3043
Lys Ser Ser Ile Pro Ser Asn Ser His Phe Glu Ser Phe Ile Arg Ser	
970 975 980	
gga tta gct gag ctt tct ttc gaa gtt gac gac aca gcc gga gat atc	3091
Gly Leu Ala Glu Leu Ser Phe Glu Val Asp Asp Thr Ala Gly Asp Ile	
985 990 995	
cat cgc gtt ccc tgg atc ggc ctg atc cag gaa atg aac gac ctc aga	3139

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<210> 288  
 <211> 1233  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 288  
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           20                  25                  30  
 Lys Leu Gln Ala Arg Ile Ser Gly Ile Gly Asn Asp Gly Lys Lys Ile  
           35                  40                  45  
 Thr Arg Pro Thr Pro Leu Leu Ala Leu Asp Phe Gln Leu Thr Val Glu  
   50                  55                  60  
 Glu Tyr Glu Thr Ile Ile Ala Ile Leu Val Glu Ala Val Gly Gly Asn  
   65                  70                  75                  80  
 Gln Ser Lys Pro Ala Ile Leu Lys Asp Leu Phe Ile Glu Tyr Pro Leu  
           85                  90                  95  
 Val Phe Leu Ala Ala Leu Ser Gly Thr Ala Met Leu Asp Ala Gln Glu  
           100                  105                  110  
 Gly Phe Trp Pro Ala Phe Trp Lys Arg Thr Gln Val Ser Val Pro Glu  
           115                  120                  125  
 His Val Tyr Asp Ala Ile Arg Lys Glu Leu Val Asn Ser Ile Arg Lys  
   130                  135                  140  
 Asn Gly Leu Glu Thr Phe Ser Leu Ala Asp Leu Asn Arg Arg Glu Tyr  
  145                  150                  155                  160  
 Val Gly Leu Ile Gln Leu His Ser Gly Leu Ser Ala Lys Asp Met Leu  
           165                  170                  175  
 Ala Leu Val Lys Phe Ile Asp His Thr Arg Ala Glu Asn Gln Gly Trp  
           180                  185                  190  
 Asp Ser Gly Glu Asp Phe Ala Ser Tyr Ala Lys Ser Val Phe Ser Ser  
           195                  200                  205  
 Gly Asp Asn Leu Leu Thr Thr Glu Ser Leu Lys Gln Leu Val Thr His  
   210                  215                  220  
 Ile Pro Ala Arg Ser Val Asp Phe Ile Ala Arg Val Tyr Glu Leu Thr  
  225                  230                  235                  240  
 Asn Trp Tyr Arg Asp Leu Lys Asp Leu Asn Glu Val Glu Ala Phe Val  
           245                  250                  255  
 Gly Thr His Gly Leu Pro Glu Leu Ser Phe Lys Phe Leu Leu Glu Cys  
           260                  265                  270  
 Leu Ser Gly Glu Ala Glu Gln Ile Ala Glu Lys Thr Lys Ala Ala Pro  
           275                  280                  285

Ala Ser Leu Glu Asn Leu Glu Pro Pro His Leu Tyr Leu Asp Pro Gln  
 290 295 300  
 Ser Phe Glu Leu Ser Leu Val Phe Pro Ala Ile Ser Lys Thr Ala Ala  
 305 310 315 320  
 Leu Gln Ile Pro Ala Pro Glu Trp Thr Val Ile Tyr Asp Gly Asn Ser  
 325 330 335  
 Ile Lys Val Arg Pro Glu Gln Asp Trp Ser Tyr Gly Gly Phe Ala Glu  
 340 345 350  
 Tyr Arg Leu Pro Leu Asp Lys Pro Leu Ser Ser Leu Arg Val Ile Thr  
 355 360 365  
 Pro Thr Glu Lys Ser Leu Ile Leu Ile Glu Gly Phe Gly His Lys Asn  
 370 375 380  
 Pro Ile Met Phe Phe Lys Asn Asn Gly Gln Pro Tyr Ala Asn Gln Glu  
 385 390 395 400  
 Met Leu Ser Gly Asn Ala Val Thr Ala Ile Val Pro Ala Ala Ala Ile  
 405 410 415  
 Ile Arg Ala Arg Met Arg Ala Ser Lys Thr Phe Asn Tyr Gln Asp Leu  
 420 425 430  
 Gly Pro Leu Ser Gly Trp Asn Lys Trp Val Ile Arg Ser Ile Pro Leu  
 435 440 445  
 Lys Arg Ala Glu Ser Ile Thr Val Ser His Gly Gly Phe Arg Lys Glu  
 450 455 460  
 Leu Pro Val Arg Arg Lys Val Asp Val Gln Trp Ile Thr Glu Asp Leu  
 465 470 475 480  
 Thr Ile Glu Asn Leu Gln Gly Leu Asp His Glu Pro Val Phe His Thr  
 485 490 495  
 Ser Pro Arg Ile Glu Phe Pro Thr Ser Gly Ser Asn Trp Val Ile Gln  
 500 505 510  
 Tyr Ser Gln Ile Leu Pro Asp Gly Ser Leu Ile Glu Met Glu Asp Tyr  
 515 520 525  
 Pro Val Glu Pro Glu Asn Phe Gly Tyr Glu Leu Asp Leu Phe Glu Glu  
 530 535 540  
 Ser Asp Asp Pro Trp Val Gly Gln Phe Leu Val Thr Leu Leu Lys Asp  
 545 550 555 560  
 Glu Lys Val Tyr Glu Thr Arg Lys Phe Asn Leu Ala Glu Gly Leu Asp  
 565 570 575  
 Leu Ser Leu Thr Phe Ser Gly Gly Gly Pro Glu Asn Arg Phe Arg Tyr  
 580 585 590  
 Pro Ser Ile Asn Gln Gly Gln Thr Gly Leu Thr Lys Thr Phe Ala Arg  
 595 600 605  
 Phe Ser Ser Asn Ser Glu Lys His Ile Arg Phe Pro Asp Glu Ile Ile

610					615					620					
Gly 625	Leu	Asp	Ala	Phe	Thr 630	Ser	Gln	Lys	Ala	Phe 635	Asn	Ile	Ala	Ser	Gly 640
Asp	Phe	Pro	Glu	Asp 645	Tyr	Asn	Leu	Asp	Val 650	Phe	Ile	Thr	Pro	Pro	Gln 655
Leu	His	Tyr	Gln 660	Val	Pro	Val	Thr	His 665	Ser	Gln	Thr	Lys	Trp 670	Glu	Ser
Thr	Lys	Thr	Thr 675	Leu	Asp	Phe	Asn 680	Asp	Phe	Ala	Asp	Gly 685	Asn	Leu	Gln
Ile 690	Arg	Phe	Pro	Asn	Glu	Val 695	Tyr	Asp	Pro	Asn	Leu 700	Lys	Ile	Ile	Lys
Met 705	Val	Ala	Tyr	Lys	Lys 710	Pro	Glu	Ser	Ser	Glu 715	Pro	Lys	Tyr	Leu	Ser 720
Lys	Ile	Gly	Ser	Ser 725	Lys	Val	Trp	Ser	Ile 730	Pro	Met	Asp	Arg	Ile	Lys 735
Glu	Leu	Met	Asp 740	Asp	Asp	Ala	Gln 745	Phe	Leu	Leu	Ile	Ala	Glu 750	Trp	Phe
Ala	Glu	Ser 755	Lys	Asp	Gln	His	Arg 760	Glu	Lys	Ile	Ile	Ser 765	Glu	Ala	Lys
Arg	Thr 770	Gly	Lys	Ile	Ser	Asn 775	Ala	Ala	Leu	Lys	Ser 780	Ala	Arg	Pro	Gln
Pro 785	Gln	Ala	Ser	Ser 790	His	Ile	Ala	Thr	Ile 795	Glu	Lys	Lys	Pro	Leu	Leu 800
Ala	Ala	Ala	Glu	Ile 805	Lys	Leu	Ser	Thr	Val 810	Glu	Leu	Glu	Leu	Gly 815	Arg
His	Thr	Ser	Lys 820	Arg	Leu	Glu	Gly 825	Trp	Ala	Trp	Ser	Ala	Leu 830	Asn	Pro
Leu	Asp	Pro 835	Pro	Ile	Lys	Val 840	Asp	Phe	Gln	Gly	Thr 845	Ser	Gly	Ser	Leu
Pro 850	Asp	Thr	His	Phe	Val 855	Val	Gly	Pro	Leu	Ile	Val 860	Glu	Val	Arg	Glu
Lys 865	Glu	Phe	Leu	Ser	Gln 870	Trp	Gln	Pro	Lys	Val 875	Pro	Ser	Val	Lys	Ala 880
Val	Val	Ala	Asn 885	Asp	Pro	Ser	Phe	Glu	Leu 890	Asp	Pro	Gln	Phe	Asp 895	Pro
Phe	Leu	Thr 900	His	Arg	Trp	Met	Phe	Ala 905	Pro	Arg	Ser	Gly	Lys 910	Val	Leu
Leu	Pro	Gln 915	Glu	Ile	Arg	Thr	Val 920	Trp	Asp	Ala	Arg	Phe	Asn	Met	Arg
His 930	Val	Leu	Ala	Gln	Arg	Glu 935	Asn	Leu	His	Val	Lys 940	Ser	Ile	Gln	Asp

Phe Asp Asp Ala Thr Ser Thr Tyr Leu Thr Ser Asp Pro Arg Val Ala  
 945 950 955 960  
 Leu Asp Glu Leu Asp Lys Ser Ser Ile Pro Ser Asn Ser His Phe Glu  
 965 970 975  
 Ser Phe Ile Arg Ser Gly Leu Ala Glu Leu Ser Phe Glu Val Asp Asp  
 980 985 990  
 Thr Ala Gly Asp Ile His Arg Val Pro Trp Ile Gly Leu Ile Gln Glu  
 995 1000 1005  
 Met Asn Asp Leu Arg Ile Leu Gln Ile Gln Gly Tyr Glu Thr Glu Glu  
 1010 1015 1020  
 Arg Ala Ile Glu Arg Arg Asn Ser Gln Ser Tyr Ile Arg Glu Ile Gly  
 1025 1030 1035 1040  
 Gly Ser Glu Leu Trp Asn Ile Leu Lys Gly Asn Ser Glu Gly Leu Ser  
 1045 1050 1055  
 Leu Ala Gln Lys Cys Ala Pro Gln Ala Thr Glu Ile Asn Val Ile Arg  
 1060 1065 1070  
 Asn Ser Gly Leu Glu Ala Met Arg Asn Gly Leu Gly Ala Asp Gln Phe  
 1075 1080 1085  
 Ser Ala Glu Phe Ile Ser Ala Asp Ser Arg Leu Arg Ala Gln Leu Glu  
 1090 1095 1100  
 Trp Leu Glu Asn Arg Arg Glu Leu Asn Asp Leu Gly Gln Leu Pro Thr  
 1105 1110 1115 1120  
 Leu Phe Asp Phe Ala Glu Lys Tyr Glu Tyr Leu Ile Asp His Leu Gly  
 1125 1130 1135  
 Asp Asp Arg Ile Lys Val Thr Ala Arg Glu Leu Ser Thr Leu Ala Ser  
 1140 1145 1150  
 Glu His Arg Arg Gly Asn Ala Glu Asn Trp Leu Tyr Ala Pro Tyr Val  
 1155 1160 1165  
 Ser Phe Ile Tyr Ser Leu Leu Asn Arg Met Ile Ala His Glu Val Ile  
 1170 1175 1180  
 Arg Pro Ile Ala Gln Ile Asn Tyr Ser Arg His Asp Trp Ala Asn Ala  
 1185 1190 1195 1200  
 Ala Arg Leu Ile Pro Arg Leu Thr Gly Phe Asp Leu Val Ser Ala Glu  
 1205 1210 1215  
 Ala Lys Val Leu Ser Ala Ile Asn Asn Asn Asn Ile Ile Pro Thr Ala  
 1220 1225 1230

Ile

&lt;210&gt; 289

&lt;211&gt; 1005

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(982)

&lt;223&gt; RXN02506

&lt;400&gt; 289

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atatccatct	cttgcatacc	ggccgaaagg	tttagcacac	atg	cac	ctc	aat	cag	115
				Met	His	Leu	Asn	Gln	
				1				5	

ctc	gaa	ttt	ttc	atc	gca	gta	gcc	caa	cac	gga	cag	atc	aac	cgc	gcc	163
Leu	Glu	Phe	Phe	Ile	Ala	Val	Ala	Gln	His	Gly	Gln	Ile	Asn	Arg	Ala	
			10						15					20		

gcc	gaa	gaa	ctc	ctc	att	tcc	caa	ccc	gct	ctc	agc	cga	cag	atc	tcc	211
Ala	Glu	Glu	Leu	Leu	Ile	Ser	Gln	Pro	Ala	Leu	Ser	Arg	Gln	Ile	Ser	
			25					30					35			

gca	ctt	gaa	aaa	tcc	gtc	gga	gct	cca	ctc	ttc	gaa	cgc	cat	tcc	cgc	259
Ala	Leu	Glu	Lys	Ser	Val	Gly	Ala	Pro	Leu	Phe	Glu	Arg	His	Ser	Arg	
		40					45					50				

ggc	gtc	tcc	ctc	aca	aag	gcc	gga	gaa	atc	ctc	cac	gaa	gaa	gcc	ctc	307
Gly	Val	Ser	Leu	Thr	Lys	Ala	Gly	Glu	Ile	Leu	His	Glu	Glu	Ala	Leu	
	55					60					65					

cga	acg	ctt	agc	agg	atg	caa	tcg	gta	gtc	gat	gaa	atc	caa	tcc	ggc	355
Arg	Thr	Leu	Ser	Arg	Met	Gln	Ser	Val	Val	Asp	Glu	Ile	Gln	Ser	Gly	
	70				75					80					85	

gag	cac	ctc	atc	acc	agc	atc	aac	atc	gga	gtt	ccc	cct	gga	atc	ccc	403
Glu	His	Leu	Ile	Thr	Ser	Ile	Asn	Ile	Gly	Val	Pro	Pro	Gly	Ile	Pro	
				90					95					100		

atc	gac	tgg	ttg	cgc	tgc	caa	ctc	atc	gat	tta	ggc	ccc	gag	acc	cgc	451
Ile	Asp	Trp	Leu	Arg	Cys	Gln	Leu	Ile	Asp	Leu	Gly	Pro	Glu	Thr	Arg	
			105				110						115			

att	tca	ctg	atc	gaa	tcc	ccc	acc	gat	gat	cag	cta	aaa	ctt	ctt	aaa	499
Ile	Ser	Leu	Ile	Glu	Ser	Pro	Thr	Asp	Asp	Gln	Leu	Lys	Leu	Leu	Lys	
		120					125					130				

caa	cgc	gaa	ctc	gac	atc	gcc	ctt	tgt	cga	cgc	caa	agc	gag	gcc	ttt	547
Gln	Arg	Glu	Leu	Asp	Ile	Ala	Leu	Cys	Arg	Arg	Gln	Ser	Glu	Ala	Phe	
		135				140					145					

gcc	acc	aca	ctt	gtc	cac	gaa	caa	gaa	ctg	gga	atc	gtc	gtc	cga	aaa	595
Ala	Thr	Thr	Leu	Val	His	Glu	Gln	Glu	Leu	Gly	Ile	Val	Val	Arg	Lys	
	150				155				160					165		

aac	tcc	gaa	ctg	cac	caa	aaa	gtc	gca	gga	aaa	gac	aac	gcc	aca	ctc	643
Asn	Ser	Glu	Leu	His	Gln	Lys	Val	Ala	Gly	Lys	Asp	Asn	Ala	Thr	Leu	
				170					175					180		

ttc	gat	ctt	gaa	ggg	ctt	cga	gtc	ctc	gca	cac	tcc	cgc	ggc	gaa	gta	691
Phe	Asp	Leu	Glu	Gly	Leu	Arg	Val	Leu	Ala	His	Ser	Arg	Gly	Glu	Val	

185										190										195										
aga	att	cag	gaa	gaa	atc	ctc	aaa	aac	gcc	atg	ctc	gcc	gca	gga	gtt	739														
Arg	Ile	Gln	Glu	Glu	Ile	Leu	Lys	Asn	Ala	Met	Leu	Ala	Ala	Gly	Val															
200										210																				
aat	gcc	acg	tgg	atc	ttc	cga	aaa	ttt	ggg	caa	tat	agc	tca	ctg	atc	787														
Asn	Ala	Thr	Trp	Ile	Phe	Arg	Lys	Phe	Gly	Gln	Tyr	Ser	Ser	Leu	Ile															
215										225																				
gca	gac	ctt	gtc	cag	gcc	gat	gtc	gca	ctc	aca	aca	gag	gaa	tcc	gcc	835														
Ala	Asp	Leu	Val	Gln	Ala	Asp	Val	Ala	Leu	Thr	Thr	Glu	Glu	Ser	Ala															
230										245																				
cgc	acc	aac	ttc	ccc	agc	tgg	caa	tgg	gtc	ccc	atc	gaa	ggc	gaa	gac	883														
Arg	Thr	Asn	Phe	Pro	Ser	Trp	Gln	Trp	Val	Pro	Ile	Glu	Gly	Glu	Asp															
250										260																				
gcc	tcc	gga	aat	gac	ctt	gtt	gtt	cgc	acc	tgg	atc	acc	tgg	aac	ccc	931														
Ala	Ser	Gly	Asn	Asp	Leu	Val	Val	Arg	Thr	Trp	Ile	Thr	Trp	Asn	Pro															
265										275																				
caa	ccc	acc	ccc	gcg	gtg	aag	gcc	ctg	atc	cag	aaa	ttt	att	gac	gga	979														
Gln	Pro	Thr	Pro	Ala	Val	Lys	Ala	Leu	Ile	Gln	Lys	Phe	Ile	Asp	Gly															
280										290																				
aac	tgagttctaa	acagccgcca	tga												1005															
Asn																														

&lt;210&gt; 290

&lt;211&gt; 294

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 290

Met	His	Leu	Asn	Gln	Leu	Glu	Phe	Phe	Ile	Ala	Val	Ala	Gln	His	Gly
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Gln	Ile	Asn	Arg	Ala	Ala	Glu	Glu	Leu	Leu	Ile	Ser	Gln	Pro	Ala	Leu
		20						25					30		
Ser	Arg	Gln	Ile	Ser	Ala	Leu	Glu	Lys	Ser	Val	Gly	Ala	Pro	Leu	Phe
		35					40					45			
Glu	Arg	His	Ser	Arg	Gly	Val	Ser	Leu	Thr	Lys	Ala	Gly	Glu	Ile	Leu
	50				55					60					
His	Glu	Glu	Ala	Leu	Arg	Thr	Leu	Ser	Arg	Met	Gln	Ser	Val	Val	Asp
	65				70					75					80
Glu	Ile	Gln	Ser	Gly	Glu	His	Leu	Ile	Thr	Ser	Ile	Asn	Ile	Gly	Val
				85					90					95	
Pro	Pro	Gly	Ile	Pro	Ile	Asp	Trp	Leu	Arg	Cys	Gln	Leu	Ile	Asp	Leu
		100						105					110		
Gly	Pro	Glu	Thr	Arg	Ile	Ser	Leu	Ile	Glu	Ser	Pro	Thr	Asp	Asp	Gln
		115					120					125			



Leu Lys Leu Leu Lys Gln Arg Glu Leu Asp Ile Ala Leu Cys Arg Arg  
 130 135 140  
 Gln Ser Glu Ala Phe Ala Thr Thr Leu Val His Glu Gln Glu Leu Gly  
 145 150 155 160  
 Ile Val Val Arg Lys Asn Ser Glu Leu His Gln Lys Val Ala Gly Lys  
 165 170 175  
 Asp Asn Ala Thr Leu Phe Asp Leu Glu Gly Leu Arg Val Leu Ala His  
 180 185 190  
 Ser Arg Gly Glu Val Arg Ile Gln Glu Glu Ile Leu Lys Asn Ala Met  
 195 200 205  
 Leu Ala Ala Gly Val Asn Ala Thr Trp Ile Phe Arg Lys Phe Gly Gln  
 210 215 220  
 Tyr Ser Ser Leu Ile Ala Asp Leu Val Gln Ala Asp Val Ala Leu Thr  
 225 230 235 240  
 Thr Glu Glu Ser Ala Arg Thr Asn Phe Pro Ser Trp Gln Trp Val Pro  
 245 250 255  
 Ile Glu Gly Glu Asp Ala Ser Gly Asn Asp Leu Val Val Arg Thr Trp  
 260 265 270  
 Ile Thr Trp Asn Pro Gln Pro Thr Pro Ala Val Lys Ala Leu Ile Gln  
 275 280 285  
 Lys Phe Ile Asp Gly Asn  
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<210> 291  
 <211> 789  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(766)  
 <223> RXN02620

<400> 291  
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 Met Ala Gly Ala Val  
 1 5  
 gga cgc ccc cgg aga tca gct ccg cga cgg gca ggc aag aat cct cgc 163  
 Gly Arg Pro Arg Arg Ser Ala Pro Arg Arg Ala Gly Lys Asn Pro Arg  
 10 15 20  
 gag gag att ctt gac gcc tct gct gag ctt ttc acc cgt caa ggc ttc 211  
 Glu Glu Ile Leu Asp Ala Ser Ala Glu Leu Phe Thr Arg Gln Gly Phe  
 25 30 35  
 gca aca acc tcc acg cat caa atc gct gat gcc gtg gga atc cgc caa 259  
 Ala Thr Thr Ser Thr His Gln Ile Ala Asp Ala Val Gly Ile Arg Gln

40	45	50	
gcc tcg ctg tat tat cac ttc ccg tcc aag acg gaa atc ttc ctc acc			307
Ala Ser Leu Tyr Tyr His Phe Pro Ser Lys Thr Glu Ile Phe Leu Thr			
55	60	65	
ctg ctg aaa tct act gtc gag ccg tcc act gtg ctc gcc gaa gac tta			355
Leu Leu Lys Ser Thr Val Glu Pro Ser Thr Val Leu Ala Glu Asp Leu			
70	75	80	85
agc acc ctg gac gcc gga cct gag atg cgc ctc tgg gca atc gtt gcc			403
Ser Thr Leu Asp Ala Gly Pro Glu Met Arg Leu Trp Ala Ile Val Ala			
	90	95	100
tcc gaa gtg cgt ctg ctg ctg tcc acc aag tgg aac gtc ggt cgc ctg			451
Ser Glu Val Arg Leu Leu Leu Ser Thr Lys Trp Asn Val Gly Arg Leu			
	105	110	115
tac caa ctc ccc atc gtt ggt tct gaa gag ttc gcc gag tac cac agc			499
Tyr Gln Leu Pro Ile Val Gly Ser Glu Glu Phe Ala Glu Tyr His Ser			
	120	125	130
cag cgc gaa gcc ctc acc aac gtc ttc cgc gac ctc gcc acc gaa atc			547
Gln Arg Glu Ala Leu Thr Asn Val Phe Arg Asp Leu Ala Thr Glu Ile			
	135	140	145
gtc ggt gac gac ccc cgc gca gaa ctc ccc ttc cac atc acc atg tcg			595
Val Gly Asp Asp Pro Arg Ala Glu Leu Pro Phe His Ile Thr Met Ser			
	150	155	160
gtg atc gaa atg cgt cgc aac gac ggc aag att cca agc ccg ctt tcc			643
Val Ile Glu Met Arg Arg Asn Asp Gly Lys Ile Pro Ser Pro Leu Ser			
	170	175	180
gca gac agc ctc ccg gag acc gca att atg ctt gcc gac gcc tcc ctc			691
Ala Asp Ser Leu Pro Glu Thr Ala Ile Met Leu Ala Asp Ala Ser Leu			
	185	190	195
gcc gtc ctc ggc gcg ccg ctg ccc gcc gac cgg gtc gaa aaa acg ctt			739
Ala Val Leu Gly Ala Pro Leu Pro Ala Asp Arg Val Glu Lys Thr Leu			
	200	205	210
gaa cta atc aag cag gct gac gcg aaa taaccatccg cgctgcgaa atc			789
Glu Leu Ile Lys Gln Ala Asp Ala Lys			
	215	220	

&lt;210&gt; 292

&lt;211&gt; 222

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 292

Met	Ala	Gly	Ala	Val	Gly	Arg	Pro	Arg	Arg	Ser	Ala	Pro	Arg	Arg	Ala
1				5					10						15

Gly	Lys	Asn	Pro	Arg	Glu	Glu	Ile	Leu	Asp	Ala	Ser	Ala	Glu	Leu	Phe
			20					25					30		

Thr	Arg	Gln	Gly	Phe	Ala	Thr	Thr	Ser	Thr	His	Gln	Ile	Ala	Asp	Ala
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<210> 293
<211> 654
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(631)
<223> RXN00826
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<400> 293																
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ccgtgtccat	tcagactggg	ttctttaagt	tcttgggcac	atg	atc	aca	ggt	tta								115
				Met	Ile	Thr	Val	Leu								
				1				5								
att	gat	gga	caa	tcc	ggt	gcg	ggc	aaa	acc	acc	ttg	gcg	ggt	gag	tta	163
Ile	Asp	Gly	Gln	Ser	Gly	Ala	Gly	Lys	Thr	Thr	Leu	Ala	Gly	Glu	Leu	
				10				15						20		
gct	gcc	cg	acc	ggg	ttt	cag	ttg	ggt	cat	ttg	gat	gac	ttt	tat	cct	211
Ala	Ala	Arg	Thr	Gly	Phe	Gln	Leu	Val	His	Leu	Asp	Asp	Phe	Tyr	Pro	
			25				30						35			

ggt tgg act ggc ctt gaa gcg gca tcg gag att gtt gca cgc cat gtt 259  
 Gly Trp Thr Gly Leu Glu Ala Ala Ser Glu Ile Val Ala Arg His Val  
 40 45 50

ttg gac gcg gac aac ccc ggt ttc ttc acg tgg gat tgg cac aac aat 307  
 Leu Asp Ala Asp Asn Pro Gly Phe Phe Thr Trp Asp Trp His Asn Asn  
 55 60 65

tgc caa ggc gat tgg atc aag ttg gag cct ggt cga agt ctc att atc 355  
 Cys Gln Gly Asp Trp Ile Lys Leu Glu Pro Gly Arg Ser Leu Ile Ile  
 70 75 80 85

gaa ggc tct gga tca atc act gct gca aca aaa cgc aag gca tcg ctg 403  
 Glu Gly Ser Gly Ser Ile Thr Ala Ala Thr Lys Arg Lys Ala Ser Leu  
 90 95 100

ttg ggc gag ctg gtg acc gtt cgt atc act ggt cct gag gct tta aga 451  
 Leu Gly Glu Leu Val Thr Val Arg Ile Thr Gly Pro Glu Ala Leu Arg  
 105 110 115

aaa cag cgc gcc ctc aac cgc gat cct gat tac gca cca ttt tgg aaa 499  
 Lys Gln Arg Ala Leu Asn Arg Asp Pro Asp Tyr Ala Pro Phe Trp Lys  
 120 125 130

gtg tgg gcg cag cag gag caa cgc cat ttc tct tta ggc gtt gag gtg 547  
 Val Trp Ala Gln Gln Glu Gln Arg His Phe Ser Leu Gly Val Glu Val  
 135 140 145

gat cat gag att gtg cta ggt tct gat gag gct tcg gga cga ccc gaa 595  
 Asp His Glu Ile Val Leu Gly Ser Asp Glu Ala Ser Gly Arg Pro Glu  
 150 155 160 165

gaa atc tat gac agc ctg gga acg gcc cag agt tct taagaaagtt 641  
 Glu Ile Tyr Asp Ser Leu Gly Thr Ala Gln Ser Ser  
 170 175

tgactagaga aca 654

&lt;210&gt; 294

&lt;211&gt; 177

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 294

Met Ile Thr Val Leu Ile Asp Gly Gln Ser Gly Ala Gly Lys Thr Thr  
 1 5 10 15

Leu Ala Gly Glu Leu Ala Ala Arg Thr Gly Phe Gln Leu Val His Leu  
 20 25 30

Asp Asp Phe Tyr Pro Gly Trp Thr Gly Leu Glu Ala Ala Ser Glu Ile  
 35 40 45

Val Ala Arg His Val Leu Asp Ala Asp Asn Pro Gly Phe Phe Thr Trp  
 50 55 60

Asp Trp His Asn Asn Cys Gln Gly Asp Trp Ile Lys Leu Glu Pro Gly  
 65 70 75 80

Arg Ser Leu Ile Ile Glu Gly Ser Gly Ser Ile Thr Ala Ala Thr Lys

	85	90	95
Arg Lys Ala Ser Leu Leu Gly Glu Leu Val Thr Val Arg Ile Thr Gly	100	105	110
Pro Glu Ala Leu Arg Lys Gln Arg Ala Leu Asn Arg Asp Pro Asp Tyr	115	120	125
Ala Pro Phe Trp Lys Val Trp Ala Gln Gln Glu Gln Arg His Phe Ser	130	135	140
Leu Gly Val Glu Val Asp His Glu Ile Val Leu Gly Ser Asp Glu Ala	145	150	155
Ser Gly Arg Pro Glu Glu Ile Tyr Asp Ser Leu Gly Thr Ala Gln Ser	165	170	175
Ser			

<210> 295  
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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(532)  
 <223> RXS00070

<400> 295  
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 Val Gly Ile Asn Arg 5  
 atc agc caa ggc tct gcc ccg aag ctg gga gtg cga agc acc aga cag 163  
 Ile Ser Gln Gly Ser Ala Pro Lys Leu Gly Val Arg Ser Thr Arg Gln 20  
 cga aaa gcc gta att gac gtt ctt gag gaa atc gat aac ttc gct tcc 211  
 Arg Lys Ala Val Ile Asp Val Leu Glu Glu Ile Asp Asn Phe Ala Ser 35  
 gcc aaa gaa atc cat cac gag cta tcc acc agg gaa cac aac gtc ggc 259  
 Ala Lys Glu Ile His His Glu Leu Ser Thr Arg Glu His Asn Val Gly 50  
 ctc aca acc gtc tac cga acc ctc caa tcc ctc gcc gac atc gga gca 307  
 Leu Thr Thr Val Tyr Arg Thr Leu Gln Ser Leu Ala Asp Ile Gly Ala 65  
 gtc gac gta ctt acc gtc acg ggt gga gaa act ctg tac cgc caa tgc 355  
 Val Asp Val Leu Thr Val Thr Gly Gly Glu Thr Leu Tyr Arg Gln Cys 85  
 cac gac gag gga cac cac cat cac ctg gtc tgc acc aat tgc ggt cgc 403  
 His Asp Glu Gly His His His His Leu Val Cys Thr Asn Cys Gly Arg 100

aca gtc gaa atc gat ggc ggt cca gta gag aca tgg gca cag gaa att 451  
 Thr Val Glu Ile Asp Gly Gly Pro Val Glu Thr Trp Ala Gln Glu Ile  
                   105                                  110                                  115

gcc act aaa aac ggc ttt gct ctc agt agt cac gag gct gaa atc ttt 499  
 Ala Thr Lys Asn Gly Phe Ala Leu Ser Ser His Glu Ala Glu Ile Phe  
                   120                                  125                                  130

gga ctt tgc gct gat tgt aag gaa aaa gtt acg tagttcaagg acatatgaag 552  
 Gly Leu Cys Ala Asp Cys Lys Glu Lys Val Thr  
                   135                                  140

ctg 555

<210> 296

<211> 144

<212> PRT

<213> Corynebacterium glutamicum

<400> 296

Val Gly Ile Asn Arg Ile Ser Gln Gly Ser Ala Pro Lys Leu Gly Val  
           1                                  5                                  10                                  15

Arg Ser Thr Arg Gln Arg Lys Ala Val Ile Asp Val Leu Glu Glu Ile  
                   20                                  25                                  30

Asp Asn Phe Ala Ser Ala Lys Glu Ile His His Glu Leu Ser Thr Arg  
                   35                                  40                                  45

Glu His Asn Val Gly Leu Thr Thr Val Tyr Arg Thr Leu Gln Ser Leu  
           50                                  55                                  60

Ala Asp Ile Gly Ala Val Asp Val Leu Thr Val Thr Gly Gly Glu Thr  
           65                                  70                                  75                                  80

Leu Tyr Arg Gln Cys His Asp Glu Gly His His His His Leu Val Cys  
                   85                                  90                                  95

Thr Asn Cys Gly Arg Thr Val Glu Ile Asp Gly Gly Pro Val Glu Thr  
                   100                                  105                                  110

Trp Ala Gln Glu Ile Ala Thr Lys Asn Gly Phe Ala Leu Ser Ser His  
           115                                  120                                  125

Glu Ala Glu Ile Phe Gly Leu Cys Ala Asp Cys Lys Glu Lys Val Thr  
           130                                  135                                  140

<210> 297

<211> 936

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(913)

&lt;223&gt; RXS00133

&lt;400&gt; 297

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aatttgaagg tggataccca gcggattaaa gatgatgaag atg cta ttc gtt cgg 115  
 Met Leu Phe Val Arg  
 1 5

cgg ctg aca tcg ctg aaa acc gca aca ggc atc cca gtc acc atg ttc 163  
 Arg Leu Thr Ser Leu Lys Thr Ala Thr Gly Ile Pro Val Thr Met Phe  
 10 15 20

gcc act gtg ttg cag gac aat cgc ctg caa att act cag tgg gtt ggg 211  
 Ala Thr Val Leu Gln Asp Asn Arg Leu Gln Ile Thr Gln Trp Val Gly  
 25 30 35

ttg cgt acc ccg gct ctg cag aat ctg gtc att gaa cca ggt gtg ggc 259  
 Leu Arg Thr Pro Ala Leu Gln Asn Leu Val Ile Glu Pro Gly Val Gly  
 40 45 50

gtt ggt gga cgc gtc gtc gca acc cgt cgt ccg gtt ggt gtg agt gat 307  
 Val Gly Gly Arg Val Val Ala Thr Arg Arg Pro Val Gly Val Ser Asp  
 55 60 65

tac acc agg gca aat gtc att tca cat gag aag gat tcc gcg att cag 355  
 Tyr Thr Arg Ala Asn Val Ile Ser His Glu Lys Asp Ser Ala Ile Gln  
 70 75 80 85

gat gag ggc ctt cat tcc att gtc gca gtt ccc gtg atc gtg cac cgc 403  
 Asp Glu Gly Leu His Ser Ile Val Ala Val Pro Val Ile Val His Arg  
 90 95 100

gaa att cgt ggc gtt ttg tat gtt ggc gtt cac tct gcg gtg cgt ctc 451  
 Glu Ile Arg Gly Val Leu Tyr Val Gly Val His Ser Ala Val Arg Leu  
 105 110 115

ggc gac act gtt att gaa gaa gtc acc atg act gcg cgc acg ttg gaa 499  
 Gly Asp Thr Val Ile Glu Glu Val Thr Met Thr Ala Arg Thr Leu Glu  
 120 125 130

caa aac ctg gcg atc aac tcc gcg ctt cgc cgc aat ggc gtt cct gat 547  
 Gln Asn Leu Ala Ile Asn Ser Ala Leu Arg Arg Asn Gly Val Pro Asp  
 135 140 145

ggt cgc ggt tcc ctc aaa gct aac cgc gtg atg aat ggg gcg gag tgg 595  
 Gly Arg Gly Ser Leu Lys Ala Asn Arg Val Met Asn Gly Ala Glu Trp  
 150 155 160 165

gag cag gtt cgt tcc act cat tcc aag ctg cgc atg ctg gca aat cgt 643  
 Glu Gln Val Arg Ser Thr His Ser Lys Leu Arg Met Leu Ala Asn Arg  
 170 175 180

gtg acc gat gag gat ctg cgc cgc gat ttg gaa gag ctt tgc gat cag 691  
 Val Thr Asp Glu Asp Leu Arg Arg Asp Leu Glu Glu Leu Cys Asp Gln  
 185 190 195

atg gtc acc cca gtc cgc atc aag cag acc acc aag ctg tcc gcg cgt 739  
 Met Val Thr Pro Val Arg Ile Lys Gln Thr Thr Lys Leu Ser Ala Arg  
 200 205 210

gag ttg gac gtg ctg gct tgt gtc gcg ctc ggt cac acc aac gtc gaa 787  
 Glu Leu Asp Val Leu Ala Cys Val Ala Leu Gly His Thr Asn Val Glu  
 215 220 225  
 gct gct gaa gag atg ggc atc ggc gcg gaa acc gtc aag agc tac ctg 835  
 Ala Ala Glu Glu Met Gly Ile Gly Ala Glu Thr Val Lys Ser Tyr Leu  
 230 235 240 245  
 cgc tcg gtc atg cgc aag ctc ggc gcc cac acg cgc tac gag gca gtc 883  
 Arg Ser Val Met Arg Lys Leu Gly Ala His Thr Arg Tyr Glu Ala Val  
 250 255 260  
 aac gca gca cgc cgg atc ggc gca ctg cct taaaaagatt ttgctttacg acg 936  
 Asn Ala Ala Arg Arg Ile Gly Ala Leu Pro  
 265 270

<210> 298  
 <211> 271  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 298  
 Met Leu Phe Val Arg Arg Leu Thr Ser Leu Lys Thr Ala Thr Gly Ile  
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 Pro Val Thr Met Phe Ala Thr Val Leu Gln Asp Asn Arg Leu Gln Ile  
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 Thr Gln Trp Val Gly Leu Arg Thr Pro Ala Leu Gln Asn Leu Val Ile  
 35 40 45  
 Glu Pro Gly Val Gly Val Gly Gly Arg Val Val Ala Thr Arg Arg Pro  
 50 55 60  
 Val Gly Val Ser Asp Tyr Thr Arg Ala Asn Val Ile Ser His Glu Lys  
 65 70 75 80  
 Asp Ser Ala Ile Gln Asp Glu Gly Leu His Ser Ile Val Ala Val Pro  
 85 90 95  
 Val Ile Val His Arg Glu Ile Arg Gly Val Leu Tyr Val Gly Val His  
 100 105 110  
 Ser Ala Val Arg Leu Gly Asp Thr Val Ile Glu Glu Val Thr Met Thr  
 115 120 125  
 Ala Arg Thr Leu Glu Gln Asn Leu Ala Ile Asn Ser Ala Leu Arg Arg  
 130 135 140  
 Asn Gly Val Pro Asp Gly Arg Gly Ser Leu Lys Ala Asn Arg Val Met  
 145 150 155 160  
 Asn Gly Ala Glu Trp Glu Gln Val Arg Ser Thr His Ser Lys Leu Arg  
 165 170 175  
 Met Leu Ala Asn Arg Val Thr Asp Glu Asp Leu Arg Arg Asp Leu Glu  
 180 185 190  
 Glu Leu Cys Asp Gln Met Val Thr Pro Val Arg Ile Lys Gln Thr Thr



195	200	205
Lys Leu Ser Ala Arg Glu Leu Asp Val Leu Ala Cys Val Ala Leu Gly		
210	215	220
His Thr Asn Val Glu Ala Ala Glu Glu Met Gly Ile Gly Ala Glu Thr		
225	230	235
Val Lys Ser Tyr Leu Arg Ser Val Met Arg Lys Leu Gly Ala His Thr		
245	250	255
Arg Tyr Glu Ala Val Asn Ala Ala Arg Arg Ile Gly Ala Leu Pro		
260	265	270

&lt;210&gt; 299

&lt;211&gt; 699

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(676)

&lt;223&gt; RXS00144

&lt;400&gt; 299

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ctttaacgga ccgcacagag aggcggggaa ggaggtcacg atg agc gaa cgt aat	115
Met Ser Glu Arg Asn	
1 5	

agt gct gta cta gaa ctc ctt aat gag gac gac gtc agc cgt acc atc	163
Ser Ala Val Leu Glu Leu Leu Asn Glu Asp Asp Val Ser Arg Thr Ile	
10 15 20	

gca cgc atc gcg cac cag att att gag aaa acc gcg ctt gat tcc aaa	211
Ala Arg Ile Ala His Gln Ile Ile Glu Lys Thr Ala Leu Asp Ser Lys	
25 30 35	

gac gcg gat cgg gtc atg ttg tta ggt att ccc tca ggt gga gtc cca	259
Asp Ala Asp Arg Val Met Leu Leu Gly Ile Pro Ser Gly Gly Val Pro	
40 45 50	

ttg gcc cgt agg ctc gct gaa aag atc gaa gaa ttt tcc ggc gtt tcg	307
Leu Ala Arg Arg Leu Ala Glu Lys Ile Glu Glu Phe Ser Gly Val Ser	
55 60 65	

gta gat acc ggc gct gtt gat atc acc ttg tac agg gat gat ctt cga	355
Val Asp Thr Gly Ala Val Asp Ile Thr Leu Tyr Arg Asp Asp Leu Arg	
70 75 80 85	

aac aaa cca cac cgc gca ctg cag ccc acc tct att cca gca ggt ggt	403
Asn Lys Pro His Arg Ala Leu Gln Pro Thr Ser Ile Pro Ala Gly Gly	
90 95 100	

atc gat aac acc acc gtg att ttg gtg gat gat gtg ctg ttt tcc ggt	451
Ile Asp Asn Thr Thr Val Ile Leu Val Asp Asp Val Leu Phe Ser Gly	
105 110 115	

cgt acc atc cgc gct gca ctt gat gct ttg cgc gac gtt gga cgc ccc	499
---	-----

Arg Thr Ile Arg Ala Ala Leu Asp Ala Leu Arg Asp Val Gly Arg Pro  
 120 125 130

aac tac atc cag tta gct gtg ttg gtt gac cgc ggt cat cgc cag ctg 547  
 Asn Tyr Ile Gln Leu Ala Val Leu Val Asp Arg Gly His Arg Gln Leu  
 135 140 145

ccc att cgc gct gac tat gtg ggc aaa aat ctc ccc acc gca cgc gcg 595  
 Pro Ile Arg Ala Asp Tyr Val Gly Lys Asn Leu Pro Thr Ala Arg Ala  
 150 155 160 165

gaa gac gtt tcc gtc atg ctt aca gaa atc gac ggc cgc gat gca gtc 643  
 Glu Asp Val Ser Val Met Leu Thr Glu Ile Asp Gly Arg Asp Ala Val  
 170 175 180

acg ctc acc cga gaa gac tct gaa ggg gat tcc tagatgaagc acctcctatc 696  
 Thr Leu Thr Arg Glu Asp Ser Glu Gly Asp Ser  
 185 190

cat 699

<210> 300  
 <211> 192  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 300  
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Val Ser Arg Thr Ile Ala Arg Ile Ala His Gln Ile Ile Glu Lys Thr  
 20 25 30

Ala Leu Asp Ser Lys Asp Ala Asp Arg Val Met Leu Leu Gly Ile Pro  
 35 40 45

Ser Gly Gly Val Pro Leu Ala Arg Arg Leu Ala Glu Lys Ile Glu Glu  
 50 55 60

Phe Ser Gly Val Ser Val Asp Thr Gly Ala Val Asp Ile Thr Leu Tyr  
 65 70 75 80

Arg Asp Asp Leu Arg Asn Lys Pro His Arg Ala Leu Gln Pro Thr Ser  
 85 90 95

Ile Pro Ala Gly Gly Ile Asp Asn Thr Thr Val Ile Leu Val Asp Asp  
 100 105 110

Val Leu Phe Ser Gly Arg Thr Ile Arg Ala Ala Leu Asp Ala Leu Arg  
 115 120 125

Asp Val Gly Arg Pro Asn Tyr Ile Gln Leu Ala Val Leu Val Asp Arg  
 130 135 140

Gly His Arg Gln Leu Pro Ile Arg Ala Asp Tyr Val Gly Lys Asn Leu  
 145 150 155 160

Pro Thr Ala Arg Ala Glu Asp Val Ser Val Met Leu Thr Glu Ile Asp  
 165 170 175

Gly Arg Asp Ala Val Thr Leu Thr Arg Glu Asp Ser Glu Gly Asp Ser  
 180 185 190

<210> 301  
 <211> 1230  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1207)  
 <223> RXS00205

<400> 301  
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 atcccacaat aggggtacct tccagaaagt tgggtgaggag atg gct tcc gaa acc 115  
 Met Ala Ser Glu Thr  
 1 5  
 tcc agc ccg aag aag cgg gcc acc acg ctc aaa gac atc gcg caa gca 163  
 Ser Ser Pro Lys Lys Arg Ala Thr Thr Leu Lys Asp Ile Ala Gln Ala  
 10 15 20  
 aca cag ctt tca gtc agc acg gtg tcc cgg gca ttg gcc aac aac gcg 211  
 Thr Gln Leu Ser Val Ser Thr Val Ser Arg Ala Leu Ala Asn Asn Ala  
 25 30 35  
 agc att ccg gaa tcc aca cgc atc cga gtg gtt gaa gcc gct caa aag 259  
 Ser Ile Pro Glu Ser Thr Arg Ile Arg Val Val Glu Ala Ala Gln Lys  
 40 45 50  
 ctg aac tac cgt ccc aat gcc caa gct cgt gca ttg cgg aag tcg agg 307  
 Leu Asn Tyr Arg Pro Asn Ala Gln Ala Arg Ala Leu Arg Lys Ser Arg  
 55 60 65  
 aca gac acc atc ggt gtc atc att cca aac att gag aac cca tat ttc 355  
 Thr Asp Thr Ile Gly Val Ile Ile Pro Asn Ile Glu Asn Pro Tyr Phe  
 70 75 80 85  
 tcc tca cta gca gca tcg att caa aaa gct gct cgt gaa gct ggg gtg 403  
 Ser Ser Leu Ala Ala Ser Ile Gln Lys Ala Ala Arg Glu Ala Gly Val  
 90 95 100  
 tcc acc att ttg tcc aac tct gaa gaa aac cca gag ctg ctt ggt cag 451  
 Ser Thr Ile Leu Ser Asn Ser Glu Glu Asn Pro Glu Leu Leu Gly Gln  
 105 110 115  
 act ttg gcg atc atg gat gac caa cgc ctc gat gga atc atc gtg gtg 499  
 Thr Leu Ala Ile Met Asp Asp Gln Arg Leu Asp Gly Ile Ile Val Val  
 120 125 130  
 cca cac att cag tca gag gaa caa gtc act gac ttg gtt aac agg gga 547  
 Pro His Ile Gln Ser Glu Glu Gln Val Thr Asp Leu Val Asn Arg Gly  
 135 140 145  
 gtg cca gta gtg ctg gca gac cgt agt ttt gtt aac tcg tct att cct 595

Val 150	Pro	Val	Val	Leu	Ala 155	Asp	Arg	Ser	Phe	Val 160	Asn	Ser	Ser	Ile	Pro 165	
tcg	gtt	acc	tca	gat	cca	gtt	ccg	ggc	atg	act	gaa	gct	gtg	gac	tta	643
Ser	Val	Thr	Ser	Asp 170	Pro	Val	Pro	Gly	Met 175	Thr	Glu	Ala	Val	Asp 180	Leu	
ctc	ctg	gca	gct	gac	gtg	caa	ttg	ggc	tac	ctt	gcc	ggc	ccg	cag	gat	691
Leu	Leu	Ala	Ala	Asp 185	Val	Gln	Leu	Gly	Tyr 190	Leu	Ala	Gly	Pro	Gln	Asp	
act	tcc	act	ggt	cag	ctg	cgt	ctt	aac	act	ttt	gaa	aga	cta	tgc	gtg	739
Thr	Ser	Thr	Gly	Gln	Leu	Arg	Leu	Asn	Thr	Phe	Glu	Arg	Leu	Cys	Val	
		200					205					210				
gac	cgc	ggc	atc	gtc	gga	gca	tct	gtc	tat	tac	ggt	ggc	tac	cgc	caa	787
Asp	Arg	Gly	Ile	Val	Gly	Ala	Ser	Val	Tyr	Tyr	Gly	Gly	Tyr	Arg	Gln	
	215					220					225					
gaa	tct	gga	tat	gac	ggc	atc	aag	gtg	ctg	atc	aag	cag	gga	gcc	aat	835
Glu	Ser	Gly	Tyr	Asp	Gly	Ile	Lys	Val	Leu	Ile	Lys	Gln	Gly	Ala	Asn	
230					235					240					245	
gcg	att	atc	gct	ggt	gac	tcc	atg	atg	acc	atc	ggt	gcg	ttg	ttg	gct	883
Ala	Ile	Ile	Ala	Gly	Asp	Ser	Met	Met	Thr	Ile	Gly	Ala	Leu	Leu	Ala	
				250					255						260	
ctt	cat	gag	atg	aat	ttg	aag	atc	ggt	gag	gat	gtg	cag	ctc	att	ggg	931
Leu	His	Glu	Met	Asn	Leu	Lys	Ile	Gly	Glu	Asp	Val	Gln	Leu	Ile	Gly	
			265					270					275			
ttt	gat	aac	aac	cca	att	ttc	cgg	ctg	cag	aat	cca	ccg	ctg	agc	atc	979
Phe	Asp	Asn	Asn	Pro	Ile	Phe	Arg	Leu	Gln	Asn	Pro	Pro	Leu	Ser	Ile	
		280					285					290				
att	gac	cag	cac	gta	caa	gag	atc	ggt	aag	cgt	gcg	ttt	gag	att	ctg	1027
Ile	Asp	Gln	His	Val	Gln	Glu	Ile	Gly	Lys	Arg	Ala	Phe	Glu	Ile	Leu	
	295					300					305					
cag	aag	ctg	atc	aat	ggg	gac	acc	gcg	caa	aaa	tct	gtg	gtg	att	cca	1075
Gln	Lys	Leu	Ile	Asn	Gly	Asp	Thr	Ala	Gln	Lys	Ser	Val	Val	Ile	Pro	
310					315					320					325	
acg	cag	ctc	agc	atc	aat	gga	tca	acg	gcg	gtt	tcc	caa	aag	gcg	gcc	1123
Thr	Gln	Leu	Ser	Ile	Asn	Gly	Ser	Thr	Ala	Val	Ser	Gln	Lys	Ala	Ala	
				330					335					340		
gca	aag	gca	gca	aaa	gca	gcc	caa	aaa	gca	gcc	gcg	aaa	gcc	gca	cag	1171
Ala	Lys	Ala	Ala	Lys	Ala	Ala	Gln	Lys	Ala	Ala	Ala	Lys	Ala	Ala	Gln	
			345					350					355			
aac	acg	caa	cac	gag	gtg	agc	cta	gat	ggt	gaa	ctc	tga	aca	agcg		1217
Asn	Thr	Gln	His	Glu	Val	Ser	Leu	Asp	Gly	Glu	Leu					
		360					365									
cttc	atc	agc	atg													1230

&lt;210&gt; 302

&lt;211&gt; 369

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 302

Met Ala Ser Glu Thr Ser Ser Pro Lys Lys Arg Ala Thr Thr Leu Lys  
 1 5 10 15  
 Asp Ile Ala Gln Ala Thr Gln Leu Ser Val Ser Thr Val Ser Arg Ala  
 20 25 30  
 Leu Ala Asn Asn Ala Ser Ile Pro Glu Ser Thr Arg Ile Arg Val Val  
 35 40 45  
 Glu Ala Ala Gln Lys Leu Asn Tyr Arg Pro Asn Ala Gln Ala Arg Ala  
 50 55 60  
 Leu Arg Lys Ser Arg Thr Asp Thr Ile Gly Val Ile Ile Pro Asn Ile  
 65 70 75 80  
 Glu Asn Pro Tyr Phe Ser Ser Leu Ala Ala Ser Ile Gln Lys Ala Ala  
 85 90 95  
 Arg Glu Ala Gly Val Ser Thr Ile Leu Ser Asn Ser Glu Glu Asn Pro  
 100 105 110  
 Glu Leu Leu Gly Gln Thr Leu Ala Ile Met Asp Asp Gln Arg Leu Asp  
 115 120 125  
 Gly Ile Ile Val Val Pro His Ile Gln Ser Glu Glu Gln Val Thr Asp  
 130 135 140  
 Leu Val Asn Arg Gly Val Pro Val Val Leu Ala Asp Arg Ser Phe Val  
 145 150 155 160  
 Asn Ser Ser Ile Pro Ser Val Thr Ser Asp Pro Val Pro Gly Met Thr  
 165 170 175  
 Glu Ala Val Asp Leu Leu Leu Ala Ala Asp Val Gln Leu Gly Tyr Leu  
 180 185 190  
 Ala Gly Pro Gln Asp Thr Ser Thr Gly Gln Leu Arg Leu Asn Thr Phe  
 195 200 205  
 Glu Arg Leu Cys Val Asp Arg Gly Ile Val Gly Ala Ser Val Tyr Tyr  
 210 215 220  
 Gly Gly Tyr Arg Gln Glu Ser Gly Tyr Asp Gly Ile Lys Val Leu Ile  
 225 230 235 240  
 Lys Gln Gly Ala Asn Ala Ile Ile Ala Gly Asp Ser Met Met Thr Ile  
 245 250 255  
 Gly Ala Leu Leu Ala Leu His Glu Met Asn Leu Lys Ile Gly Glu Asp  
 260 265 270  
 Val Gln Leu Ile Gly Phe Asp Asn Asn Pro Ile Phe Arg Leu Gln Asn  
 275 280 285  
 Pro Pro Leu Ser Ile Ile Asp Gln His Val Gln Glu Ile Gly Lys Arg  
 290 295 300  
 Ala Phe Glu Ile Leu Gln Lys Leu Ile Asn Gly Asp Thr Ala Gln Lys

305		310		315		320
Ser Val Val Ile	Pro Thr Gln Leu Ser Ile	Asn Gly Ser Thr	Ala Val			
	325	330	335			
Ser Gln Lys Ala	Ala Ala Lys Ala	Ala Lys Ala Ala	Gln Lys Ala Ala			
	340	345	350			
Ala Lys Ala Ala	Gln Asn Thr Gln His Glu Val	Ser Leu Asp Gly Glu				
	355	360	365			

Leu

<210> 303  
 <211> 1392  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1369)  
 <223> RXS00470

<400> 303  
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 Met Gly Glu Ser Pro 5  
 1  
 gaa aag gtg gcg ttc agg gtc ttc cct gat ggt ttg gtg tcg cag ggg 163  
 Glu Lys Val Ala Phe Arg Val Phe Pro Asp Gly Leu Val Ser Gln Gly 20  
 10 15  
 cat gac atg atc gaa gat atg agt aac aca cct gcg cct tat acc ccg 211  
 His Asp Met Ile Glu Asp Met Ser Asn Thr Pro Ala Pro Tyr Thr Pro 35  
 25 30  
 cag cct gcg ggg caa gcg gtg cct tta tat ccc acg ttt acc cgg tca 259  
 Gln Pro Ala Gly Gln Ala Val Pro Leu Tyr Pro Thr Phe Thr Arg Ser 50  
 40 45  
 aga gat ggt cgg gtt gtt gcg ggt gtc gca tcg ggg ctg gca aag cat 307  
 Arg Asp Gly Arg Val Val Ala Gly Val Ala Ser Gly Leu Ala Lys His 65  
 55 60  
 ctt aat gtg tcg gtg ttt tgg gtt cgt gcg ctg ctg att ttt gcg gcg 355  
 Leu Asn Val Ser Val Phe Trp Val Arg Ala Leu Leu Ile Phe Ala Ala 85  
 70 75 80  
 ttg ctg agc ggt gcg ggt ctt ttt gcg tat gcc ttg att tgg att ttt 403  
 Leu Leu Ser Gly Ala Gly Leu Phe Ala Tyr Ala Leu Ile Trp Ile Phe 100  
 90 95  
 acg cgc att gag aaa aag ggg agt ggg gag gcg tcg aca agc aag cgc 451  
 Thr Arg Ile Glu Lys Lys Gly Ser Gly Glu Ala Ser Thr Ser Lys Arg 115  
 105 110  
 tgg gtg tcg tgg tgc ctg gtg ctg ctc gct atc ggt ggt gct gcg gcg 499

Trp	Val	Ser	Trp	Cys	Leu	Val	Leu	Leu	Ala	Ile	Gly	Gly	Ala	Ala	Ala		
		120					125					130					
tcg	gtg	atg	ctg	agc	acc	ggc	ttc	gcg	gtg	ggc	acg	ttg	gtg	ccc	atc	547	
Ser	Val	Met	Leu	Ser	Thr	Gly	Phe	Ala	Val	Gly	Thr	Leu	Val	Pro	Ile		
	135					140					145						
ggc	gtg	gtc	ggc	gtg	ggc	ctg	ttg	atg	gtg	tgg	ctg	gcg	tat	gac	cgc	595	
Gly	Val	Val	Gly	Val	Gly	Leu	Leu	Met	Val	Trp	Leu	Ala	Tyr	Asp	Arg		
150					155					160					165		
ggg	gtg	gaa	tcc	ggc	ccg	aat	ctg	ctg	att	att	gcc	acc	ggc	ggc	gtg	643	
Gly	Val	Glu	Ser	Gly	Pro	Asn	Leu	Leu	Ile	Ile	Ala	Thr	Gly	Gly	Val		
				170					175					180			
ttg	atg	ctg	gtg	gcg	atc	gtg	ctg	atc	gtg	atg	aat	tgg	aac	acc	cag	691	
Leu	Met	Leu	Val	Ala	Ile	Val	Leu	Ile	Val	Met	Asn	Trp	Asn	Thr	Gln		
			185				190						195				
gac	ggc	ttc	gtc	atg	gcg	ctg	gtg	gcc	gtg	gtg	ctc	acg	ctg	gtg	ggc	739	
Asp	Gly	Phe	Val	Met	Ala	Leu	Val	Ala	Val	Val	Leu	Thr	Leu	Val	Gly		
		200					205					210					
gtg	gct	gcg	ctg	ggc	gtt	ccg	ctg	tgg	gtg	cgg	atg	tgg	gat	cag	ctg	787	
Val	Ala	Ala	Leu	Gly	Val	Pro	Leu	Trp	Val	Arg	Met	Trp	Asp	Gln	Leu		
	215					220					225						
ggc	gag	gag	cgc	gcg	gaa	aaa	gcc	gca	gct	gct	gag	cgc	gca	gat	att	835	
Gly	Glu	Glu	Arg	Ala	Glu	Lys	Ala	Ala	Ala	Ala	Glu	Arg	Ala	Asp	Ile		
230					235					240					245		
gct	tcc	cgc	ctg	cat	gat	tcg	gta	ctg	cag	acc	ttg	gcg	ctg	att	caa	883	
Ala	Ser	Arg	Leu	His	Asp	Ser	Val	Leu	Gln	Thr	Leu	Ala	Leu	Ile	Gln		
				250					255					260			
aag	cgt	gcc	gac	gac	ccc	gcc	gaa	gtc	gcc	cgc	ctg	gcc	cgc	ggg	cag	931	
Lys	Arg	Ala	Asp	Asp	Pro	Ala	Glu	Val	Ala	Arg	Leu	Ala	Arg	Gly	Gln		
			265					270					275				
gaa	cgc	gag	ctg	cgt	caa	tgg	ctg	ttt	gat	tcc	caa	gat	aaa	aca	cct	979	
Glu	Arg	Glu	Leu	Arg	Gln	Trp	Leu	Phe	Asp	Ser	Gln	Asp	Lys	Thr	Pro		
		280					285					290					
caa	aca	acc	ggc	act	gtc	ttt	act	gcg	ttg	gag	cgc	gcc	tgc	ggc	gaa	1027	
Gln	Thr	Thr	Gly	Thr	Val	Phe	Thr	Ala	Leu	Glu	Arg	Ala	Cys	Gly	Glu		
	295					300					305						
gtc	gag	gat	att	tac	gct	ctg	cgt	atc	gtg	cct	gtg	acc	gtg	gga	acc	1075	
Val	Glu	Asp	Ile	Tyr	Ala	Leu	Arg	Ile	Val	Pro	Val	Thr	Val	Gly	Thr		
310					315					320					325		
gat	gaa	gcg	ctg	act	gag	aaa	acg	cag	gca	gcg	gtg	atg	gca	gtc	cgc	1123	
Asp	Glu	Ala	Leu	Thr	Glu	Lys	Thr	Gln	Ala	Ala	Val	Met	Ala	Val	Arg		
				330					335					340			
gaa	gca	ctc	gtg	aac	gtg	gcc	aag	cat	gcc	ggc	gtg	gaa	acc	gcc	gat	1171	
Glu	Ala	Leu	Val	Asn	Val	Ala	Lys	His	Ala	Gly	Val	Glu	Thr	Ala	Asp		
			345					350					355				
gtg	tac	gcc	gaa	att	atg	ctc	ggc	gaa	ctg	aac	att	ttc	gtc	cgc	gac	1219	
Val	Tyr	Ala	Glu	Ile	Met	Leu	Gly	Glu	Leu	Asn	Ile	Phe	Val	Arg	Asp		

360	365	370	
cgc ggt gca gga ttc gac ccc gac aac atc ccc gac ggg cac cac ggg			1267
Arg Gly Ala Gly Phe Asp Pro Asp Asn Ile Pro Asp Gly His His Gly			
375	380	385	
ctc gcc gaa tcc gtc caa ggc cgc gtc gaa cga gcc ggc gga aaa gta			1315
Leu Ala Glu Ser Val Gln Gly Arg Val Glu Arg Ala Gly Gly Lys Val			
390	395	400	405
cgc atc aaa tct gaa atc ggc gaa ggc acc gaa gtg gca atc acc atg			1363
Arg Ile Lys Ser Glu Ile Gly Glu Gly Thr Glu Val Ala Ile Thr Met			
410	415	420	
gat gtg tagttggtcg tacgcgcgtg tct			1392
Asp Val			

<210> 304  
 <211> 423  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 304  
 Met Gly Glu Ser Pro Glu Lys Val Ala Phe Arg Val Phe Pro Asp Gly  
 1 5 10 15

Leu Val Ser Gln Gly His Asp Met Ile Glu Asp Met Ser Asn Thr Pro  
 20 25 30

Ala Pro Tyr Thr Pro Gln Pro Ala Gly Gln Ala Val Pro Leu Tyr Pro  
 35 40 45

Thr Phe Thr Arg Ser Arg Asp Gly Arg Val Val Ala Gly Val Ala Ser  
 50 55 60

Gly Leu Ala Lys His Leu Asn Val Ser Val Phe Trp Val Arg Ala Leu  
 65 70 75 80

Leu Ile Phe Ala Ala Leu Leu Ser Gly Ala Gly Leu Phe Ala Tyr Ala  
 85 90 95

Leu Ile Trp Ile Phe Thr Arg Ile Glu Lys Lys Gly Ser Gly Glu Ala  
 100 105 110

Ser Thr Ser Lys Arg Trp Val Ser Trp Cys Leu Val Leu Leu Ala Ile  
 115 120 125

Gly Gly Ala Ala Ala Ser Val Met Leu Ser Thr Gly Phe Ala Val Gly  
 130 135 140

Thr Leu Val Pro Ile Gly Val Val Gly Val Gly Leu Leu Met Val Trp  
 145 150 155 160

Leu Ala Tyr Asp Arg Gly Val Glu Ser Gly Pro Asn Leu Leu Ile Ile  
 165 170 175

Ala Thr Gly Gly Val Leu Met Leu Val Ala Ile Val Leu Ile Val Met  
 180 185 190



Asn Trp Asn Thr Gln Asp Gly Phe Val Met Ala Leu Val Ala Val Val  
 195 200 205  
 Leu Thr Leu Val Gly Val Ala Ala Leu Gly Val Pro Leu Trp Val Arg  
 210 215 220  
 Met Trp Asp Gln Leu Gly Glu Glu Arg Ala Glu Lys Ala Ala Ala Ala  
 225 230 235 240  
 Glu Arg Ala Asp Ile Ala Ser Arg Leu His Asp Ser Val Leu Gln Thr  
 245 250 255  
 Leu Ala Leu Ile Gln Lys Arg Ala Asp Asp Pro Ala Glu Val Ala Arg  
 260 265 270  
 Leu Ala Arg Gly Gln Glu Arg Glu Leu Arg Gln Trp Leu Phe Asp Ser  
 275 280 285  
 Gln Asp Lys Thr Pro Gln Thr Thr Gly Thr Val Phe Thr Ala Leu Glu  
 290 295 300  
 Arg Ala Cys Gly Glu Val Glu Asp Ile Tyr Ala Leu Arg Ile Val Pro  
 305 310 315 320  
 Val Thr Val Gly Thr Asp Glu Ala Leu Thr Glu Lys Thr Gln Ala Ala  
 325 330 335  
 Val Met Ala Val Arg Glu Ala Leu Val Asn Val Ala Lys His Ala Gly  
 340 345 350  
 Val Glu Thr Ala Asp Val Tyr Ala Glu Ile Met Leu Gly Glu Leu Asn  
 355 360 365  
 Ile Phe Val Arg Asp Arg Gly Ala Gly Phe Asp Pro Asp Asn Ile Pro  
 370 375 380  
 Asp Gly His His Gly Leu Ala Glu Ser Val Gln Gly Arg Val Glu Arg  
 385 390 395 400  
 Ala Gly Gly Lys Val Arg Ile Lys Ser Glu Ile Gly Glu Gly Thr Glu  
 405 410 415  
 Val Ala Ile Thr Met Asp Val  
 420

&lt;210&gt; 305

&lt;211&gt; 813

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(790)

&lt;223&gt; RXS00471

&lt;400&gt; 305

acgcatcaaa tctgaaatcg gcgaaggcac cgaagtggca atcaccatgg atgtgtagtt 60

 ggctgtacgc gcgtgtcttc ggggctgtaa cctgaaaggc atg gtt gat gtg ttt 115  
 Met Val Asp Val Phe

	1	5	
ttg gtc gat gac cac tcc gtg ttt cgc tcc ggc gtc aaa gca gaa cta			163
Leu Val Asp Asp His Ser Val Phe Arg Ser Gly Val Lys Ala Glu Leu			
	10	15	20
ggc aac gcc gtc aca gta gtc ggc gaa gca ggg acg gtg gcc gac gcc			211
Gly Asn Ala Val Thr Val Val Gly Glu Ala Gly Thr Val Ala Asp Ala			
	25	30	35
gta gcc ggc atc aag gca agc aaa cca gag gta gtg ctt ctc gac gtc			259
Val Ala Gly Ile Lys Ala Ser Lys Pro Glu Val Val Leu Leu Asp Val			
	40	45	50
cac atg ccc gac ggc ggc ggc ctc gca gtg ctc cag cag atc aac gac			307
His Met Pro Asp Gly Gly Gly Leu Ala Val Leu Gln Gln Ile Asn Asp			
	55	60	65
tcc gat gtg gac acc att ttc ttg gca ctc agt gtc tct gat gct gcg			355
Ser Asp Val Asp Thr Ile Phe Leu Ala Leu Ser Val Ser Asp Ala Ala			
	70	75	80
gaa gat gtc atc gcc atc atc cgt ggc ggt gcc agg gga tac gtg acc			403
Glu Asp Val Ile Ala Ile Ile Arg Gly Gly Ala Arg Gly Tyr Val Thr			
	90	95	100
aaa tca atc tcc ggt gaa gaa ctc atc gaa gcc atc aac cgc gtg aaa			451
Lys Ser Ile Ser Gly Glu Glu Leu Ile Glu Ala Ile Asn Arg Val Lys			
	105	110	115
tcc ggc gac gca ttc ttc tca cca cgc ctg gca ggc ttt gtc ctc gac			499
Ser Gly Asp Ala Phe Phe Ser Pro Arg Leu Ala Gly Phe Val Leu Asp			
	120	125	130
gcc ttc gcc gcc ccc gat tcc gca gct ggc gca ggc att gtc gac gca			547
Ala Phe Ala Ala Pro Asp Ser Ala Ala Gly Ala Gly Ile Val Asp Ala			
	135	140	145
ccc gaa aaa gac gcc gcc gta gaa tcc gga aaa atc ctc gac gac cca			595
Pro Glu Lys Asp Ala Ala Val Glu Ser Gly Lys Ile Leu Asp Asp Pro			
	150	155	160
gtt gtc gac gcc ctc acc cgc cgc gaa ctc gaa gtc ctc cgc cta cta			643
Val Val Asp Ala Leu Thr Arg Arg Glu Leu Glu Val Leu Arg Leu Leu			
	170	175	180
gcc cgc ggc tac acc tac aaa gaa atc ggc aaa gaa ctg ttc att tcc			691
Ala Arg Gly Tyr Thr Tyr Lys Glu Ile Gly Lys Glu Leu Phe Ile Ser			
	185	190	195
gtc aaa acc gtg gaa acc cac gcc tca aac att ctg cgg aaa acc caa			739
Val Lys Thr Val Glu Thr His Ala Ser Asn Ile Leu Arg Lys Thr Gln			
	200	205	210
caa tcc aac cgc cac gcg ttg acc cgg tgg gct cac tcg agg gat ctt			787
Gln Ser Asn Arg His Ala Leu Thr Arg Trp Ala His Ser Arg Asp Leu			
	215	220	225
gac taatggcggc taaaaagagt ggc			813
Asp			
230			

&lt;210&gt; 306

&lt;211&gt; 230

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 306

Met Val Asp Val Phe Leu Val Asp Asp His Ser Val Phe Arg Ser Gly  
 1 5 10 15

Val Lys Ala Glu Leu Gly Asn Ala Val Thr Val Val Gly Glu Ala Gly  
 20 25 30

Thr Val Ala Asp Ala Val Ala Gly Ile Lys Ala Ser Lys Pro Glu Val  
 35 40 45

Val Leu Leu Asp Val His Met Pro Asp Gly Gly Gly Leu Ala Val Leu  
 50 55 60

Gln Gln Ile Asn Asp Ser Asp Val Asp Thr Ile Phe Leu Ala Leu Ser  
 65 70 75 80

Val Ser Asp Ala Ala Glu Asp Val Ile Ala Ile Ile Arg Gly Gly Ala  
 85 90 95

Arg Gly Tyr Val Thr Lys Ser Ile Ser Gly Glu Glu Leu Ile Glu Ala  
 100 105 110

Ile Asn Arg Val Lys Ser Gly Asp Ala Phe Phe Ser Pro Arg Leu Ala  
 115 120 125

Gly Phe Val Leu Asp Ala Phe Ala Ala Pro Asp Ser Ala Ala Gly Ala  
 130 135 140

Gly Ile Val Asp Ala Pro Glu Lys Asp Ala Ala Val Glu Ser Gly Lys  
 145 150 155 160

Ile Leu Asp Asp Pro Val Val Asp Ala Leu Thr Arg Arg Glu Leu Glu  
 165 170 175

Val Leu Arg Leu Leu Ala Arg Gly Tyr Thr Tyr Lys Glu Ile Gly Lys  
 180 185 190

Glu Leu Phe Ile Ser Val Lys Thr Val Glu Thr His Ala Ser Asn Ile  
 195 200 205

Leu Arg Lys Thr Gln Gln Ser Asn Arg His Ala Leu Thr Arg Trp Ala  
 210 215 220

His Ser Arg Asp Leu Asp  
 225 230

&lt;210&gt; 307

&lt;211&gt; 708

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(685)

&lt;223&gt; RXS00481

&lt;400&gt; 307

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gtccataaaa ataatgtgcc tacaagaaat ttatagtatc ccatgagtta atatttttaa 60

aaataaactt tatctgactt tgtagaaaaa ggtgattact atg ctg aat atg cag 115
                                         Met Leu Asn Met Gln
                                         1 5

gaa cca gat aaa atc cat ccg gca gaa cct aca ctt cgt aat att tat 163
Glu Pro Asp Lys Ile His Pro Ala Glu Pro Thr Leu Arg Asn Ile Tyr
                        10 15 20

gac gtt aaa act agt gat ccc aaa agt gaa tta gtt gat cgt tct ggc 211
Asp Val Lys Thr Ser Asp Pro Lys Ser Glu Leu Val Asp Arg Ser Gly
                        25 30 35

atg tcg gaa gaa gac att gcg caa att ggg cgg cta atg aaa tcg ttg 259
Met Ser Glu Glu Asp Ile Ala Gln Ile Gly Arg Leu Met Lys Ser Leu
                        40 45 50

gcc agt ctt cgc gat gtg gaa cgt agt att ggt gaa gcc tcg gca cgt 307
Ala Ser Leu Arg Asp Val Glu Arg Ser Ile Gly Glu Ala Ser Ala Arg
                        55 60 65

tat atg gag cta agt gcc cct gat atg cga gct ttg cac tat ttg att 355
Tyr Met Glu Leu Ser Ala Pro Asp Met Arg Ala Leu His Tyr Leu Ile
                        70 75 80 85

gtg gcg ggc aat gcg ggc gaa gtg gtg act cca gga atg ctt gga gct 403
Val Ala Gly Asn Ala Gly Glu Val Val Thr Pro Gly Met Leu Gly Ala
                        90 95 100

cac ctt aag ctt tcc ccg gca tct gta aca aag acg ctt aat agg cta 451
His Leu Lys Leu Ser Pro Ala Ser Val Thr Lys Thr Leu Asn Arg Leu
                        105 110 115

gaa aaa ggt ggg cat att gtt cgt aat gtg cac ccc gtc gac cgc agg 499
Glu Lys Gly Gly His Ile Val Arg Asn Val His Pro Val Asp Arg Arg
                        120 125 130

gct ttc gcc ctc atg gtc act gat gcc act cgt gga gag gcg atg cgg 547
Ala Phe Ala Leu Met Val Thr Asp Ala Thr Arg Gly Glu Ala Met Arg
                        135 140 145

acg ctt ggt aag cat cag gcg cgt cgt ttt gat gct gct aaa cga tta 595
Thr Leu Gly Lys His Gln Ala Arg Arg Phe Asp Ala Ala Lys Arg Leu
                        150 155 160 165

act cca caa gag cgt gaa gtg gtt atc cga ttc ctt cag gat atg gca 643
Thr Pro Gln Glu Arg Glu Val Val Ile Arg Phe Leu Gln Asp Met Ala
                        170 175 180

cag gag tta tcc ctt aat aat gca cca tgg ctc aac acg gag 685
Gln Glu Leu Ser Leu Asn Asn Ala Pro Trp Leu Asn Thr Glu
                        185 190 195

tagatgacca tctacgttaa tta 708

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<210> 308  
 <211> 195  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 308  
 Met Leu Asn Met Gln Glu Pro Asp Lys Ile His Pro Ala Glu Pro Thr  
   1                  5                  10                  15  
 Leu Arg Asn Ile Tyr Asp Val Lys Thr Ser Asp Pro Lys Ser Glu Leu  
                   20                  25                  30  
 Val Asp Arg Ser Gly Met Ser Glu Glu Asp Ile Ala Gln Ile Gly Arg  
           35                  40                  45  
 Leu Met Lys Ser Leu Ala Ser Leu Arg Asp Val Glu Arg Ser Ile Gly  
       50                  55                  60  
 Glu Ala Ser Ala Arg Tyr Met Glu Leu Ser Ala Pro Asp Met Arg Ala  
   65                  70                  75                  80  
 Leu His Tyr Leu Ile Val Ala Gly Asn Ala Gly Glu Val Val Thr Pro  
                   85                  90                  95  
 Gly Met Leu Gly Ala His Leu Lys Leu Ser Pro Ala Ser Val Thr Lys  
           100                  105                  110  
 Thr Leu Asn Arg Leu Glu Lys Gly Gly His Ile Val Arg Asn Val His  
       115                  120                  125  
 Pro Val Asp Arg Arg Ala Phe Ala Leu Met Val Thr Asp Ala Thr Arg  
       130                  135                  140  
 Gly Glu Ala Met Arg Thr Leu Gly Lys His Gln Ala Arg Arg Phe Asp  
 145                  150                  155                  160  
 Ala Ala Lys Arg Leu Thr Pro Gln Glu Arg Glu Val Val Ile Arg Phe  
                   165                  170                  175  
 Leu Gln Asp Met Ala Gln Glu Leu Ser Leu Asn Asn Ala Pro Trp Leu  
       180                  185                  190  
 Asn Thr Glu  
       195

<210> 309  
 <211> 579  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(556)  
 <223> RXS00649

<400> 309  
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 cattttgtgc aagatgcaat agctggcaaa ctggagagcc atg agc acc gac ccc 115  
                   Met Ser Thr Asp Pro

1 5  
 atc gcg gcc ttg gaa tac gaa tcc acc atc ttc gcc cgt cac cgg aat 163  
 Ile Ala Ala Leu Glu Tyr Glu Ser Thr Ile Phe Ala Arg His Arg Asn  
 10 15 20  
 caa tac acc ggc caa gca ggt acg aat gct ggc gtc ctc gat tcc agc 211  
 Gln Tyr Thr Gly Gln Ala Gly Thr Asn Ala Gly Val Leu Asp Ser Ser  
 25 30 35  
 ggc tac aac cta ctc acg ctg ctc cag tta cgt ggc ccc tcc acc atc 259  
 Gly Tyr Asn Leu Leu Thr Leu Leu Gln Leu Arg Gly Pro Ser Thr Ile  
 40 45 50  
 ggc gaa ctc agc gcc atc acc ggc cta gac gca tct acc ctt aac cgt 307  
 Gly Glu Leu Ser Ala Ile Thr Gly Leu Asp Ala Ser Thr Leu Asn Arg  
 55 60 65  
 cag aca aaa gcc cta cta acc aaa gga ttt gtc gaa cgc atc cca gat 355  
 Gln Thr Lys Ala Leu Leu Thr Lys Gly Phe Val Glu Arg Ile Pro Asp  
 70 75 80 85  
 ccc gac ggt gga atc gct cgg aaa ttc cac ccc acc gac ctc ggc aat 403  
 Pro Asp Gly Gly Ile Ala Arg Lys Phe His Pro Thr Asp Leu Gly Asn  
 90 95 100  
 gaa ctg ctc aac gag gaa cgc aca tcc agc caa gaa aaa tat gcc gag 451  
 Glu Leu Leu Asn Glu Glu Arg Thr Ser Ser Gln Glu Lys Tyr Ala Glu  
 105 110 115  
 tta ctt tca gac tgg ccc gaa gag gat cta cgc acc ttc gtc aaa ctt 499  
 Leu Leu Ser Asp Trp Pro Glu Glu Asp Leu Arg Thr Phe Val Lys Leu  
 120 125 130  
 ctt gaa aaa cta aat aaa gcc gtg gag aca cgc gtc gga aag cat tgg 547  
 Leu Glu Lys Leu Asn Lys Ala Val Glu Thr Arg Val Gly Lys His Trp  
 135 140 145  
 ccg cgc ccc tgactcagcc caagccagag ccc 579  
 Pro Arg Pro  
 150

&lt;210&gt; 310

&lt;211&gt; 152

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 310

Met Ser Thr Asp Pro Ile Ala Ala Leu Glu Tyr Glu Ser Thr Ile Phe  
 1 5 10 15  
 Ala Arg His Arg Asn Gln Tyr Thr Gly Gln Ala Gly Thr Asn Ala Gly  
 20 25 30  
 Val Leu Asp Ser Ser Gly Tyr Asn Leu Leu Thr Leu Leu Gln Leu Arg  
 35 40 45  
 Gly Pro Ser Thr Ile Gly Glu Leu Ser Ala Ile Thr Gly Leu Asp Ala  
 50 55 60

Ser Thr Leu Asn Arg Gln Thr Lys Ala Leu Leu Thr Lys Gly Phe Val  
65 70 75 80

Glu Arg Ile Pro Asp Pro Asp Gly Gly Ile Ala Arg Lys Phe His Pro  
85 90 95

Thr Asp Leu Gly Asn Glu Leu Leu Asn Glu Glu Arg Thr Ser Ser Gln  
100 105 110

Glu Lys Tyr Ala Glu Leu Leu Ser Asp Trp Pro Glu Glu Asp Leu Arg  
115 120 125

Thr Phe Val Lys Leu Leu Glu Lys Leu Asn Lys Ala Val Glu Thr Arg  
130 135 140

Val Gly Lys His Trp Pro Arg Pro  
145 150

<210> 311  
<211> 759  
<212> DNA  
<213> Corynebacterium glutamicum

<220>  
<221> CDS  
<222> (101)..(736)  
<223> RXS00650

<400> 311  
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cgaaaacgaag tgcgccattg ggaaggacct agttcaaaca atg att cgc gtg ctg 115  
Met Ile Arg Val Leu  
1 5

ctt gct gat gac cac gaa atc gtg agg ctc gga ctc cga gct gtg ctg 163  
Leu Ala Asp Asp His Glu Ile Val Arg Leu Gly Leu Arg Ala Val Leu  
10 15 20

gaa agc gcc gag gac att gaa gtg gtg ggc gaa gtc tcc acc gcc gaa 211  
Glu Ser Ala Glu Asp Ile Glu Val Val Gly Glu Val Ser Thr Ala Glu  
25 30 35

ggt gcg gtg cag gca gcc caa gaa ggc gga atc gac gtc atc ttg atg 259  
Gly Ala Val Gln Ala Ala Gln Glu Gly Gly Ile Asp Val Ile Leu Met  
40 45 50

gac ctc cga ttc ggc ccc ggc gtc caa gga acc cag gtt tcc aca ggc 307  
Asp Leu Arg Phe Gly Pro Gly Val Gln Gly Thr Gln Val Ser Thr Gly  
55 60 65

gca gac gcc acc gca gcc atc aag cga aac atc gat aac ccg cca aaa 355  
Ala Asp Ala Thr Ala Ala Ile Lys Arg Asn Ile Asp Asn Pro Pro Lys  
70 75 80 85

gtc ctg gtc gtg acc aac tac gac acc gac aca gac atc ctc ggc gca 403  
Val Leu Val Val Thr Asn Tyr Asp Thr Asp Thr Asp Ile Leu Gly Ala  
90 95 100

atc gaa gcc ggc gca ctg ggc tac ctg ctc aaa gac gcc cca ccg agc 451

Ile Glu Ala Gly Ala Leu Gly Tyr Leu Leu Lys Asp Ala Pro Pro Ser  
                   105                  110                  115

gaa ctc ctg gca gca gta cga tcc gca gca gaa ggt gac tcc aca ctg 499  
 Glu Leu Leu Ala Ala Val Arg Ser Ala Ala Glu Gly Asp Ser Thr Leu  
                   120                  125                  130

tca ccc atg gtt gcg aac cgc ctg atg act cgc gtg cgc acc ccc aaa 547  
 Ser Pro Met Val Ala Asn Arg Leu Met Thr Arg Val Arg Thr Pro Lys  
                   135                  140                  145

acc tca ctc acc cca cgt gaa ctg gaa gtt ctc aag ctg gtt gcc ggt 595  
 Thr Ser Leu Thr Pro Arg Glu Leu Glu Val Leu Lys Leu Val Ala Gly  
                   150                  155                  160                  165

gga tcc tcc aac cgc gac att ggc cgt atc ctc ttc ctc tca gaa gcc 643  
 Gly Ser Ser Asn Arg Asp Ile Gly Arg Ile Leu Phe Leu Ser Glu Ala  
                   170                  175                  180

acg gtg aaa tcc cac ctc gtg cac atc tac gac aag ctc ggc gtg cgg 691  
 Thr Val Lys Ser His Leu Val His Ile Tyr Asp Lys Leu Gly Val Arg  
                   185                  190                  195

tca cgt acc tcc gct gtc gca gcc gca cgt gag cag ggg ctg ctg 736  
 Ser Arg Thr Ser Ala Val Ala Ala Ala Arg Glu Gln Gly Leu Leu  
                   200                  205                  210

tagcgggggt tgctgcaagg ctt 759

&lt;210&gt; 312

&lt;211&gt; 212

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 312

Met Ile Arg Val Leu Leu Ala Asp Asp His Glu Ile Val Arg Leu Gly  
   1                  5                  10                  15

Leu Arg Ala Val Leu Glu Ser Ala Glu Asp Ile Glu Val Val Gly Glu  
                   20                  25                  30

Val Ser Thr Ala Glu Gly Ala Val Gln Ala Ala Gln Glu Gly Gly Ile  
                   35                  40                  45

Asp Val Ile Leu Met Asp Leu Arg Phe Gly Pro Gly Val Gln Gly Thr  
                   50                  55                  60

Gln Val Ser Thr Gly Ala Asp Ala Thr Ala Ala Ile Lys Arg Asn Ile  
   65                  70                  75                  80

Asp Asn Pro Pro Lys Val Leu Val Val Thr Asn Tyr Asp Thr Asp Thr  
                   85                  90                  95

Asp Ile Leu Gly Ala Ile Glu Ala Gly Ala Leu Gly Tyr Leu Leu Lys  
                   100                  105                  110

Asp Ala Pro Pro Ser Glu Leu Leu Ala Ala Val Arg Ser Ala Ala Glu  
                   115                  120                  125

Gly Asp Ser Thr Leu Ser Pro Met Val Ala Asn Arg Leu Met Thr Arg



130	135	140
Val Arg Thr Pro Lys Thr Ser Leu Thr Pro Arg Glu Leu Glu Val Leu		
145	150	155 160
Lys Leu Val Ala Gly Gly Ser Ser Asn Arg Asp Ile Gly Arg Ile Leu		
	165	170 175
Phe Leu Ser Glu Ala Thr Val Lys Ser His Leu Val His Ile Tyr Asp		
	180	185 190
Lys Leu Gly Val Arg Ser Arg Thr Ser Ala Val Ala Ala Ala Arg Glu		
	195	200 205
Gln Gly Leu Leu		
210		

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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(1003)  
 <223> RXS00657

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 Met Ser Thr Glu Asp  
 1 5  
 att gtc gtc gta gca gta gat ggc tcg gac gcc tca aaa caa gct gtt 163  
 Ile Val Val Val Ala Val Asp Gly Ser Asp Ala Ser Lys Gln Ala Val  
 10 15 20  
 cgg tgg gct gca aat acc gcc aac aaa cgt ggc att cca ctt cgc ttg 211  
 Arg Trp Ala Ala Asn Thr Ala Asn Lys Arg Gly Ile Pro Leu Arg Leu  
 25 30 35  
 gct tcc agc tac acc atg cct cag ttc ctc tac gca gag gga atg gtt 259  
 Ala Ser Ser Tyr Thr Met Pro Gln Phe Leu Tyr Ala Glu Gly Met Val  
 40 45 50  
 cca cca caa gag ctt ttc gat gac ctc cag gcc gaa gcc ctg gaa aag 307  
 Pro Pro Gln Glu Leu Phe Asp Asp Leu Gln Ala Glu Ala Leu Glu Lys  
 55 60 65  
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 Ile Asn Glu Ala Arg Asp Ile Ala His Glu Val Ala Pro Glu Ile Lys  
 70 75 80 85  
 atc ggg cac acc atc gct gaa ggc agt ccc atc gac atg ctg ttg gaa 403  
 Ile Gly His Thr Ile Ala Glu Gly Ser Pro Ile Asp Met Leu Leu Glu  
 90 95 100  
 atg tct ccc gat gcc aca atg atc gtc atg ggt tcc cgc gga ctc ggc 451  
 Met Ser Pro Asp Ala Thr Met Ile Val Met Gly Ser Arg Gly Leu Gly

105	110	115	
gga ctc tcc gga atg gtc atg ggc tcc gtc tcc ggt gca gtg gtc agc Gly Leu Ser Gly Met Val Met Gly Ser Val Ser Gly Ala Val Val Ser 120 125 130			499
cac gca aag tgt cca gtc gtt gtt gtc cgt gaa gac agc gca gtc aac His Ala Lys Cys Pro Val Val Val Arg Glu Asp Ser Ala Val Asn 135 140 145			547
gaa gac agc aag tac ggc cca gtc gtc gtc ggt gtg gat ggc tcc gaa Glu Asp Ser Lys Tyr Gly Pro Val Val Val Gly Val Asp Gly Ser Glu 150 155 160 165			595
gtc tcc caa cag gca acc gaa tac gca ttt gcg gaa gct gaa gct cgt Val Ser Gln Gln Ala Thr Glu Tyr Ala Phe Ala Glu Ala Glu Ala Arg 170 175 180			643
ggc gcc gaa ctc gtt gca gtt cac acc tgg atg gac atg cag gta cag Gly Ala Glu Leu Val Ala Val His Thr Trp Met Asp Met Gln Val Gln 185 190 195			691
gca tca ctt gca ggt ctt gca gct gct caa cag cag tgg gat gaa gtg Ala Ser Leu Ala Gly Leu Ala Ala Gln Gln Gln Trp Asp Glu Val 200 205 210			739
gaa cgt cag caa acc gac atg ctg atc gaa cgc ctc gca cca ctg gtg Glu Arg Gln Gln Thr Asp Met Leu Ile Glu Arg Leu Ala Pro Leu Val 215 220 225			787
gaa aag tac cca agt gta acc gtc aag aag atc atc acc cgt gac cgc Glu Lys Tyr Pro Ser Val Thr Val Lys Lys Ile Ile Thr Arg Asp Arg 230 235 240 245			835
cca gtt cgc gca ctt gca gaa gca tct gaa aac gcg cag ctc cta gtc Pro Val Arg Ala Leu Ala Glu Ala Ser Glu Asn Ala Gln Leu Leu Val 250 255 260			883
gtt ggt tcc cat ggt cgt ggc gga ttt aag ggc atg ctc ctt ggc tcc Val Gly Ser His Gly Arg Gly Gly Phe Lys Gly Met Leu Leu Gly Ser 265 270 275			931
acc tcc cgc gca ctg ctg caa tcc gca ccg tgc cca atg atg gtg gtt Thr Ser Arg Ala Leu Leu Gln Ser Ala Pro Cys Pro Met Met Val Val 280 285 290			979
cgc cca cct gag aag att aag aag tagttttcttt taagtttcga tgc Arg Pro Pro Glu Lys Ile Lys Lys 295 300			1026

&lt;210&gt; 314

&lt;211&gt; 301

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 314

Met	Ser	Thr	Glu	Asp	Ile	Val	Val	Val	Ala	Val	Asp	Gly	Ser	Asp	Ala
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Ser Lys Gln Ala Val Arg Trp Ala Ala Asn Thr Ala Asn Lys Arg Gly

20					25					30						
Ile	Pro	Leu	Arg	Leu	Ala	Ser	Ser	Tyr	Thr	Met	Pro	Gln	Phe	Leu	Tyr	
35					40					45						
Ala	Glu	Gly	Met	Val	Pro	Pro	Gln	Glu	Leu	Phe	Asp	Asp	Leu	Gln	Ala	
50					55					60						
Glu	Ala	Leu	Glu	Lys	Ile	Asn	Glu	Ala	Arg	Asp	Ile	Ala	His	Glu	Val	
65					70					75					80	
Ala	Pro	Glu	Ile	Lys	Ile	Gly	His	Thr	Ile	Ala	Glu	Gly	Ser	Pro	Ile	
85					90					95						
Asp	Met	Leu	Leu	Glu	Met	Ser	Pro	Asp	Ala	Thr	Met	Ile	Val	Met	Gly	
100					105					110						
Ser	Arg	Gly	Leu	Gly	Gly	Leu	Ser	Gly	Met	Val	Met	Gly	Ser	Val	Ser	
115					120					125						
Gly	Ala	Val	Val	Ser	His	Ala	Lys	Cys	Pro	Val	Val	Val	Val	Arg	Glu	
130					135					140						
Asp	Ser	Ala	Val	Asn	Glu	Asp	Ser	Lys	Tyr	Gly	Pro	Val	Val	Val	Gly	
145					150					155					160	
Val	Asp	Gly	Ser	Glu	Val	Ser	Gln	Gln	Ala	Thr	Glu	Tyr	Ala	Phe	Ala	
165					170					175						
Glu	Ala	Glu	Ala	Arg	Gly	Ala	Glu	Leu	Val	Ala	Val	His	Thr	Trp	Met	
180					185					190						
Asp	Met	Gln	Val	Gln	Ala	Ser	Leu	Ala	Gly	Leu	Ala	Ala	Ala	Gln	Gln	
195					200					205						
Gln	Trp	Asp	Glu	Val	Glu	Arg	Gln	Gln	Thr	Asp	Met	Leu	Ile	Glu	Arg	
210					215					220						
Leu	Ala	Pro	Leu	Val	Glu	Lys	Tyr	Pro	Ser	Val	Thr	Val	Lys	Lys	Ile	
225					230					235					240	
Ile	Thr	Arg	Asp	Arg	Pro	Val	Arg	Ala	Leu	Ala	Glu	Ala	Ser	Glu	Asn	
245					250					255						
Ala	Gln	Leu	Leu	Val	Val	Gly	Ser	His	Gly	Arg	Gly	Gly	Phe	Lys	Gly	
260					265					270						
Met	Leu	Leu	Gly	Ser	Thr	Ser	Arg	Ala	Leu	Leu	Gln	Ser	Ala	Pro	Cys	
275					280					285						
Pro	Met	Met	Val	Val	Arg	Pro	Pro	Glu	Lys	Ile	Lys	Lys				
290					295					300						

&lt;210&gt; 315

&lt;211&gt; 1752

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1729)

&lt;223&gt; RXS00719

&lt;400&gt; 315

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tcatccacct agtgggaagcc tccgctgaaa ggagcaacca gtg act gat aaa cac 115
Val Thr Asp Lys His
1 5

acc atg cct ggt gaa gag gac gac acc gta ttc gtc tac cac acc cac 163
Thr Met Pro Gly Glu Glu Asp Asp Thr Val Phe Val Tyr His Thr His
10 15 20

aaa ggc gaa atg gac gtc gaa ggt gcg ttt gct gac gaa gaa gaa cta 211
Lys Gly Glu Met Asp Val Glu Gly Ala Phe Ala Asp Glu Glu Glu Leu
25 30 35

gca cca cac ggc ggt tgg gct tcc gca gat ttc gac cca gca gaa ttc 259
Ala Pro His Gly Gly Trp Ala Ser Ala Asp Phe Asp Pro Ala Glu Phe
40 45 50

ggc tac gaa gac tct gac gat gac ttc gat gca gag gac ttt gac gaa 307
Gly Tyr Glu Asp Ser Asp Asp Asp Phe Asp Ala Glu Asp Phe Asp Glu
55 60 65

aca gag ttc tcc aac cct gat ttc ggc gaa gac tac tct gat gaa gac 355
Thr Glu Phe Ser Asn Pro Asp Phe Gly Glu Asp Tyr Ser Asp Glu Asp
70 75 80 85

tgg gaa gaa atc gag acc gca ttc gga ttc gac cca agc cac ctt gaa 403
Trp Glu Glu Ile Glu Thr Ala Phe Gly Phe Asp Pro Ser His Leu Glu
90 95 100

gaa gct ctc tgc acg gtc gct atc gtc gga cgc cca aat gtt ggt aaa 451
Glu Ala Leu Cys Thr Val Ala Ile Val Gly Arg Pro Asn Val Gly Lys
105 110 115

tca acc ttg gtg aac cgc ttt att gga cgt cga gaa gca gtc gtg gaa 499
Ser Thr Leu Val Asn Arg Phe Ile Gly Arg Arg Glu Ala Val Val Glu
120 125 130

gat ttc ccc ggc gta acc cgt gac cgc atc tcc tac atc tct gac tgg 547
Asp Phe Pro Gly Val Thr Arg Asp Arg Ile Ser Tyr Ile Ser Asp Trp
135 140 145

ggt gga cac cgt ttc tgg gtt cag gac aca ggc gga tgg gat cct aac 595
Gly Gly His Arg Phe Trp Val Gln Asp Thr Gly Gly Trp Asp Pro Asn
150 155 160 165

gtc aag ggc atc cac gca tcg atc gca cag caa gca gaa gtt gct atg 643
Val Lys Gly Ile His Ala Ser Ile Ala Gln Gln Ala Glu Val Ala Met
170 175 180

agc act gcc gat gtc atc gta ttc gtc gtg gac acc aag gtg ggc atc 691
Ser Thr Ala Asp Val Ile Val Phe Val Val Asp Thr Lys Val Gly Ile
185 190 195

acc gaa act gac tca gtg atg gca gca aaa ctg ttg cgc tcg gaa gtg 739
Thr Glu Thr Asp Ser Val Met Ala Ala Lys Leu Leu Arg Ser Glu Val
200 205 210

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cca	gtg	atc	ttg	gtt	gcg	aac	aaa	ttc	gac	tcc	gac	agc	cag	tgg	gct	787
Pro	Val	Ile	Leu	Val	Ala	Asn	Lys	Phe	Asp	Ser	Asp	Ser	Gln	Trp	Ala	
	215					220					225					
gac	atg	gct	gag	ttc	tac	agc	ctc	ggc	ctt	ggc	gat	cca	tac	cca	gtt	835
Asp	Met	Ala	Glu	Phe	Tyr	Ser	Leu	Gly	Leu	Gly	Asp	Pro	Tyr	Pro	Val	
	230				235					240					245	
tca	gcc	cag	cat	gga	cgt	ggc	ggc	gct	gac	gtt	ttg	gac	aaa	gtc	ctt	883
Ser	Ala	Gln	His	Gly	Arg	Gly	Gly	Ala	Asp	Val	Leu	Asp	Lys	Val	Leu	
				250					255					260		
gaa	ctc	ttc	cca	gaa	gag	cct	cgc	tcc	aag	tcc	atc	gtg	gaa	ggc	cct	931
Glu	Leu	Phe	Pro	Glu	Glu	Pro	Arg	Ser	Lys	Ser	Ile	Val	Glu	Gly	Pro	
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Arg	Arg	Val	Ala	Leu	Val	Gly	Lys	Pro	Asn	Val	Gly	Lys	Ser	Ser	Leu	
		280					285					290				
ctc	aac	aag	ttt	gct	ggc	gag	acc	cgc	tct	gtc	gtg	gac	aat	gtt	gca	1027
Leu	Asn	Lys	Phe	Ala	Gly	Glu	Thr	Arg	Ser	Val	Val	Asp	Asn	Val	Ala	
	295					300					305					
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Gly	Thr	Thr	Val	Asp	Pro	Val	Asp	Ser	Leu	Ile	Gln	Leu	Asp	Gln	Lys	
	310				315					320					325	
ctg	tgg	aaa	ttc	gtg	gat	act	gct	ggc	ctt	cgc	aaa	aag	gtc	aag	act	1123
Leu	Trp	Lys	Phe	Val	Asp	Thr	Ala	Gly	Leu	Arg	Lys	Lys	Val	Lys	Thr	
				330					335					340		
gca	tct	ggc	cac	gag	tac	tac	gca	tca	ctg	cgt	acc	cac	ggc	gcc	atc	1171
Ala	Ser	Gly	His	Glu	Tyr	Tyr	Ala	Ser	Leu	Arg	Thr	His	Gly	Ala	Ile	
			345					350					355			
gat	gca	gct	gag	ctg	tgt	gtt	ttg	ctt	atc	gat	tcc	tcc	gaa	ccc	atc	1219
Asp	Ala	Ala	Glu	Leu	Cys	Val	Leu	Leu	Ile	Asp	Ser	Ser	Glu	Pro	Ile	
		360					365					370				
acc	gag	cag	gat	cag	cgc	gtg	ctc	gca	atg	atc	acc	gat	gcc	ggc	aag	1267
Thr	Glu	Gln	Asp	Gln	Arg	Val	Leu	Ala	Met	Ile	Thr	Asp	Ala	Gly	Lys	
		375				380					385					
gca	ctg	gtt	att	gcg	ttc	aac	aag	tgg	gat	ctc	atg	gat	gaa	gat	cgc	1315
Ala	Leu	Val	Ile	Ala	Phe	Asn	Lys	Trp	Asp	Leu	Met	Asp	Glu	Asp	Arg	
	390				395					400					405	
cgc	atc	gat	ttg	gat	cgc	gaa	ctt	gat	ctc	cag	ttg	gca	cac	gtg	cct	1363
Arg	Ile	Asp	Leu	Asp	Arg	Glu	Leu	Asp	Leu	Gln	Leu	Ala	His	Val	Pro	
			410						415					420		
tgg	gca	aag	cgc	atc	aac	atc	tcc	gcc	aaa	acc	ggc	cgt	gca	ctg	cag	1411
Trp	Ala	Lys	Arg	Ile	Asn	Ile	Ser	Ala	Lys	Thr	Gly	Arg	Ala	Leu	Gln	
			425					430					435			
cgc	ctc	gag	cca	gca	atg	ttg	gaa	gcg	ctc	gac	aac	tgg	gat	cgc	cgt	1459
Arg	Leu	Glu	Pro	Ala	Met	Leu	Glu	Ala	Leu	Asp	Asn	Trp	Asp	Arg	Arg	
		440					445					450				

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 Ile Ser Thr Gly Gln Leu Asn Thr Trp Leu Arg Glu Ala Ile Ala Ala  
 455 460 465  
 aac cca cca cca atg cgt ggc gga cgt ttg cct cga gtg ctg ttt gcc 1555  
 Asn Pro Pro Pro Met Arg Gly Gly Arg Leu Pro Arg Val Leu Phe Ala  
 470 475 480 485  
 acc cag gca tct act cag cca cca gtg atc gta ctg ttc acc acc ggc 1603  
 Thr Gln Ala Ser Thr Gln Pro Pro Val Ile Val Leu Phe Thr Thr Gly  
 490 495 500  
 ttc ctc gaa gca ggt tac cga cga tac ctg gag cgc aag ttc cgt gaa 1651  
 Phe Leu Glu Ala Gly Tyr Arg Arg Tyr Leu Glu Arg Lys Phe Arg Glu  
 505 510 515  
 cgt ttc ggc ttt gaa ggc act cca gtg cga atc gct gtg cgt gtt cgc 1699  
 Arg Phe Gly Phe Glu Gly Thr Pro Val Arg Ile Ala Val Arg Val Arg  
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 535 540

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 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 316  
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 35 40 45  
 Asp Pro Ala Glu Phe Gly Tyr Glu Asp Ser Asp Asp Phe Asp Ala  
 50 55 60  
 Glu Asp Phe Asp Glu Thr Glu Phe Ser Asn Pro Asp Phe Gly Glu Asp  
 65 70 75 80  
 Tyr Ser Asp Glu Asp Trp Glu Glu Ile Glu Thr Ala Phe Gly Phe Asp  
 85 90 95  
 Pro Ser His Leu Glu Glu Ala Leu Cys Thr Val Ala Ile Val Gly Arg  
 100 105 110  
 Pro Asn Val Gly Lys Ser Thr Leu Val Asn Arg Phe Ile Gly Arg Arg  
 115 120 125  
 Glu Ala Val Val Glu Asp Phe Pro Gly Val Thr Arg Asp Arg Ile Ser  
 130 135 140  
 Tyr Ile Ser Asp Trp Gly Gly His Arg Phe Trp Val Gln Asp Thr Gly  
 145 150 155 160

Gly Trp Asp Pro Asn Val Lys Gly Ile His Ala Ser Ile Ala Gln Gln  
 165 170 175  
 Ala Glu Val Ala Met Ser Thr Ala Asp Val Ile Val Phe Val Val Asp  
 180 185 190  
 Thr Lys Val Gly Ile Thr Glu Thr Asp Ser Val Met Ala Ala Lys Leu  
 195 200 205  
 Leu Arg Ser Glu Val Pro Val Ile Leu Val Ala Asn Lys Phe Asp Ser  
 210 215 220  
 Asp Ser Gln Trp Ala Asp Met Ala Glu Phe Tyr Ser Leu Gly Leu Gly  
 225 230 235 240  
 Asp Pro Tyr Pro Val Ser Ala Gln His Gly Arg Gly Gly Ala Asp Val  
 245 250 255  
 Leu Asp Lys Val Leu Glu Leu Phe Pro Glu Glu Pro Arg Ser Lys Ser  
 260 265 270  
 Ile Val Glu Gly Pro Arg Arg Val Ala Leu Val Gly Lys Pro Asn Val  
 275 280 285  
 Gly Lys Ser Ser Leu Leu Asn Lys Phe Ala Gly Glu Thr Arg Ser Val  
 290 295 300  
 Val Asp Asn Val Ala Gly Thr Thr Val Asp Pro Val Asp Ser Leu Ile  
 305 310 315 320  
 Gln Leu Asp Gln Lys Leu Trp Lys Phe Val Asp Thr Ala Gly Leu Arg  
 325 330 335  
 Lys Lys Val Lys Thr Ala Ser Gly His Glu Tyr Tyr Ala Ser Leu Arg  
 340 345 350  
 Thr His Gly Ala Ile Asp Ala Ala Glu Leu Cys Val Leu Leu Ile Asp  
 355 360 365  
 Ser Ser Glu Pro Ile Thr Glu Gln Asp Gln Arg Val Leu Ala Met Ile  
 370 375 380  
 Thr Asp Ala Gly Lys Ala Leu Val Ile Ala Phe Asn Lys Trp Asp Leu  
 385 390 395 400  
 Met Asp Glu Asp Arg Arg Ile Asp Leu Asp Arg Glu Leu Asp Leu Gln  
 405 410 415  
 Leu Ala His Val Pro Trp Ala Lys Arg Ile Asn Ile Ser Ala Lys Thr  
 420 425 430  
 Gly Arg Ala Leu Gln Arg Leu Glu Pro Ala Met Leu Glu Ala Leu Asp  
 435 440 445  
 Asn Trp Asp Arg Arg Ile Ser Thr Gly Gln Leu Asn Thr Trp Leu Arg  
 450 455 460  
 Glu Ala Ile Ala Ala Asn Pro Pro Pro Met Arg Gly Gly Arg Leu Pro  
 465 470 475 480

Arg Val Leu Phe Ala Thr Gln Ala Ser Thr Gln Pro Pro Val Ile Val  
                     485                    490                    495  
 Leu Phe Thr Thr Gly Phe Leu Glu Ala Gly Tyr Arg Arg Tyr Leu Glu  
                     500                    505                    510  
 Arg Lys Phe Arg Glu Arg Phe Gly Phe Glu Gly Thr Pro Val Arg Ile  
                     515                    520                    525  
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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(363)  
 <223> RXS00738

<400> 317  
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 ccc ggt gag cgc cgg tcg tat ggc act ttg ctt aac gac gcc acg acg 96  
 Pro Gly Glu Arg Arg Ser Tyr Gly Thr Leu Leu Asn Asp Ala Thr Thr  
                     20                    25                    30  
 cag gtg tcg cac atc ctc ggc aat gcc ttc acc cga tct ggg ctc aac 144  
 Gln Val Ser His Ile Leu Gly Asn Ala Phe Thr Arg Ser Gly Leu Asn  
                     35                    40                    45  
 gct gag tac gcg aat ctt tat ggt cag gcg ttg gtg ggc atg gtg tcg 192  
 Ala Glu Tyr Ala Asn Leu Tyr Gly Gln Ala Leu Val Gly Met Val Ser  
                     50                    55                    60  
 atg acg gcg caa tgg tgg ttg gat gag cgc act ccg ccg aag gaa gaa 240  
 Met Thr Ala Gln Trp Trp Leu Asp Glu Arg Thr Pro Pro Lys Glu Glu  
   65                    70                    75                    80  
 gtt gcc gca cat att gtt aat ctt tgt tgg aat ggt ttg acg ggg atg 288  
 Val Ala Ala His Ile Val Asn Leu Cys Trp Asn Gly Leu Thr Gly Met  
                     85                    90                    95  
 gaa gcc gat ccg aag tta act ccc atc agt tct gct gag ggt gcg att 336  
 Glu Ala Asp Pro Lys Leu Thr Pro Ile Ser Ser Ala Glu Gly Ala Ile  
                     100                    105                    110  
 ttt ggt caa gaa aag gag agt gaa gcg tgacacctat gctcgcgggg 383  
 Phe Gly Gln Glu Lys Glu Ser Glu Ala  
                     115                    120  
 ctg 386

<210> 318  
 <211> 121



&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 318

Cys Gln Glu Glu Thr Asp Gly Phe Phe Asp Phe Gly Arg Asp Met Arg  
 1 5 10 15  
 Pro Gly Glu Arg Arg Ser Tyr Gly Thr Leu Leu Asn Asp Ala Thr Thr  
 20 25 30  
 Gln Val Ser His Ile Leu Gly Asn Ala Phe Thr Arg Ser Gly Leu Asn  
 35 40 45  
 Ala Glu Tyr Ala Asn Leu Tyr Gly Gln Ala Leu Val Gly Met Val Ser  
 50 55 60  
 Met Thr Ala Gln Trp Trp Leu Asp Glu Arg Thr Pro Pro Lys Glu Glu  
 65 70 75 80  
 Val Ala Ala His Ile Val Asn Leu Cys Trp Asn Gly Leu Thr Gly Met  
 85 90 95  
 Glu Ala Asp Pro Lys Leu Thr Pro Ile Ser Ser Ala Glu Gly Ala Ile  
 100 105 110  
 Phe Gly Gln Glu Lys Glu Ser Glu Ala  
 115 120

&lt;210&gt; 319

&lt;211&gt; 783

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(760)

&lt;223&gt; RXS01082

&lt;400&gt; 319

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 Leu Thr Gln Trp Gly  
 1 5  
 aat tcg aat gtt gtg gag gac tat ctc aca gca ctt ttc cgt gca gaa 163  
 Asn Ser Asn Val Val Glu Asp Tyr Leu Thr Ala Leu Phe Arg Ala Glu  
 10 15 20  
 gaa tgg gat gag gaa cca aca aca gga aaa ctc gct gaa gta att gga 211  
 Glu Trp Asp Glu Glu Pro Thr Thr Gly Lys Leu Ala Glu Val Ile Gly  
 25 30 35  
 gtt acc gca tca acg gtg tcg gcg acg ctc aaa aaa ctc aac cct gag 259  
 Val Thr Ala Ser Thr Val Ser Ala Thr Leu Lys Lys Leu Asn Pro Glu  
 40 45 50  
 ggc ttc gtc aat tac cgt ccc tac ggg gac atc gag ctg acg ccc gca 307  
 Gly Phe Val Asn Tyr Arg Pro Tyr Gly Asp Ile Glu Leu Thr Pro Ala  
 55 60 65

ggt cga gac atc gcc atc aac gtg atc agg cgg cgc cgg atc att gag 355  
 Gly Arg Asp Ile Ala Ile Asn Val Ile Arg Arg Arg Arg Ile Ile Glu  
 70 75 80 85  
 acc tat ctg tct gag aag ctt gga tta ggc gct cat gaa cta cac ggc 403  
 Thr Tyr Leu Ser Glu Lys Leu Gly Leu Gly Ala His Glu Leu His Gly  
 90 95 100  
 gag gca gat tta tta gag cac gca gtg tct cca ctg gtg ttg gag aag 451  
 Glu Ala Asp Leu Leu Glu His Ala Val Ser Pro Leu Val Leu Glu Lys  
 105 110 115  
 atg ttt cag gca gtg ggc tat cca acg ttg gat cct cac ggg gat ccc 499  
 Met Phe Gln Ala Val Gly Tyr Pro Thr Leu Asp Pro His Gly Asp Pro  
 120 125 130  
 atc ccc acc gaa tct ggg gag atg acc atc aat gat gga ctc atg ctt 547  
 Ile Pro Thr Glu Ser Gly Glu Met Thr Ile Asn Asp Gly Leu Met Leu  
 135 140 145  
 ttg gga cta aaa gct ggc gca tct gcc acg gtt aca cgt gtt agg gac 595  
 Leu Gly Leu Lys Ala Gly Ala Ser Ala Thr Val Thr Arg Val Arg Asp  
 150 155 160 165  
 gga aac cca tca gtg gtt cgg tac ctc act gga gtg gga att acc gtg 643  
 Gly Asn Pro Ser Val Val Arg Tyr Leu Thr Gly Val Gly Ile Thr Val  
 170 175 180  
 ggc aca acg gtc acg gtc gtt gaa gct ctt agc gat att gcc aca ctg 691  
 Gly Thr Thr Val Thr Val Val Glu Ala Leu Ser Asp Ile Ala Thr Leu  
 185 190 195  
 cgc ctg cag atc ggg gaa atg ttt caa gac att ccc ctt gca gtg gca 739  
 Arg Leu Gln Ile Gly Glu Met Phe Gln Asp Ile Pro Leu Ala Val Ala  
 200 205 210  
 aac gca gtg cgc gta tca cgt tagttcagcg tgcccagcgc gct 783  
 Asn Ala Val Arg Val Ser Arg  
 215 220

&lt;210&gt; 320

&lt;211&gt; 220

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 320

Leu Thr Gln Trp Gly Asn Ser Asn Val Val Glu Asp Tyr Leu Thr Ala  
 1 5 10 15  
 Leu Phe Arg Ala Glu Glu Trp Asp Glu Glu Pro Thr Thr Gly Lys Leu  
 20 25 30  
 Ala Glu Val Ile Gly Val Thr Ala Ser Thr Val Ser Ala Thr Leu Lys  
 35 40 45  
 Lys Leu Asn Pro Glu Gly Phe Val Asn Tyr Arg Pro Tyr Gly Asp Ile  
 50 55 60  
 Glu Leu Thr Pro Ala Gly Arg Asp Ile Ala Ile Asn Val Ile Arg Arg

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Met Arg Thr Leu Ala																
1 5																
gcg gag cta aat atc aag gcg ccg tcg ctg tac aag cat gta aaa acg																163
Ala Glu Leu Asn Ile Lys Ala Pro Ser Leu Tyr Lys His Val Lys Thr																
10 15 20																
cgc gag gat atc gcc gca cac atc gcc acg aag gca ttt att cag ctg																211
Arg Glu Asp Ile Ala Ala His Ile Ala Thr Lys Ala Phe Ile Gln Leu																
25 30 35																
ggg caa agc ctg cat gaa cat tgt gaa agt gtg gag gat ttg ctt gcg																259
Gly Gln Ser Leu His Glu His Cys Glu Ser Val Glu Asp Leu Leu Ala																
40 45 50																
gaa tac cgc tcc atg gct cgg gaa aat cca aat att tac cgg ctt ctc																307
Glu Tyr Arg Ser Met Ala Arg Glu Asn Pro Asn Ile Tyr Arg Leu Leu																

55	60	65	
acc agt tca gag ttc ccc cgc gag cta ctt cca gaa ggc cta gaa act			355
Thr Ser Ser Glu Phe Pro Arg Glu Leu Leu Pro Glu Gly Leu Glu Thr			
70	75	80	85
tgg gca gga acg cca ttc tac ctg gtc acc ggc cac gat ccg atc aag			403
Trp Ala Gly Thr Pro Phe Tyr Leu Val Thr Gly His Asp Pro Ile Lys			
	90	95	100
ggt caa gca ctg tgg gca ttc gcg cac ggc atg gcc atc ctg gaa atc			451
Gly Gln Ala Leu Trp Ala Phe Ala His Gly Met Ala Ile Leu Glu Ile			
	105	110	115
gac gcc cga ttc gcc ggc ccc aac aat gga tcc ccc gcg gat ggc gtg			499
Asp Ala Arg Phe Ala Gly Pro Asn Asn Gly Ser Pro Ala Asp Gly Val			
	120	125	130
tgg gag atc ggc gcg cgg gca ttt gac aca caa gta ttc gac caa ggc			547
Trp Glu Ile Gly Ala Arg Ala Phe Asp Thr Gln Val Phe Asp Gln Gly			
	135	140	145
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<210> 322			
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<212> PRT			
<213> Corynebacterium glutamicum			
<400> 322			
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Lys His Val Lys Thr Arg Glu Asp Ile Ala Ala His Ile Ala Thr Lys			
	20	25	30
Ala Phe Ile Gln Leu Gly Gln Ser Leu His Glu His Cys Glu Ser Val			
	35	40	45
Glu Asp Leu Leu Ala Glu Tyr Arg Ser Met Ala Arg Glu Asn Pro Asn			
	50	55	60
Ile Tyr Arg Leu Leu Thr Ser Ser Glu Phe Pro Arg Glu Leu Leu Pro			
	65	70	75
Glu Gly Leu Glu Thr Trp Ala Gly Thr Pro Phe Tyr Leu Val Thr Gly			
	85	90	95
His Asp Pro Ile Lys Gly Gln Ala Leu Trp Ala Phe Ala His Gly Met			
	100	105	110
Ala Ile Leu Glu Ile Asp Ala Arg Phe Ala Gly Pro Asn Asn Gly Ser			
	115	120	125
Pro Ala Asp Gly Val Trp Glu Ile Gly Ala Arg Ala Phe Asp Thr Gln			
	130	135	140
Val Phe Asp Gln Gly			
145			

gca gcg cac ctc gcg ccg gga acc acc cgc aac tat tta tcc caa gct 643  
Ala Ala His Leu Ala Pro Gly Thr Thr Arg Asn Tyr Leu Ser Gln Ala  
170 175 180

atg aca aaa gta ggc gcg cag aat cgc ttt gaa gcg ttc acg cgc gcc 691  
 Met Thr Lys Val Gly Ala Gln Asn Arg Phe Glu Ala Phe Thr Arg Ala  
 185 190 195

agg gaa ttg ggc tgg ttg tagcttgtgg cttatctcct att 732  
 Arg Glu Leu Gly Trp Leu  
 200

<210> 324

<211> 203

<212> PRT

<213> Corynebacterium glutamicum

<400> 324

Met Ile Ser Ile Ser Ile Ala Asp Asp Glu Ala Leu Ile Ala Ser Ser  
 1 5 10 15

Leu Ala Thr Leu Leu Ser Leu Glu Pro Asp Leu Asp Val Arg Pro Thr  
 20 25 30

Ala Gly Ser Gly Glu Glu Leu Ile Glu Thr Trp Ala Asp Pro Ser Asn  
 35 40 45

Arg Thr Asp Val Cys Val Leu Asp Leu Gln Leu Gly Gly Ile Asp Gly  
 50 55 60

Ile Asp Thr Ala Thr Arg Leu Met Glu Thr Thr Pro Asp Leu Ala Val  
 65 70 75 80

Leu Ile Val Thr Ser His Ala Arg Pro Arg Gln Leu Lys Arg Ala Leu  
 85 90 95

Ala Ala Gly Val Leu Gly Phe Leu Pro Lys Thr Ser Thr Ala Asp Glu  
 100 105 110

Phe Ala Thr Ala Ile Arg Thr Val His Ala Gly Arg Arg Tyr Ile Asp  
 115 120 125

Pro Glu Leu Ala Ala Met Thr Ile Ser Ala Gly Glu Ser Pro Leu Thr  
 130 135 140

Asn Arg Glu Glu Glu Val Leu Glu Leu Ala Gly Gln Gly Leu Ser Ala  
 145 150 155 160

Glu Glu Ile Ala Val Ala Ala His Leu Ala Pro Gly Thr Thr Arg Asn  
 165 170 175

Tyr Leu Ser Gln Ala Met Thr Lys Val Gly Ala Gln Asn Arg Phe Glu  
 180 185 190

Ala Phe Thr Arg Ala Arg Glu Leu Gly Trp Leu  
 195 200

<210> 325

<211> 900

<212> DNA

<213> Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(877)

&lt;223&gt; RXS01242

&lt;400&gt; 325

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gacatatatta gtaaattggc tttttgcttt aaggagtgc atg tac gca gag gag 115
Met Tyr Ala Glu Glu
1 5

cgc cgt cga cag att gcc tca tta acg gca gtt gag gga cgt gta aat 163
Arg Arg Arg Gln Ile Ala Ser Leu Thr Ala Val Glu Gly Arg Val Asn
10 15 20

gtc aca gaa tta gcg ggc cga ttc gat gtc act gca gag acg att cga 211
Val Thr Glu Leu Ala Gly Arg Phe Asp Val Thr Ala Glu Thr Ile Arg
25 30 35

cga gac ctt gcg gtg cta gac cgc gag gga att gtt cac cgc gtt cac 259
Arg Asp Leu Ala Val Leu Asp Arg Glu Gly Ile Val His Arg Val His
40 45 50

ggt ggc gca gta gcc acc caa tct ttc caa acc aca gag ttg agc ttg 307
Gly Gly Ala Val Ala Thr Gln Ser Phe Gln Thr Thr Glu Leu Ser Leu
55 60 65

gat act cgt ttc agg tct gca tgc tca gca aag tac tcc att gcc aag 355
Asp Thr Arg Phe Arg Ser Ala Ser Ser Ala Lys Tyr Ser Ile Ala Lys
70 75 80 85

gca gcg atg cag ttc ctg ccc gct gag cat ggc gga ctg ttc ctc gat 403
Ala Ala Met Gln Phe Leu Pro Ala Glu His Gly Gly Leu Phe Leu Asp
90 95 100

gcg gga act act gtt act gct ttg gcc gat ctc att tct gag cat cct 451
Ala Gly Thr Thr Val Thr Ala Leu Ala Asp Leu Ile Ser Glu His Pro
105 110 115

agc tcc aag cag tgg tgc atc gtg acc aac tgc ctc ccc atc gca ctt 499
Ser Ser Lys Gln Trp Ser Ile Val Thr Asn Cys Leu Pro Ile Ala Leu
120 125 130

aat ctg gcc aac gcc ggg ctt gat gat gtc cag ctg ctt gga gga agc 547
Asn Leu Ala Asn Ala Gly Leu Asp Asp Val Gln Leu Leu Gly Gly Ser
135 140 145

gtt cgc gcg atc acc cag gct gtt gtg ggt gac act gcg ctt cgt act 595
Val Arg Ala Ile Thr Gln Ala Val Val Gly Asp Thr Ala Leu Arg Thr
150 155 160 165

ctc gcg ctg atg cgt gcg gat gta gtg ttc atc ggc acc aac gcg ttg 643
Leu Ala Leu Met Arg Ala Asp Val Val Phe Ile Gly Thr Asn Ala Leu
170 175 180

acg ttg gat cac gga ttg tct acg gcc gat tcc caa gag gct gcc atg 691
Thr Leu Asp His Gly Leu Ser Thr Ala Asp Ser Gln Glu Ala Ala Met
185 190 195

aaa tct gcg atg atc acc aac gcc cac aag gtg gtg gtg ttg tgt gac 739

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Lys Ser Ala Met Ile Thr Asn Ala His Lys Val Val Val Leu Cys Asp  
 200 205 210  
 tcc acc aag atg ggc acc gac tac ctc gtg agc ttt ggc gca atc agc 787  
 Ser Thr Lys Met Gly Thr Asp Tyr Leu Val Ser Phe Gly Ala Ile Ser  
 215 220 225  
 gat atc gat gtg gtg gtc acc gat gcg ggt gca cca gca agt ttc gtt 835  
 Asp Ile Asp Val Val Val Thr Asp Ala Gly Ala Pro Ala Ser Phe Val  
 230 235 240 245  
 gag cag ttg cga gaa cgc gat gta gaa gtt gtg att gca gaa 877  
 Glu Gln Leu Arg Glu Arg Asp Val Glu Val Val Ile Ala Glu  
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<210> 326  
 <211> 259  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 326  
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 Glu Gly Arg Val Asn Val Thr Glu Leu Ala Gly Arg Phe Asp Val Thr  
 20 25 30  
 Ala Glu Thr Ile Arg Arg Asp Leu Ala Val Leu Asp Arg Glu Gly Ile  
 35 40 45  
 Val His Arg Val His Gly Gly Ala Val Ala Thr Gln Ser Phe Gln Thr  
 50 55 60  
 Thr Glu Leu Ser Leu Asp Thr Arg Phe Arg Ser Ala Ser Ser Ala Lys  
 65 70 75 80  
 Tyr Ser Ile Ala Lys Ala Ala Met Gln Phe Leu Pro Ala Glu His Gly  
 85 90 95  
 Gly Leu Phe Leu Asp Ala Gly Thr Thr Val Thr Ala Leu Ala Asp Leu  
 100 105 110  
 Ile Ser Glu His Pro Ser Ser Lys Gln Trp Ser Ile Val Thr Asn Cys  
 115 120 125  
 Leu Pro Ile Ala Leu Asn Leu Ala Asn Ala Gly Leu Asp Asp Val Gln  
 130 135 140  
 Leu Leu Gly Gly Ser Val Arg Ala Ile Thr Gln Ala Val Val Gly Asp  
 145 150 155 160  
 Thr Ala Leu Arg Thr Leu Ala Leu Met Arg Ala Asp Val Val Phe Ile  
 165 170 175  
 Gly Thr Asn Ala Leu Thr Leu Asp His Gly Leu Ser Thr Ala Asp Ser  
 180 185 190  
 Gln Glu Ala Ala Met Lys Ser Ala Met Ile Thr Asn Ala His Lys Val



195	200	205
Val Val Leu Cys Asp Ser Thr Lys Met Gly Thr Asp Tyr Leu Val Ser		
210	215	220
Phe Gly Ala Ile Ser Asp Ile Asp Val Val Val Thr Asp Ala Gly Ala		
225	230	235
Pro Ala Ser Phe Val Glu Gln Leu Arg Glu Arg Asp Val Glu Val Val		
245	250	255

Ile Ala Glu

<210> 327  
 <211> 753  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(730)  
 <223> RXS01607

<400> 327  
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tttccgcccg ttttccctat ccacaaaagg accaagataa gtg atc cgt att ctg 115  
 Val Ile Arg Ile Leu  
 1 5

ttg gct gat gat cat ccc gtt gtt cgc gca ggc ctt gcc tcc ttg ctg 163  
 Leu Ala Asp Asp His Pro Val Val Arg Ala Gly Leu Ala Ser Leu Leu  
 10 15 20

gtg agt gaa gat gat ttt gag ata gtg gac atg gtg ggc acc cca gat 211  
 Val Ser Glu Asp Asp Phe Glu Ile Val Asp Met Val Gly Thr Pro Asp  
 25 30 35

gat gcc gtt gcg cgc gcc gcg gaa ggc ggg gtg gat gtg gtg ttg atg 259  
 Asp Ala Val Ala Arg Ala Ala Glu Gly Gly Val Asp Val Val Leu Met  
 40 45 50

gat ctg cgt ttt ggt gat caa cca ggc atc gag gtc gcc ggc ggg gta 307  
 Asp Leu Arg Phe Gly Asp Gln Pro Gly Ile Glu Val Ala Gly Gly Val  
 55 60 65

gag gca acg cgt cgc atc cgt gcg ctg gac aac ccg cca cag gta ctg 355  
 Glu Ala Thr Arg Arg Ile Arg Ala Leu Asp Asn Pro Pro Gln Val Leu  
 70 75 80 85

gtg gtg acc aac tac tcc aca gac ggc gat gtg gtg ggc gca gta tct 403  
 Val Val Thr Asn Tyr Ser Thr Asp Gly Asp Val Val Gly Ala Val Ser  
 90 95 100

gct ggt gcc gtg ggg tat ttg ctc aaa gat agc tcc cca gaa gat ctc 451  
 Ala Gly Ala Val Gly Tyr Leu Leu Lys Asp Ser Ser Pro Glu Asp Leu  
 105 110 115

att gcc ggt gtt cgc gat gcc gcg cgg gga gaa tca gtg ctt tca aag 499

Ile Ala Gly Val Arg Asp Ala Ala Arg Gly Glu Ser Val Leu Ser Lys  
 120 125 130  
 cag gtc gcc agc aag atc atg ggg cgg atg aac aac ccc atg act gct 547  
 Gln Val Ala Ser Lys Ile Met Gly Arg Met Asn Asn Pro Met Thr Ala  
 135 140 145  
 ctc agt gcc aga gaa att gaa gtg ctg tcc ttg gtg gcg caa ggg caa 595  
 Leu Ser Ala Arg Glu Ile Glu Val Leu Ser Leu Val Ala Gln Gly Gln  
 150 155 160 165  
 agc aat aga gaa atc ggc aag aaa ctt ttc ctc act gag gcc acg gtg 643  
 Ser Asn Arg Glu Ile Gly Lys Lys Leu Phe Leu Thr Glu Ala Thr Val  
 170 175 180  
 aaa agt cac atg ggg cat gtg ttc aac aag ctg gat gtc acc tct aga 691  
 Lys Ser His Met Gly His Val Phe Asn Lys Leu Asp Val Thr Ser Arg  
 185 190 195  
 aca gct gcg gta gct gaa gcc aga cag cgc gga att atc tagacgcaca 740  
 Thr Ala Ala Val Ala Glu Ala Arg Gln Arg Gly Ile Ile  
 200 205 210  
 cgtgttggtgta acc 753

<210> 328  
 <211> 210  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 328  
 Val Ile Arg Ile Leu Leu Ala Asp Asp His Pro Val Val Arg Ala Gly  
 1 5 10 15  
 Leu Ala Ser Leu Leu Val Ser Glu Asp Asp Phe Glu Ile Val Asp Met  
 20 25 30  
 Val Gly Thr Pro Asp Asp Ala Val Ala Arg Ala Ala Glu Gly Gly Val  
 35 40 45  
 Asp Val Val Leu Met Asp Leu Arg Phe Gly Asp Gln Pro Gly Ile Glu  
 50 55 60  
 Val Ala Gly Gly Val Glu Ala Thr Arg Arg Ile Arg Ala Leu Asp Asn  
 65 70 75 80  
 Pro Pro Gln Val Leu Val Val Thr Asn Tyr Ser Thr Asp Gly Asp Val  
 85 90 95  
 Val Gly Ala Val Ser Ala Gly Ala Val Gly Tyr Leu Leu Lys Asp Ser  
 100 105 110  
 Ser Pro Glu Asp Leu Ile Ala Gly Val Arg Asp Ala Ala Arg Gly Glu  
 115 120 125  
 Ser Val Leu Ser Lys Gln Val Ala Ser Lys Ile Met Gly Arg Met Asn  
 130 135 140  
 Asn Pro Met Thr Ala Leu Ser Ala Arg Glu Ile Glu Val Leu Ser Leu  
 145 150 155 160

<400> 329																
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cggtagacgg tacttttcata tccacccata taatgttgat atg gat aat ggg tgg																115
Met Asp Asn Gly Trp																
1 5																
ccg aac ctg caa act ctc gca ctc ttt gtg gcg att gtg gaa gag ggg																163
Pro Asn Leu Gln Thr Leu Ala Leu Phe Val Ala Ile Val Glu Glu Gly																
10 15 20																
agc ctc ggt gcc ggt gct cga aaa gtc gga atg gcc caa cct aat gcc																211
Ser Leu Gly Ala Gly Ala Arg Lys Val Gly Met Ala Gln Pro Asn Ala																
25 30 35																
agt cgg gct atc gca gag ctt gag gca gac atg aaa gcc gaa ttg ttg																259
Ser Arg Ala Ile Ala Glu Leu Glu Ala Asp Met Lys Ala Glu Leu Leu																
40 45 50																
gta cgt cat cct cga gga tca cat cca aca gct gct gga ctt gcg ctt																307
Val Arg His Pro Arg Gly Ser His Pro Thr Ala Ala Gly Leu Ala Leu																
55 60 65																
gtt gag cat tcg cgc gat ctg ctt caa tct gta caa gaa ttt act gaa																355
Val Glu His Ser Arg Asp Leu Leu Gln Ser Val Gln Glu Phe Thr Glu																
70 75 80 85																
tgg gtg aca gag gga cga act gag cag ccg ctg aaa ttg cat gtt ggg																403
Trp Val Thr Glu Gly Arg Thr Glu Gln Pro Leu Lys Leu His Val Gly																
90 95 100																
gcc agt atg acc att gcc gag gct cta ctt cca gct tgg gtt gcg gac																451
Ala Ser Met Thr Ile Ala Glu Ala Leu Leu Pro Ala Trp Val Ala Asp																
105 110 115																
atg cgc acg cgt ttt cct gcc tgc cgt gtc gac gtc tct gtg atg aat																499
Met Arg Thr Arg Phe Pro Ala Cys Arg Val Asp Val Ser Val Met Asn																

120	125	130	
tct tct caa gta att gaa gcc gtc cag aaa ggg cac ttg caa cta ggt			547
Ser Ser Gln Val Ile Glu Ala Val Gln Lys Gly His Leu Gln Leu Gly			
135	140	145	
ttt att gaa aca ccg cat gtt ccc gta cgg ctt cat gct cgt gtg gtg			595
Phe Ile Glu Thr Pro His Val Pro Val Arg Leu His Ala Arg Val Val			
150	155	160	165
caa gag gac aag ctg att gtg gtg att tct cct aat cat gag tgg gct			643
Gln Glu Asp Lys Leu Ile Val Val Ile Ser Pro Asn His Glu Trp Ala			
	170	175	180
aat cgc acg ggt agg atc agt ctt cgg gag ttg tcg gaa act ccg ctg			691
Asn Arg Thr Gly Arg Ile Ser Leu Arg Glu Leu Ser Glu Thr Pro Leu			
	185	190	195
ata gtg agg gaa gtc ggc tca ggt acc cga gaa gca tta caa gaa tta			739
Ile Val Arg Glu Val Gly Ser Gly Thr Arg Glu Ala Leu Gln Glu Leu			
	200	205	210
ctt gcg gat tat gac atg gct gag ccg att caa gtg tta aac agc aat			787
Leu Ala Asp Tyr Asp Met Ala Glu Pro Ile Gln Val Leu Asn Ser Asn			
	215	220	225
gct gcg gta cgt gtt gtt gtt gaa gca ggg gca ggt cct gca gta ctt			835
Ala Ala Val Arg Val Val Val Glu Ala Gly Ala Gly Pro Ala Val Leu			
230	235	240	245
ggt gaa tta gcc ttg cgt gat cat ctt gcg ctc ggc agg ctg ttg agt			883
Gly Glu Leu Ala Leu Arg Asp His Leu Ala Leu Gly Arg Leu Leu Ser			
	250	255	260
gtg cca ttt gaa ggc agt gga gtt act cgt cct ctt aca gct gtg tgg			931
Val Pro Phe Glu Gly Ser Gly Val Thr Arg Pro Leu Thr Ala Val Trp			
	265	270	275
agt gga ccc cgc aga ttg ccg att cta gcg gga gaa tta gtg tcc atc			979
Ser Gly Pro Arg Arg Leu Pro Ile Leu Ala Gly Glu Leu Val Ser Ile			
	280	285	290
gca tcg aac cac atc tgattttgag ccctggctaa cgg			1017
Ala Ser Asn His Ile			
295			

&lt;210&gt; 330

&lt;211&gt; 298

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 330

Met	Asp	Asn	Gly	Trp	Pro	Asn	Leu	Gln	Thr	Leu	Ala	Leu	Phe	Val	Ala
1					5				10					15	

Ile	Val	Glu	Glu	Gly	Ser	Leu	Gly	Ala	Gly	Ala	Arg	Lys	Val	Gly	Met
		20						25					30		

Ala	Gln	Pro	Asn	Ala	Ser	Arg	Ala	Ile	Ala	Glu	Leu	Glu	Ala	Asp	Met
		35					40					45			

Lys Ala Glu Leu Leu Val Arg His Pro Arg Gly Ser His Pro Thr Ala  
 50 55 60  
 Ala Gly Leu Ala Leu Val Glu His Ser Arg Asp Leu Leu Gln Ser Val  
 65 70 75 80  
 Gln Glu Phe Thr Glu Trp Val Thr Glu Gly Arg Thr Glu Gln Pro Leu  
 85 90 95  
 Lys Leu His Val Gly Ala Ser Met Thr Ile Ala Glu Ala Leu Leu Pro  
 100 105 110  
 Ala Trp Val Ala Asp Met Arg Thr Arg Phe Pro Ala Cys Arg Val Asp  
 115 120 125  
 Val Ser Val Met Asn Ser Ser Gln Val Ile Glu Ala Val Gln Lys Gly  
 130 135 140  
 His Leu Gln Leu Gly Phe Ile Glu Thr Pro His Val Pro Val Arg Leu  
 145 150 155 160  
 His Ala Arg Val Val Gln Glu Asp Lys Leu Ile Val Val Ile Ser Pro  
 165 170 175  
 Asn His Glu Trp Ala Asn Arg Thr Gly Arg Ile Ser Leu Arg Glu Leu  
 180 185 190  
 Ser Glu Thr Pro Leu Ile Val Arg Glu Val Gly Ser Gly Thr Arg Glu  
 195 200 205  
 Ala Leu Gln Glu Leu Leu Ala Asp Tyr Asp Met Ala Glu Pro Ile Gln  
 210 215 220  
 Val Leu Asn Ser Asn Ala Ala Val Arg Val Val Val Glu Ala Gly Ala  
 225 230 235 240  
 Gly Pro Ala Val Leu Gly Glu Leu Ala Leu Arg Asp His Leu Ala Leu  
 245 250 255  
 Gly Arg Leu Leu Ser Val Pro Phe Glu Gly Ser Gly Val Thr Arg Pro  
 260 265 270  
 Leu Thr Ala Val Trp Ser Gly Pro Arg Arg Leu Pro Ile Leu Ala Gly  
 275 280 285  
 Glu Leu Val Ser Ile Ala Ser Asn His Ile  
 290 295

&lt;210&gt; 331

&lt;211&gt; 928

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(928)

&lt;223&gt; RXS01872

&lt;400&gt; 331

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                                         Met Gly Asn Asp Gly
                                         1                               5

gga gac ctg cga atc gac gac cta cgc agc ttc att tca gtc gct caa 163
Gly Asp Leu Arg Ile Asp Asp Leu Arg Ser Phe Ile Ser Val Ala Gln
                               10                               15                               20

tca ggc cac cta acc gaa act gcc caa aga tta ggc atc ccg cag ccc 211
Ser Gly His Leu Thr Glu Thr Ala Gln Arg Leu Gly Ile Pro Gln Pro
                               25                               30                               35

aca ctt tcc aga cga atc agc cga gtg gaa aaa cac gca ggc acc cca 259
Thr Leu Ser Arg Arg Ile Ser Arg Val Glu Lys His Ala Gly Thr Pro
                               40                               45                               50

ctt ttc gac cgc gcc ggc cgc aaa ctc gtc ctc aac caa cga ggc cac 307
Leu Phe Asp Arg Ala Gly Arg Lys Leu Val Leu Asn Gln Arg Gly His
                               55                               60                               65

gcc ttc ctc aac cac gcc agc gcc atc gtc gca gaa ttc aac tcc gcc 355
Ala Phe Leu Asn His Ala Ser Ala Ile Val Ala Glu Phe Asn Ser Ala
                               70                               75                               80                               85

gca act gaa atc aaa cgc ctc atg gac cca gaa aaa ggc aca atc cga 403
Ala Thr Glu Ile Lys Arg Leu Met Asp Pro Glu Lys Gly Thr Ile Arg
                               90                               95                               100

ctg gac ttc atg cat tcc ttg ggc act tgg atg gtc ccc gaa ctt atc 451
Leu Asp Phe Met His Ser Leu Gly Thr Trp Met Val Pro Glu Leu Ile
                               105                               110                               115

cga aca ttc cgc gcc gaa cac ccc aac gta gaa ttc caa ctc cac caa 499
Arg Thr Phe Arg Ala Glu His Pro Asn Val Glu Phe Gln Leu His Gln
                               120                               125                               130

gcg gca gca atg ctc ctg gta gat cgt gtt ttg gct gat gaa act gac 547
Ala Ala Ala Met Leu Leu Val Asp Arg Val Leu Ala Asp Glu Thr Asp
                               135                               140                               145

ctc gca tta gtt ggc ccc aaa cct gcc gag gtt ggt acc tct tta ggg 595
Leu Ala Leu Val Gly Pro Lys Pro Ala Glu Val Gly Thr Ser Leu Gly
                               150                               155                               160                               165

tgg gcg cca ctg ctt cgt caa cga ctt gcc cta gct gtt ccc gca gat 643
Trp Ala Pro Leu Leu Arg Gln Arg Leu Ala Leu Ala Val Pro Ala Asp
                               170                               175                               180

cac cgg ctt gcc tcc ttt tct ggc caa gga gaa ttg ccg ttg att act 691
His Arg Leu Ala Ser Phe Ser Gly Gln Gly Glu Leu Pro Leu Ile Thr
                               185                               190                               195

gcg gcg gaa gaa cct ttc gtg gcg atg cga gca ggt ttc ggc acc cga 739
Ala Ala Glu Glu Pro Phe Val Ala Met Arg Ala Gly Phe Gly Thr Arg
                               200                               205                               210

ctc ctc atg gat gca tta gcc gaa gaa gcc ggt ttt gtt ccc aat gtg 787
Leu Leu Met Asp Ala Leu Ala Glu Glu Ala Gly Phe Val Pro Asn Val
                               215                               220                               225

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gtt ttc gaa tcc atg gaa ctc acc acc gtc gca ggg ctt gtc agc gca 835  
 Val Phe Glu Ser Met Glu Leu Thr Thr Val Ala Gly Leu Val Ser Ala  
 230 235 240 245

ggt ctc ggc gtt ggt gtg gtt ccg atg gat gat ccc tac ctt tcc aca 883  
 Gly Leu Gly Val Gly Val Val Pro Met Asp Asp Pro Tyr Leu Ser Thr  
 250 255 260

gtg gga atc gtg caa cgc cca ctt agt cca ccc gct tat agg gaa 928  
 Val Gly Ile Val Gln Arg Pro Leu Ser Pro Pro Ala Tyr Arg Glu  
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<210> 332

<211> 276

<212> PRT

<213> Corynebacterium glutamicum

<400> 332

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Gly Ile Pro Gln Pro Thr Leu Ser Arg Arg Ile Ser Arg Val Glu Lys  
 35 40 45

His Ala Gly Thr Pro Leu Phe Asp Arg Ala Gly Arg Lys Leu Val Leu  
 50 55 60

Asn Gln Arg Gly His Ala Phe Leu Asn His Ala Ser Ala Ile Val Ala  
 65 70 75 80

Glu Phe Asn Ser Ala Ala Thr Glu Ile Lys Arg Leu Met Asp Pro Glu  
 85 90 95

Lys Gly Thr Ile Arg Leu Asp Phe Met His Ser Leu Gly Thr Trp Met  
 100 105 110

Val Pro Glu Leu Ile Arg Thr Phe Arg Ala Glu His Pro Asn Val Glu  
 115 120 125

Phe Gln Leu His Gln Ala Ala Ala Met Leu Leu Val Asp Arg Val Leu  
 130 135 140

Ala Asp Glu Thr Asp Leu Ala Leu Val Gly Pro Lys Pro Ala Glu Val  
 145 150 155 160

Gly Thr Ser Leu Gly Trp Ala Pro Leu Leu Arg Gln Arg Leu Ala Leu  
 165 170 175

Ala Val Pro Ala Asp His Arg Leu Ala Ser Phe Ser Gly Gln Gly Glu  
 180 185 190

Leu Pro Leu Ile Thr Ala Ala Glu Glu Pro Phe Val Ala Met Arg Ala  
 195 200 205

Gly Phe Gly Thr Arg Leu Leu Met Asp Ala Leu Ala Glu Glu Ala Gly  
 210 215 220

Phe Val Pro Asn Val Val Phe Glu Ser Met Glu Leu Thr Thr Val Ala  
225 230 235 240

Gly Leu Val Ser Ala Gly Leu Gly Val Gly Val Val Pro Met Asp Asp  
245 250 255

Pro Tyr Leu Ser Thr Val Gly Ile Val Gln Arg Pro Leu Ser Pro Pro  
260 265 270

Ala Tyr Arg Glu  
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<210> 333

<211> 597

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(574)

<223> RXS02117

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ctatgagtcc agacgttttt aaagggagcg aattaccata gtg tct aca gat cca 115  
Val Ser Thr Asp Pro  
1 5

gaa gag ttc gac caa gct gaa acc ctc gat caa ctc gcg tat gag atc 163  
Glu Glu Phe Asp Gln Ala Glu Thr Leu Asp Gln Leu Ala Tyr Glu Ile  
10 15 20

atc ctg ctc acc cggtat ggt gtc caa aac aca ccg acc aac aag cgc 211  
Ile Leu Leu Thr Arg Tyr Gly Val Gln Asn Thr Pro Thr Asn Lys Arg  
25 30 35

gaa gcc atc atg gat cgc agc gcc ctc atc ttg ctc acc cgc ctt gac 259  
Glu Ala Ile Met Asp Arg Ser Ala Leu Ile Leu Leu Thr Arg Leu Asp  
40 45 50

gct caa gga cct atg aca gtt aat gag cta gct gaa agc ttt gga ctt 307  
Ala Gln Gly Pro Met Thr Val Asn Glu Leu Ala Glu Ser Phe Gly Leu  
55 60 65

aac gtt tct acc gtg cac cgc caa ctc aaa gca gcc att gcc aat ggc 355  
Asn Val Ser Thr Val His Arg Gln Leu Lys Ala Ala Ile Ala Asn Gly  
70 75 80 85

tta att gaa gtc gtc gat gat caa gca tgc ccc gct aaa ctt cat cgt 403  
Leu Ile Glu Val Val Asp Asp Gln Ala Cys Pro Ala Lys Leu His Arg  
90 95 100

cca act gag ttg ggt aaa gaa aaa ctg cag cag gag ctt ctt gcc cgc 451  
Pro Thr Glu Leu Gly Lys Glu Lys Leu Gln Gln Glu Leu Leu Ala Arg  
105 110 115

cag cag gat ctc acc cgc att ctt cat gat tgg gat gag gaa gac att 499  
Gln Gln Asp Leu Thr Arg Ile Leu His Asp Trp Asp Glu Glu Asp Ile



120 125 130  
 aaa acg cat gcc aag cta ttg cgg aag cac aat gaa agc ttg gaa gaa 547  
 Lys Thr His Ala Lys Leu Leu Arg Lys His Asn Glu Ser Leu Glu Glu  
 135 140 145

tac ctc gat atg aag tgg ccc cgc ccc taagtgccca taaacgcacc tct 597  
 Tyr Leu Asp Met Lys Trp Pro Arg Pro  
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<210> 334  
 <211> 158  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 334  
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 Pro Thr Asn Lys Arg Glu Ala Ile Met Asp Arg Ser Ala Leu Ile Leu  
 35 40 45  
 Leu Thr Arg Leu Asp Ala Gln Gly Pro Met Thr Val Asn Glu Leu Ala  
 50 55 60  
 Glu Ser Phe Gly Leu Asn Val Ser Thr Val His Arg Gln Leu Lys Ala  
 65 70 75 80  
 Ala Ile Ala Asn Gly Leu Ile Glu Val Val Asp Asp Gln Ala Cys Pro  
 85 90 95  
 Ala Lys Leu His Arg Pro Thr Glu Leu Gly Lys Glu Lys Leu Gln Gln  
 100 105 110  
 Glu Leu Leu Ala Arg Gln Gln Asp Leu Thr Arg Ile Leu His Asp Trp  
 115 120 125  
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 Glu Ser Leu Glu Glu Tyr Leu Asp Met Lys Trp Pro Arg Pro  
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 <223> RXS02288

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	Met Ser Gln Val Ile	
	1 5	
ccc gcc agc tca caa gaa aag cgt cgt gag cgc atc gtt tct tat gtc	163	
Pro Ala Ser Ser Gln Glu Lys Arg Arg Glu Arg Ile Val Ser Tyr Val		
	10 15 20	
acc cgt cat gga ttc gct cgt gtt gaa gca tta gct gag ctt ttt gag	211	
Thr Arg His Gly Phe Ala Arg Val Glu Ala Leu Ala Glu Leu Phe Glu		
	25 30 35	
gtc agc gca atg acc att cac cgt gat ttg gag gcg ctg gct gca gac	259	
Val Ser Ala Met Thr Ile His Arg Asp Leu Glu Ala Leu Ala Ala Asp		
	40 45 50	
aat ttg gtg gag cgc att agg ggt ggc gcg cgt tcg gtg tcg ccg tcg	307	
Asn Leu Val Glu Arg Ile Arg Gly Gly Ala Arg Ser Val Ser Pro Ser		
	55 60 65	
atg agt gag ttg gca gtg gag cag cgt cgg cat ttg cat cgc act gtt	355	
Met Ser Glu Leu Ala Val Glu Gln Arg Arg His Leu His Arg Thr Val		
	70 75 80 85	
aaa gag gcg ttg tgt act gca gca gca cgg ttg att ccg gag ggc gct	403	
Lys Glu Ala Leu Cys Thr Ala Ala Ala Arg Leu Ile Pro Glu Gly Ala		
	90 95 100	
gtg gtg gcg att gat gat tcc acc acg ttg gag tct ttg gtt gag aag	451	
Val Val Ala Ile Asp Asp Ser Thr Thr Leu Glu Ser Leu Val Glu Lys		
	105 110 115	
ttg ccg cag cgg tca cca tcg gcg ttg att acg cat tct ttg aag aca	499	
Leu Pro Gln Arg Ser Pro Ser Ala Leu Ile Thr His Ser Leu Lys Thr		
	120 125 130	
atg gcg gat cat cgt gtg cgc gcc ggg atg agc gat atc cgt ttg att	547	
Met Ala Asp His Arg Val Arg Ala Gly Met Ser Asp Ile Arg Leu Ile		
	135 140 145	
gcg tgt gcg gga ttg tat ttc gcg gag act gat tct ttc ttg ggc aag	595	
Ala Cys Ala Gly Leu Tyr Phe Ala Glu Thr Asp Ser Phe Leu Gly Lys		
	150 155 160 165	
gca act tca gcg cag ttg aat gag ctg tcg gcg gat att tct ttt gtt	643	
Ala Thr Ser Ala Gln Leu Asn Glu Leu Ser Ala Asp Ile Ser Phe Val		
	170 175 180	
tct acg act gcg gtg cgc gct acg ggg gag gtt ccg gcg ctg ttt cat	691	
Ser Thr Thr Ala Val Arg Ala Thr Gly Glu Val Pro Ala Leu Phe His		
	185 190 195	
cct gat atg gag gct gct gat acg aag cgg gcg ttg att ggg att ggt	739	
Pro Asp Met Glu Ala Ala Asp Thr Lys Arg Ala Leu Ile Gly Ile Gly		
	200 205 210	
agc gtg cgt gtg ttg gtg gtg gat tct agt aaa ttt ggt tcg gct ggt	787	
Ser Val Arg Val Leu Val Val Asp Ser Ser Lys Phe Gly Ser Ala Gly		
	215 220 225	

gtg ttc aag gtt gct tcg att gag gag ttt gac cac atc atc att gat 835  
 Val Phe Lys Val Ala Ser Ile Glu Glu Phe Asp His Ile Ile Ile Asp  
 230 235 240 245

cag cag tgc acc cgt gag cag cgg gat ctt ttg cgt aat tcg cgc gcg 883  
 Gln Gln Cys Thr Arg Glu Gln Arg Asp Leu Leu Arg Asn Ser Arg Ala  
 250 255 260

cag atc cat gtg att gac cac aat ggt gat gaa att ttg gat acc cca 931  
 Gln Ile His Val Ile Asp His Asn Gly Asp Glu Ile Leu Asp Thr Pro  
 265 270 275

acg gaa gag gat ttt taagatggct ttggttcttg gaa 969  
 Thr Glu Glu Asp Phe  
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<210> 336  
 <211> 282  
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 <213> Corynebacterium glutamicum

<400> 336  
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 20 25 30

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 35 40 45

Ala Leu Ala Ala Asp Asn Leu Val Glu Arg Ile Arg Gly Gly Ala Arg  
 50 55 60

Ser Val Ser Pro Ser Met Ser Glu Leu Ala Val Glu Gln Arg Arg His  
 65 70 75 80

Leu His Arg Thr Val Lys Glu Ala Leu Cys Thr Ala Ala Ala Arg Leu  
 85 90 95

Ile Pro Glu Gly Ala Val Val Ala Ile Asp Asp Ser Thr Thr Leu Glu  
 100 105 110

Ser Leu Val Glu Lys Leu Pro Gln Arg Ser Pro Ser Ala Leu Ile Thr  
 115 120 125

His Ser Leu Lys Thr Met Ala Asp His Arg Val Arg Ala Gly Met Ser  
 130 135 140

Asp Ile Arg Leu Ile Ala Cys Ala Gly Leu Tyr Phe Ala Glu Thr Asp  
 145 150 155 160

Ser Phe Leu Gly Lys Ala Thr Ser Ala Gln Leu Asn Glu Leu Ser Ala  
 165 170 175

Asp Ile Ser Phe Val Ser Thr Thr Ala Val Arg Ala Thr Gly Glu Val  
 180 185 190

Pro Ala Leu Phe His Pro Asp Met Glu Ala Ala Asp Thr Lys Arg Ala  
 195 200 205

Leu Ile Gly Ile Gly Ser Val Arg Val Leu Val Val Asp Ser Ser Lys  
 210 215 220  
 Phe Gly Ser Ala Gly Val Phe Lys Val Ala Ser Ile Glu Glu Phe Asp  
 225 230 235 240  
 His Ile Ile Ile Asp Gln Gln Cys Thr Arg Glu Gln Arg Asp Leu Leu  
 245 250 255  
 Arg Asn Ser Arg Ala Gln Ile His Val Ile Asp His Asn Gly Asp Glu  
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 Ile Leu Asp Thr Pro Thr Glu Glu Asp Phe  
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 <212> DNA  
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 <223> RXS02573

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 Met Thr Asn Lys Thr  
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 atg ctg gtt gct ttt gat ggc tca ccg gaa tcc cgg cgc gct ttg gaa 163  
 Met Leu Val Ala Phe Asp Gly Ser Pro Glu Ser Arg Arg Ala Leu Glu  
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 Tyr Ala Ala Lys Leu Leu Gln Pro Arg Thr Val Glu Ile Leu Thr Ala  
 25 30 35  
 tgg gag cca ttg cat cgg caa gct gcg cgc tcg gtt tcg ttg atc acc 259  
 Trp Glu Pro Leu His Arg Gln Ala Ala Arg Ser Val Ser Leu Ile Thr  
 40 45 50  
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 Leu Gly Val Glu Pro Glu Asp Pro Ala His Ser Ala Ala Leu Lys Thr  
 55 60 65  
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 Cys Gln Glu Gly Val Leu Ala Gln Ser Leu Gly Leu Glu Ala Arg  
 70 75 80 85  
 gcc cac atg gtg gaa tcc gca acg gcc gtg tgg agc gcc atc gtt gat 403  
 Ala His Met Val Glu Ser Ala Thr Ala Val Trp Ser Ala Ile Val Asp  
 90 95 100  
 gct gct gac gag ctc cgc ccc gac gtg att gtc acc ggc acc cgc ggg 451  
 Ala Ala Asp Glu Leu Arg Pro Asp Val Ile Val Thr Gly Thr Arg Gly  
 105 110 115

atc tcc gga tgg aaa tcc ctg tgg caa tcc tcc acc tca gac agc gtg 499  
 Ile Ser Gly Trp Lys Ser Leu Trp Gln Ser Ser Thr Ser Asp Ser Val  
 120 125 130

ctc cac cac gcc gac gta cca gtt ttt gtc gtt cca ccc ctg gac 544  
 Leu His His Ala Asp Val Pro Val Phe Val Val Pro Pro Leu Asp  
 135 140 145

taaaaccgag acgagaacca aga 567

<210> 338

<211> 148

<212> PRT

<213> Corynebacterium glutamicum

<400> 338

Met Thr Asn Lys Thr Met Leu Val Ala Phe Asp Gly Ser Pro Glu Ser  
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Arg Arg Ala Leu Glu Tyr Ala Ala Lys Leu Leu Gln Pro Arg Thr Val  
 20 25 30

Glu Ile Leu Thr Ala Trp Glu Pro Leu His Arg Gln Ala Ala Arg Ser  
 35 40 45

Val Ser Leu Ile Thr Leu Gly Val Glu Pro Glu Asp Pro Ala His Ser  
 50 55 60

Ala Ala Leu Lys Thr Cys Gln Glu Gly Val Glu Leu Ala Gln Ser Leu  
 65 70 75 80

Gly Leu Glu Ala Arg Ala His Met Val Glu Ser Ala Thr Ala Val Trp  
 85 90 95

Ser Ala Ile Val Asp Ala Ala Asp Glu Leu Arg Pro Asp Val Ile Val  
 100 105 110

Thr Gly Thr Arg Gly Ile Ser Gly Trp Lys Ser Leu Trp Gln Ser Ser  
 115 120 125

Thr Ser Asp Ser Val Leu His His Ala Asp Val Pro Val Phe Val Val  
 130 135 140

Pro Pro Leu Asp  
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<210> 339

<211> 866

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(843)

<223> RXS02627

<400> 339

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gga Gly	gat Asp	gct Ala	gag Glu	gct Ala	gcg Ala	ctg Leu	gaa Glu	ttc Phe	ggt Gly	gtg Val	cag Gln	cct Pro	gtg Val	ggt Gly	gca Ala	96
tca Ser	gat Asp	tgg Trp	ctc Leu	gca Ala	ttc Phe	ggt Gly	ggt Gly	gaa Glu	ggc Gly	gtg Val	gga Gly	ccg Pro	tgg Trp	att Ile	gag Glu	144
gat Asp	tct Ser	gcc Ala	tac Tyr	gat Asp	gaa Glu	gcg Ala	cca Pro	gaa Glu	ata Ile	atc Ile	gga Gly	acc Thr	atg Met	gaa Glu	ccg Pro	192
gag Glu	tat Tyr	gaa Glu	aag Lys	att Ile	gca Ala	gcg Ala	ctt Leu	gaa Glu	ccg Pro	gat Asp	ctg Leu	att Ile	ttg Leu	gac Asp	gtg Val	240
cgc Arg	agc Ser	tct Ser	ggc Gly	gac Asp	cag Gln	gaa Glu	cgc Arg	tat Tyr	gac Asp	aag Lys	ttg Leu	tct Ser	tca Ser	atc Ile	gca Ala	288
ctg Leu	acc Thr	atc Ile	ggc Gly	gtt Val	cca Pro	gaa Glu	ggt Gly	ggc Gly	gat Asp	agc Ser	tac Tyr	ctc Leu	acc Thr	cca Pro	cgc Arg	336
gct Ala	gag Glu	cag Gln	gta Val	acc Thr	atg Met	atc Ile	gcc Ala	act Thr	gct Ala	ctg Leu	ggg Gly	cag Gln	gct Ala	gaa Glu	cgt Arg	384
ggt Gly	gaa Glu	gaa Glu	gtg Val	aac Asn	gct Ala	gaa Glu	tac Tyr	gag Glu	cag Gln	ctc Leu	act Thr	gct Ala	gat Asp	att Ile	cgt Arg	432
gca Ala	gct Ala	cac His	ccg Pro	ggc Gly	tgg Trp	cct Pro	gag Glu	aag Lys	acc Thr	gcg Ala	gct Ala	gct Ala	gta Val	tct Ser	gca Ala	480
acg Thr	gca Ala	acc Thr	agc Ser	tgg Trp	ggt Gly	gca Ala	tac Tyr	atc Ile	aag Lys	ggc Gly	tcc Ser	aac Asn	cgt Arg	gta Val	gat Asp	528
act Thr	ttg Leu	ctg Leu	gac Asp	ctg Leu	ggc Gly	ttc Phe	cag Gln	gaa Glu	aac Asn	cct Pro	gag Glu	ctg Leu	gct Ala	aaa Lys	cag Gln	576
caa Gln	cct Pro	ggc Gly	gat Asp	acg Thr	ggt Gly	ttc Phe	tcc Ser	atc Ile	aaa Lys	ttc Phe	agt Ser	gaa Glu	gag Glu	act Thr	ttc Phe	624
ggc Gly	gtt Val	gtg Val	gat Asp	tcc Ser	gac Asp	ctg Leu	gtt Val	gtc Val	ggc Gly	ttt Phe	gcc Ala	atc Ile	ggt Gly	atg Met	act Thr	672
cct Pro	gag Glu	gaa Glu	atg Met	gca Ala	gag Glu	cag Gln	gtt Val	cca Pro	tgg Trp	cag Gln	atg Met	ttg Leu	acc Thr	gcc Ala	act Thr	720
cgt Arg	gac Asp	ggc Gly	cgt Arg	tcc Ser	ttt Phe	gtg Val	atg Met	ccc Pro	cgt Arg	gag Glu	att Ile	tcc Ser	aat Asn	gcg Ala	ttt Phe	768

245	250	255	
tct ttg ggt tcc ccg cag tcc act cgg ttc gcg tta gac gcc ttg gtg			816
Ser Leu Gly Ser Pro Gln Ser Thr Arg Phe Ala Leu Asp Ala Leu Val			
260	265	270	
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Pro Leu Leu Glu Glu His Ala Gly Glu			
275	280		

<210> 340  
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 <212> PRT  
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 Ser Asp Trp Leu Ala Phe Gly Gly Glu Gly Val Gly Pro Trp Ile Glu  
           35                    40                    45  
 Asp Ser Ala Tyr Asp Glu Ala Pro Glu Ile Ile Gly Thr Met Glu Pro  
       50                    55                    60  
 Glu Tyr Glu Lys Ile Ala Ala Leu Glu Pro Asp Leu Ile Leu Asp Val  
   65                    70                    75                    80  
 Arg Ser Ser Gly Asp Gln Glu Arg Tyr Asp Lys Leu Ser Ser Ile Ala  
           85                    90                    95  
 Leu Thr Ile Gly Val Pro Glu Gly Gly Asp Ser Tyr Leu Thr Pro Arg  
          100                    105                    110  
 Ala Glu Gln Val Thr Met Ile Ala Thr Ala Leu Gly Gln Ala Glu Arg  
       115                    120                    125  
 Gly Glu Glu Val Asn Ala Glu Tyr Glu Gln Leu Thr Ala Asp Ile Arg  
   130                    135                    140  
 Ala Ala His Pro Gly Trp Pro Glu Lys Thr Ala Ala Ala Val Ser Ala  
  145                    150                    155                    160  
 Thr Ala Thr Ser Trp Gly Ala Tyr Ile Lys Gly Ser Asn Arg Val Asp  
          165                    170                    175  
 Thr Leu Leu Asp Leu Gly Phe Gln Glu Asn Pro Glu Leu Ala Lys Gln  
       180                    185                    190  
 Gln Pro Gly Asp Thr Gly Phe Ser Ile Lys Phe Ser Glu Glu Thr Phe  
       195                    200                    205  
 Gly Val Val Asp Ser Asp Leu Val Val Gly Phe Ala Ile Gly Met Thr  
   210                    215                    220  
 Pro Glu Glu Met Ala Glu Gln Val Pro Trp Gln Met Leu Thr Ala Thr

225		230		235		240
Arg Asp Gly Arg Ser Phe Val Met Pro Arg Glu Ile Ser Asn Ala Phe						
		245		250		255
Ser Leu Gly Ser Pro Gln Ser Thr Arg Phe Ala Leu Asp Ala Leu Val						
	260		265		270	
Pro Leu Leu Glu Glu His Ala Gly Glu						
	275		280			

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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(907)  
 <223> RXS02691

<400> 341  
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 Met Asn Thr Met Pro  
 1 5  
 gac caa ccg ctc aac cag gac gga ttc cct acc gca tcc aaa ggg gtg 163  
 Asp Gln Pro Leu Asn Gln Asp Gly Phe Pro Thr Ala Ser Lys Gly Val  
 10 15 20  
 gaa ccc gac aac ctc ccc gac cgc gtt ctc gtg gac ggc ctt aaa cca 211  
 Glu Pro Asp Asn Leu Pro Asp Arg Val Leu Val Asp Gly Leu Lys Pro  
 25 30 35  
 aag cat cag cag ctt cgt gaa att ttg gag gaa atc tgc acc acc cag 259  
 Lys His Gln Gln Leu Arg Glu Ile Leu Glu Glu Ile Cys Thr Thr Gln  
 40 45 50  
 ctt cag cct ggg gac atg ctg cct ggt gag cgc atc ctg gaa gaa aag 307  
 Leu Gln Pro Gly Asp Met Leu Pro Gly Glu Arg Ile Leu Glu Glu Lys  
 55 60 65  
 tat ggc gtc agc cga att acg gtt cgt cgg gcg att ggt gat ctg gtc 355  
 Tyr Gly Val Ser Arg Ile Thr Val Arg Arg Ala Ile Gly Asp Leu Val  
 70 75 80 85  
 gcg tcc ggc agg ttg aag cga gct cgc ggc aaa ggt acc ttc gtg gcc 403  
 Ala Ser Gly Arg Leu Lys Arg Ala Arg Gly Lys Gly Thr Phe Val Ala  
 90 95 100  
 cac tcg ccg ttg att tcc cgc ctg cat ttg gcc tcg ttt tcc gca gag 451  
 His Ser Pro Leu Ile Ser Arg Leu His Leu Ala Ser Phe Ser Ala Glu  
 105 110 115  
 atg gcc gcc cag aag cta tcg gct acc agc agg att ttg agt tct tcc 499  
 Met Ala Ala Gln Lys Leu Ser Ala Thr Ser Arg Ile Leu Ser Ser Ser  
 120 125 130



cgc ggt ccc gcc cca gat gat att gct gat ttc ttt ggt acc gat cgc 547  
 Arg Gly Pro Ala Pro Asp Asp Ile Ala Asp Phe Phe Gly Thr Asp Arg  
 135 140 145  
 gcg gcc cag cac atc acg ttg cgc cgc ctg cgc ttt gga aat ggt cga 595  
 Ala Ala Gln His Ile Thr Leu Arg Arg Leu Arg Phe Gly Asn Gly Arg  
 150 155 160 165  
 ccc tat gcc att gac aac ggt tgg tac aac tcc gaa ttc gca cct gac 643  
 Pro Tyr Ala Ile Asp Asn Gly Trp Tyr Asn Ser Glu Phe Ala Pro Asp  
 170 175 180  
 ctg ctg gaa aat gat gtg tac aac tcc gtg tac tcc atc ctg gac cgc 691  
 Leu Leu Glu Asn Asp Val Tyr Asn Ser Val Tyr Ser Ile Leu Asp Arg  
 185 190 195  
 gtc tat ggc gtc ccc gtc acc cag gcc gag caa acg gtc acc gcc gta 739  
 Val Tyr Gly Val Pro Val Thr Gln Ala Glu Gln Thr Val Thr Ala Val  
 200 205 210  
 gca gcc gac gaa gac acc gca cgg ctt ctg gac gtc acc ccc ggc gcc 787  
 Ala Ala Asp Glu Asp Thr Ala Arg Leu Leu Asp Val Thr Pro Gly Ala  
 215 220 225  
 cca ctc ctt cgt atc ctt cga cag tca ctt tct ggc gat aag ccc gtg 835  
 Pro Leu Leu Arg Ile Leu Arg Gln Ser Leu Ser Gly Asp Lys Pro Val  
 230 235 240 245  
 gaa tgg tgc gtt tcc ttg tac cga acc gac cga tat tct tta aaa aca 883  
 Glu Trp Cys Val Ser Leu Tyr Arg Thr Asp Arg Tyr Ser Leu Lys Thr  
 250 255 260  
 ttg gtt aca cgc tcc gaa gat ctc tgacgtgaac ccattttggt ggc 930  
 Leu Val Thr Arg Ser Glu Asp Leu  
 265

&lt;210&gt; 342

&lt;211&gt; 269

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 342

Met Asn Thr Met Pro Asp Gln Pro Leu Asn Gln Asp Gly Phe Pro Thr  
 1 5 10 15  
 Ala Ser Lys Gly Val Glu Pro Asp Asn Leu Pro Asp Arg Val Leu Val  
 20 25 30  
 Asp Gly Leu Lys Pro Lys His Gln Gln Leu Arg Glu Ile Leu Glu Glu  
 35 40 45  
 Ile Cys Thr Thr Gln Leu Gln Pro Gly Asp Met Leu Pro Gly Glu Arg  
 50 55 60  
 Ile Leu Glu Glu Lys Tyr Gly Val Ser Arg Ile Thr Val Arg Arg Ala  
 65 70 75 80  
 Ile Gly Asp Leu Val Ala Ser Gly Arg Leu Lys Arg Ala Arg Gly Lys  
 85 90 95

Gly Thr Phe Val Ala His Ser Pro Leu Ile Ser Arg Leu His Leu Ala  
 100 105 110  
 Ser Phe Ser Ala Glu Met Ala Ala Gln Lys Leu Ser Ala Thr Ser Arg  
 115 120 125  
 Ile Leu Ser Ser Ser Arg Gly Pro Ala Pro Asp Asp Ile Ala Asp Phe  
 130 135 140  
 Phe Gly Thr Asp Arg Ala Ala Gln His Ile Thr Leu Arg Arg Leu Arg  
 145 150 155 160  
 Phe Gly Asn Gly Arg Pro Tyr Ala Ile Asp Asn Gly Trp Tyr Asn Ser  
 165 170 175  
 Glu Phe Ala Pro Asp Leu Leu Glu Asn Asp Val Tyr Asn Ser Val Tyr  
 180 185 190  
 Ser Ile Leu Asp Arg Val Tyr Gly Val Pro Val Thr Gln Ala Glu Gln  
 195 200 205  
 Thr Val Thr Ala Val Ala Ala Asp Glu Asp Thr Ala Arg Leu Leu Asp  
 210 215 220  
 Val Thr Pro Gly Ala Pro Leu Leu Arg Ile Leu Arg Gln Ser Leu Ser  
 225 230 235 240  
 Gly Asp Lys Pro Val Glu Trp Cys Val Ser Leu Tyr Arg Thr Asp Arg  
 245 250 255  
 Tyr Ser Leu Lys Thr Leu Val Thr Arg Ser Glu Asp Leu  
 260 265

<210> 343  
 <211> 1161  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1138)  
 <223> RXS02730

<400> 343  
 ccaacatcgc cttgcacgta ataggttaaa acacaagtga atgtaatcgt ttgcagcaat 60  
 cgattacata aaggtagata atgagataaa gcgaggcgct atg gcg acg gaa aaa 115  
 Met Ala Thr Glu Lys  
 1 5  
 ttc cga ccg act ctt aaa gat gtc gct cgt caa gca ggt gtc tcc atc 163  
 Phe Arg Pro Thr Leu Lys Asp Val Ala Arg Gln Ala Gly Val Ser Ile  
 10 15 20  
 gcc aca gca tca cga gca cta gcg gat aat ccg gcg gtt gct gca tcg 211  
 Ala Thr Ala Ser Arg Ala Leu Ala Asp Asn Pro Ala Val Ala Ala Ser  
 25 30 35  
 act cgt gaa aga atc caa caa tta gcc tct gat ctg ggt tac cgg gcc 259  
 Thr Arg Glu Arg Ile Gln Gln Leu Ala Ser Asp Leu Gly Tyr Arg Ala

40	45	50	
aat gct caa gct cgt gcg ctt cgc agt tct cgc agc aac acc att ggt			307
Asn Ala Gln Ala Arg Ala Leu Arg Ser Ser Arg Ser Asn Thr Ile Gly			
55	60	65	
gtg att gtt ccc agt ttg att aac cat tac ttc gcc gca atg gtt act			355
Val Ile Val Pro Ser Leu Ile Asn His Tyr Phe Ala Ala Met Val Thr			
70	75	80	85
gaa att caa agc acc gcc agc aaa gct gga ctt gcc acg att atc acc			403
Glu Ile Gln Ser Thr Ala Ser Lys Ala Gly Leu Ala Thr Ile Ile Thr			
	90	95	100
aac agc aat gaa gat gcg acc act atg tct ggg tct ttg gag ttt ctc			451
Asn Ser Asn Glu Asp Ala Thr Thr Met Ser Gly Ser Leu Glu Phe Leu			
	105	110	115
acc tcg cat ggt gtc gat gga atc atc tgc gta cct aat gag gaa tgc			499
Thr Ser His Gly Val Asp Gly Ile Ile Cys Val Pro Asn Glu Glu Cys			
	120	125	130
gcg aat caa cta gag gac ttg cag aag caa gga atg cca gtg gtg ttg			547
Ala Asn Gln Leu Glu Asp Leu Gln Lys Gln Gly Met Pro Val Val Leu			
	135	140	145
gtt gac cga gag ctt cca gga gac tcc acc atc cca acg gcg acc tct			595
Val Asp Arg Glu Leu Pro Gly Asp Ser Thr Ile Pro Thr Ala Thr Ser			
150	155	160	165
aac ccc caa cca gga atc gcc gca gca gta gaa ctc ctg gct cac aac			643
Asn Pro Gln Pro Gly Ile Ala Ala Ala Val Glu Leu Leu Ala His Asn			
	170	175	180
aac gcg ttg ccg att ggt tac ctc tca ggt ccc atg gac acc tca aca			691
Asn Ala Leu Pro Ile Gly Tyr Leu Ser Gly Pro Met Asp Thr Ser Thr			
	185	190	195
ggt aga gag cga tta gag gat ttc aaa gca gcc tgc gcc aac tcc aaa			739
Gly Arg Glu Arg Leu Glu Asp Phe Lys Ala Ala Cys Ala Asn Ser Lys			
	200	205	210
att ggc gaa cag ctc gtt ttt ctg ggt ggg tac gaa caa agc gtt gga			787
Ile Gly Glu Gln Leu Val Phe Leu Gly Gly Tyr Glu Gln Ser Val Gly			
215	220	225	
ttt gaa ggc gct acg aaa ttg ctc gat caa gga gct aaa act ctt ttt			835
Phe Glu Gly Ala Thr Lys Leu Leu Asp Gln Gly Ala Lys Thr Leu Phe			
230	235	240	245
gcc ggc gat tct atg atg acg atc ggt gtc att gaa gcc tgc cat aag			883
Ala Gly Asp Ser Met Met Thr Ile Gly Val Ile Glu Ala Cys His Lys			
	250	255	260
gct ggt ttg gtt atc ggc aag gat gtc agc gtg att ggt ttt gat aca			931
Ala Gly Leu Val Ile Gly Lys Asp Val Ser Val Ile Gly Phe Asp Thr			
	265	270	275
cat ccg ctt ttt gcc ctg caa cct cat ccg ttg aca gtg att gat caa			979
His Pro Leu Phe Ala Leu Gln Pro His Pro Leu Thr Val Ile Asp Gln			
	280	285	290

aat gta gaa caa cta gcc caa cga gca gtg tct atc ctc acc gaa tta 1027  
 Asn Val Glu Gln Leu Ala Gln Arg Ala Val Ser Ile Leu Thr Glu Leu  
 295 300 305

att gca ggc acg gta cct agc gtg acg aaa act acg atc ccc act gcc 1075  
 Ile Ala Gly Thr Val Pro Ser Val Thr Lys Thr Thr Ile Pro Thr Ala  
 310 315 320 325

ctt att cat cgt gaa tca atc atc aac tcc act tta agg aag aag gat 1123  
 Leu Ile His Arg Glu Ser Ile Ile Asn Ser Thr Leu Arg Lys Lys Asp  
 330 335 340

gga ctc ccc aat gag taactcaacc ggtaccgaca ttg 1161  
 Gly Leu Pro Asn Glu  
 345

<210> 344

<211> 346

<212> PRT

<213> Corynebacterium glutamicum

<400> 344

Met Ala Thr Glu Lys Phe Arg Pro Thr Leu Lys Asp Val Ala Arg Gln  
 1 5 10 15

Ala Gly Val Ser Ile Ala Thr Ala Ser Arg Ala Leu Ala Asp Asn Pro  
 20 25 30

Ala Val Ala Ala Ser Thr Arg Glu Arg Ile Gln Gln Leu Ala Ser Asp  
 35 40 45

Leu Gly Tyr Arg Ala Asn Ala Gln Ala Arg Ala Leu Arg Ser Ser Arg  
 50 55 60

Ser Asn Thr Ile Gly Val Ile Val Pro Ser Leu Ile Asn His Tyr Phe  
 65 70 75 80

Ala Ala Met Val Thr Glu Ile Gln Ser Thr Ala Ser Lys Ala Gly Leu  
 85 90 95

Ala Thr Ile Ile Thr Asn Ser Asn Glu Asp Ala Thr Thr Met Ser Gly  
 100 105 110

Ser Leu Glu Phe Leu Thr Ser His Gly Val Asp Gly Ile Ile Cys Val  
 115 120 125

Pro Asn Glu Glu Cys Ala Asn Gln Leu Glu Asp Leu Gln Lys Gln Gly  
 130 135 140

Met Pro Val Val Leu Val Asp Arg Glu Leu Pro Gly Asp Ser Thr Ile  
 145 150 155 160

Pro Thr Ala Thr Ser Asn Pro Gln Pro Gly Ile Ala Ala Ala Val Glu  
 165 170 175

Leu Leu Ala His Asn Asn Ala Leu Pro Ile Gly Tyr Leu Ser Gly Pro  
 180 185 190

Met Asp Thr Ser Thr Gly Arg Glu Arg Leu Glu Asp Phe Lys Ala Ala

195					200					205					
Cys	Ala	Asn	Ser	Lys	Ile	Gly	Glu	Gln	Leu	Val	Phe	Leu	Gly	Gly	Tyr
210						215					220				
Glu	Gln	Ser	Val	Gly	Phe	Glu	Gly	Ala	Thr	Lys	Leu	Leu	Asp	Gln	Gly
225					230					235					240
Ala	Lys	Thr	Leu	Phe	Ala	Gly	Asp	Ser	Met	Met	Thr	Ile	Gly	Val	Ile
				245					250					255	
Glu	Ala	Cys	His	Lys	Ala	Gly	Leu	Val	Ile	Gly	Lys	Asp	Val	Ser	Val
			260					265					270		
Ile	Gly	Phe	Asp	Thr	His	Pro	Leu	Phe	Ala	Leu	Gln	Pro	His	Pro	Leu
		275					280					285			
Thr	Val	Ile	Asp	Gln	Asn	Val	Glu	Gln	Leu	Ala	Gln	Arg	Ala	Val	Ser
						295					300				
Ile	Leu	Thr	Glu	Leu	Ile	Ala	Gly	Thr	Val	Pro	Ser	Val	Thr	Lys	Thr
305						310					315				320
Thr	Ile	Pro	Thr	Ala	Leu	Ile	His	Arg	Glu	Ser	Ile	Ile	Asn	Ser	Thr
				325					330					335	
Leu	Arg	Lys	Lys	Asp	Gly	Leu	Pro	Asn	Glu						
			340					345							

&lt;210&gt; 345

&lt;211&gt; 606

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(606)

&lt;223&gt; RXS02818

&lt;400&gt; 345

tcc	tat	tcc	cgg	aag	ttt	ttg	acc	cag	gtg	tgg	att	cga	gac	aat	gtc	48
Ser	Tyr	Ser	Arg	Lys	Phe	Leu	Thr	Gln	Val	Trp	Ile	Arg	Asp	Asn	Val	
1				5					10					15		

ggc	gat	tat	aaa	ggc	ctt	acc	gat	acg	gcg	ttc	cgt	aag	aag	ctg	cag	96
Gly	Asp	Tyr	Lys	Gly	Leu	Thr	Asp	Thr	Ala	Phe	Arg	Lys	Lys	Leu	Gln	
			20					25					30			

cgc	gat	ctt	gcc	tac	ctg	cgc	aga	gtt	ggc	gtt	ccg	att	gag	cag	ttc	144
Arg	Asp	Leu	Ala	Tyr	Leu	Arg	Arg	Val	Gly	Val	Pro	Ile	Glu	Gln	Phe	
		35					40					45				

acg	gtc	acc	tca	ggc	ata	gct	gaa	ggc	cag	cag	gcg	tac	cgt	ctg	gcc	192
Thr	Val	Thr	Ser	Gly	Ile	Ala	Glu	Gly	Gln	Gln	Ala	Tyr	Arg	Leu	Ala	
		50				55					60					

cag	gat	tct	tat	aag	ctc	ccc	gag	gtc	gaa	ttc	acc	cca	gat	gag	gcc	240
Gln	Asp	Ser	Tyr	Lys	Leu	Pro	Glu	Val	Glu	Phe	Thr	Pro	Asp	Glu	Ala	
65					70					75					80	

gcc gtg ctg ggc atg gca ggg gag atg ggc cat aat cag gaa ctc ggc 288  
 Ala Val Leu Gly Met Ala Gly Glu Met Gly His Asn Gln Glu Leu Gly  
                     85                    90                    95

gcc ttc gcg cgt tcg ggg tgg acc aaa ttg gcg gcc ggc ggc gcg cag 336  
 Ala Phe Ala Arg Ser Gly Trp Thr Lys Leu Ala Ala Gly Gly Ala Gln  
                     100                    105                    110

cgt gat ctg tcc acg tcc aca gcc ttg acc aat gcg ggc gat tta ggt 384  
 Arg Asp Leu Ser Thr Ser Thr Ala Leu Thr Asn Ala Gly Asp Leu Gly  
                     115                    120                    125

tcc ttg tct gca aaa acc ctc gat gcg atc atc aaa gcc cgc caa ttg 432  
 Ser Leu Ser Ala Lys Thr Leu Asp Ala Ile Ile Lys Ala Arg Gln Leu  
                     130                    135                    140

ggc aag caa atc agc ttc gaa tac cgg cgc gcc ccc aaa gac gcc ccc 480  
 Gly Lys Gln Ile Ser Phe Glu Tyr Arg Arg Ala Pro Lys Asp Ala Pro  
 145                    150                    155                    160

tcg ctt cga cac atg gat cct tgg ggt ctg gtc cct gag cgc gac cgc 528  
 Ser Leu Arg His Met Asp Pro Trp Gly Leu Val Pro Glu Arg Asp Arg  
                     165                    170                    175

atc tac ctg gtc gga ttc gac ctc gac cgc caa gaa gca cgc acc ttc 576  
 Ile Tyr Leu Val Gly Phe Asp Leu Asp Arg Gln Glu Ala Arg Thr Phe  
                     180                    185                    190

cgc atc acc cgc gtc cgc aac atc aaa ctc 606  
 Arg Ile Thr Arg Val Arg Asn Ile Lys Leu  
                     195                    200

&lt;210&gt; 346

&lt;211&gt; 202

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 346

Ser Tyr Ser Arg Lys Phe Leu Thr Gln Val Trp Ile Arg Asp Asn Val  
   1                    5                    10                    15

Gly Asp Tyr Lys Gly Leu Thr Asp Thr Ala Phe Arg Lys Lys Leu Gln  
                     20                    25                    30

Arg Asp Leu Ala Tyr Leu Arg Arg Val Gly Val Pro Ile Glu Gln Phe  
                     35                    40                    45

Thr Val Thr Ser Gly Ile Ala Glu Gly Gln Gln Ala Tyr Arg Leu Ala  
                     50                    55                    60

Gln Asp Ser Tyr Lys Leu Pro Glu Val Glu Phe Thr Pro Asp Glu Ala  
   65                    70                    75                    80

Ala Val Leu Gly Met Ala Gly Glu Met Gly His Asn Gln Glu Leu Gly  
                     85                    90                    95

Ala Phe Ala Arg Ser Gly Trp Thr Lys Leu Ala Ala Gly Gly Ala Gln  
                     100                    105                    110

Arg Asp Leu Ser Thr Ser Thr Ala Leu Thr Asn Ala Gly Asp Leu Gly

115		120		125
Ser Leu Ser Ala Lys Thr Leu Asp Ala Ile Ile Lys Ala Arg Gln Leu				
130		135		140
Gly Lys Gln Ile Ser Phe Glu Tyr Arg Arg Ala Pro Lys Asp Ala Pro				
145		150		155
Ser Leu Arg His Met Asp Pro Trp Gly Leu Val Pro Glu Arg Asp Arg				
	165		170	175
Ile Tyr Leu Val Gly Phe Asp Leu Asp Arg Gln Glu Ala Arg Thr Phe				
	180		185	190
Arg Ile Thr Arg Val Arg Asn Ile Lys Leu				
	195		200	

&lt;210&gt; 347

&lt;211&gt; 582

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)...(559)

&lt;223&gt; RXS02911

&lt;400&gt; 347

accgcataca ttaacgtggt gatcattgcc ctagtatgcg cagtagcggc tgctctgac 60

agcagttacc ttttccgcgg aaatccgaag ggagccaata atg cgc act agt aaa	115
Met Arg Thr Ser Lys	
1 5	

aaa gag atg att ctg cgc acg gcc atc gat tat atc ggc gag tac agc	163
Lys Glu Met Ile Leu Arg Thr Ala Ile Asp Tyr Ile Gly Glu Tyr Ser	
10 15 20	

ctc gag acg ctg agt tac gat tcg ctc gcc gag gcg acc ggt ctg tcc	211
Leu Glu Thr Leu Ser Tyr Asp Ser Leu Ala Glu Ala Thr Gly Leu Ser	
25 30 35	

aag tcg ggc ttg att tat cat ttc ccc agc cgc cat gcg ctg ctt tta	259
Lys Ser Gly Leu Ile Tyr His Phe Pro Ser Arg His Ala Leu Leu Leu	
40 45 50	

ggc atg cac gag ttg ctt gcc gac gac tgg gac aag gaa ttg cgc gac	307
Gly Met His Glu Leu Leu Ala Asp Asp Trp Asp Lys Glu Leu Arg Asp	
55 60 65	

ata acc cgc gac cca gag gat cca ctt gag cga ttg cgc gcc gtc gtg	355
Ile Thr Arg Asp Pro Glu Asp Pro Leu Glu Arg Leu Arg Ala Val Val	
70 75 80 85	

gtt acg ctt gct gaa aac gtt tcg cgc ccc gag ctg gtt ttg ctt atg	403
Val Thr Leu Ala Glu Asn Val Ser Arg Pro Glu Leu Val Leu Leu Met	
90 95 100	

gac gcc ccc tcc cac ccg gga ttt ctt aac gcc tgg cgc act gta aat	451
Asp Ala Pro Ser His Pro Gly Phe Leu Asn Ala Trp Arg Thr Val Asn	

105	110	115	
cat caa tgg atc ccc gac acc gat gat ctg gaa aac gat gcc cac aaa			499
His Gln Trp Ile Pro Asp Thr Asp Asp Leu Glu Asn Asp Ala His Lys			
120	125	130	
cgc gcc gtc tac tct ggt gca gct cgc agc cga tgg cct ctt cgt gca			547
Arg Ala Val Tyr Ser Gly Ala Ala Arg Ser Arg Trp Pro Leu Arg Ala			
135	140	145	
cga tta cat tca tgatgatgtc ctcagcaagt cca			582
Arg Leu His Ser			
150			

<210> 348  
 <211> 153  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 348  
 Met Arg Thr Ser Lys Lys Glu Met Ile Leu Arg Thr Ala Ile Asp Tyr  
 1 5 10 15  
 Ile Gly Glu Tyr Ser Leu Glu Thr Leu Ser Tyr Asp Ser Leu Ala Glu  
 20 25 30  
 Ala Thr Gly Leu Ser Lys Ser Gly Leu Ile Tyr His Phe Pro Ser Arg  
 35 40 45  
 His Ala Leu Leu Leu Gly Met His Glu Leu Leu Ala Asp Asp Trp Asp  
 50 55 60  
 Lys Glu Leu Arg Asp Ile Thr Arg Asp Pro Glu Asp Pro Leu Glu Arg  
 65 70 75 80  
 Leu Arg Ala Val Val Val Thr Leu Ala Glu Asn Val Ser Arg Pro Glu  
 85 90 95  
 Leu Val Leu Leu Met Asp Ala Pro Ser His Pro Gly Phe Leu Asn Ala  
 100 105 110  
 Trp Arg Thr Val Asn His Gln Trp Ile Pro Asp Thr Asp Asp Leu Glu  
 115 120 125  
 Asn Asp Ala His Lys Arg Ala Val Tyr Ser Gly Ala Ala Arg Ser Arg  
 130 135 140  
 Trp Pro Leu Arg Ala Arg Leu His Ser  
 145 150

<210> 349  
 <211> 786  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(763)  
 <223> RXS03066



&lt;400&gt; 349

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cgaaatcacc gcggcgtaat agcaccagct taaaaacctt atg aca tca gac aaa 115
                                         Met Thr Ser Asp Lys
                                         1           5

gac act gaa caa ttg gaa gcg gca ggc act gaa att tta atg cct cgc 163
Asp Thr Glu Gln Leu Glu Ala Ala Gly Thr Glu Ile Leu Met Pro Arg
                        10                        15                        20

cgc cgt ccg gca cag cag cgc agt cgt gaa cga ttc aat cga atc ctc 211
Arg Arg Pro Ala Gln Gln Arg Ser Arg Glu Arg Phe Asn Arg Ile Leu
                        25                        30                        35

acc gct gcg cgt tca gtg ctt gtc gat cta ggt ttt gaa tcg ttc acg 259
Thr Ala Ala Arg Ser Val Leu Val Asp Leu Gly Phe Glu Ser Phe Thr
                        40                        45                        50

ttt gat gaa gtc gct aag cgt gca gag gta ccg atc ggc acg ctg tac 307
Phe Asp Glu Val Ala Lys Arg Ala Glu Val Pro Ile Gly Thr Leu Tyr
                        55                        60                        65

caa ttc ttt gcc aat aag tat gta ttg atc tgc gaa ttg gat cgt gtg 355
Gln Phe Phe Ala Asn Lys Tyr Val Leu Ile Cys Glu Leu Asp Arg Val
                        70                        75                        80                        85

gat acc gca gaa gct gtc gcg gag ttg aag aaa ttc tcc gat cag gtt 403
Asp Thr Ala Glu Ala Val Ala Glu Leu Lys Lys Phe Ser Asp Gln Val
                        90                        95                        100

cct gcg ttg cag tgg ccg gat atc ctt gat gaa ttc att gag cac ttg 451
Pro Ala Leu Gln Trp Pro Asp Ile Leu Asp Glu Phe Ile Glu His Leu
                        105                        110                        115

gct agg ctc tgg cgc gat gat ccg tct cgg cgg gcc gtg tgg cat gcc 499
Ala Arg Leu Trp Arg Asp Asp Pro Ser Arg Arg Ala Val Trp His Ala
                        120                        125                        130

atc cag tcc acg ccg gca act cgt gcg aca gct gcg gcg acg gaa aaa 547
Ile Gln Ser Thr Pro Ala Thr Arg Ala Thr Ala Ala Thr Glu Lys
                        135                        140                        145

gag atg ctg gaa atc atc gcg gaa gtt atg cgc ccg ctt gcc cgc ggt 595
Glu Met Leu Glu Ile Ile Ala Glu Val Met Arg Pro Leu Ala Arg Gly
                        150                        155                        160                        165

gcc ggc tac gag gag cgc atg tca ctg gcg gga ttg ctg gtg cac acg 643
Ala Gly Tyr Glu Glu Arg Met Ser Leu Ala Gly Leu Leu Val His Thr
                        170                        175                        180

gta agt tcc ctg ctt aac tat gcc gtg cgt gat gtc aat agt tcc gaa 691
Val Ser Ser Leu Leu Asn Tyr Ala Val Arg Asp Val Asn Ser Ser Glu
                        185                        190                        195

gag gat ttc gac agc atc gtg gaa gaa ata aaa cga atg ctg att tct 739
Glu Asp Phe Asp Ser Ile Val Glu Glu Ile Lys Arg Met Leu Ile Ser
                        200                        205                        210

tac ctc ttc tcc gtg gct act gga tagtcaacac gcacgttcca ccg 786

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Tyr Leu Phe Ser Val Ala Thr Gly  
 215 220

<210> 350  
 <211> 221  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 350  
 Met Thr Ser Asp Lys Asp Thr Glu Gln Leu Glu Ala Ala Gly Thr Glu  
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 Ile Leu Met Pro Arg Arg Arg Pro Ala Gln Gln Arg Ser Arg Glu Arg  
 20 25 30  
 Phe Asn Arg Ile Leu Thr Ala Ala Arg Ser Val Leu Val Asp Leu Gly  
 35 40 45  
 Phe Glu Ser Phe Thr Phe Asp Glu Val Ala Lys Arg Ala Glu Val Pro  
 50 55 60  
 Ile Gly Thr Leu Tyr Gln Phe Phe Ala Asn Lys Tyr Val Leu Ile Cys  
 65 70 75 80  
 Glu Leu Asp Arg Val Asp Thr Ala Glu Ala Val Ala Glu Leu Lys Lys  
 85 90 95  
 Phe Ser Asp Gln Val Pro Ala Leu Gln Trp Pro Asp Ile Leu Asp Glu  
 100 105 110  
 Phe Ile Glu His Leu Ala Arg Leu Trp Arg Asp Asp Pro Ser Arg Arg  
 115 120 125  
 Ala Val Trp His Ala Ile Gln Ser Thr Pro Ala Thr Arg Ala Thr Ala  
 130 135 140  
 Ala Ala Thr Glu Lys Glu Met Leu Glu Ile Ile Ala Glu Val Met Arg  
 145 150 155 160  
 Pro Leu Ala Arg Gly Ala Gly Tyr Glu Glu Arg Met Ser Leu Ala Gly  
 165 170 175  
 Leu Leu Val His Thr Val Ser Ser Leu Leu Asn Tyr Ala Val Arg Asp  
 180 185 190  
 Val Asn Ser Ser Glu Glu Asp Phe Asp Ser Ile Val Glu Glu Ile Lys  
 195 200 205  
 Arg Met Leu Ile Ser Tyr Leu Phe Ser Val Ala Thr Gly  
 210 215 220

<210> 351  
 <211> 565  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(565)

&lt;223&gt; RXS03208

&lt;400&gt; 351

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gcataaattg agtttggaag aacaaggaag gcagcctcct gtg aag gat ctg gtc 115  
 Val Lys Asp Leu Val  
 1 5

gat acc acc gaa atg tat ctg cgc act att tac gag ctg gaa gaa gag 163  
 Asp Thr Thr Glu Met Tyr Leu Arg Thr Ile Tyr Glu Leu Glu Glu Glu  
 10 15 20

ggc att gtt cct ctg cgt gct cgt atc gca gaa cgc ctt gag cag tcc 211  
 Gly Ile Val Pro Leu Arg Ala Arg Ile Ala Glu Arg Leu Glu Gln Ser  
 25 30 35

ggc cca act gtc agc cag act gtc gcc cgt atg gaa cgc gac ggt ctt 259  
 Gly Pro Thr Val Ser Gln Thr Val Ala Arg Met Glu Arg Asp Gly Leu  
 40 45 50

gtg cac gtc agc ccc gac cgc agc ctc gaa atg act cca gag gga cgt 307  
 Val His Val Ser Pro Asp Arg Ser Leu Glu Met Thr Pro Glu Gly Arg  
 55 60 65

tcc ctc gcc atc gcc gtg atg cgt aag cac cgc cta gca gaa cgc ctc 355  
 Ser Leu Ala Ile Ala Val Met Arg Lys His Arg Leu Ala Glu Arg Leu  
 70 75 80 85

ctt acc gac atc atc ggc ttg gac atc cac aaa gtc cac gac gaa gca 403  
 Leu Thr Asp Ile Ile Gly Leu Asp Ile His Lys Val His Asp Glu Ala  
 90 95 100

tgc cgc tgg gag cac gtg atg agt gat gag gtt gaa cgt cgc ctc gtt 451  
 Cys Arg Trp Glu His Val Met Ser Asp Glu Val Glu Arg Arg Leu Val  
 105 110 115

gaa gtt ctt gac gat gtg cat cgc tcc cct ttc ggt aac cca att cct 499  
 Glu Val Leu Asp Asp Val His Arg Ser Pro Phe Gly Asn Pro Ile Pro  
 120 125 130

ggc ctc ggc gaa atc ggt ttg gat caa gca gat gag cct gat tcc ggc 547  
 Gly Leu Gly Glu Ile Gly Leu Asp Gln Ala Asp Glu Pro Asp Ser Gly  
 135 140 145

gtt cgt gcc atc gat ctg 565  
 Val Arg Ala Ile Asp Leu  
 150 155

&lt;210&gt; 352

&lt;211&gt; 155

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 352

Val Lys Asp Leu Val Asp Thr Thr Glu Met Tyr Leu Arg Thr Ile Tyr  
 1 5 10 15

Glu Leu Glu Glu Glu Gly Ile Val Pro Leu Arg Ala Arg Ile Ala Glu  
 20 25 30

Arg Leu Glu Gln Ser Gly Pro Thr Val Ser Gln Thr Val Ala Arg Met  
 35 40 45  
 Glu Arg Asp Gly Leu Val His Val Ser Pro Asp Arg Ser Leu Glu Met  
 50 55 60  
 Thr Pro Glu Gly Arg Ser Leu Ala Ile Ala Val Met Arg Lys His Arg  
 65 70 75 80  
 Leu Ala Glu Arg Leu Leu Thr Asp Ile Ile Gly Leu Asp Ile His Lys  
 85 90 95  
 Val His Asp Glu Ala Cys Arg Trp Glu His Val Met Ser Asp Glu Val  
 100 105 110  
 Glu Arg Arg Leu Val Glu Val Leu Asp Asp Val His Arg Ser Pro Phe  
 115 120 125  
 Gly Asn Pro Ile Pro Gly Leu Gly Glu Ile Gly Leu Asp Gln Ala Asp  
 130 135 140  
 Glu Pro Asp Ser Gly Val Arg Ala Ile Asp Leu  
 145 150 155

&lt;210&gt; 353

&lt;211&gt; 562

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(562)

&lt;223&gt; FRXA00307

&lt;400&gt; 353

gtgtttttaag aagtgttttt aagagaatac gcattgaagt agttttccct gctggcagcg 60

gcataaattg agtttggaag aacaaggaag gcagcctcct gtg aag gat ctg gtc 115  
 Val Lys Asp Leu Val  
 1 5

gat acc acc gaa atg tat ctg cgc act att tac gag ctg gaa gaa gag 163  
 Asp Thr Thr Glu Met Tyr Leu Arg Thr Ile Tyr Glu Leu Glu Glu Glu  
 10 15 20

ggc att gtt cct ctg cgt gct cgt atc gca gaa cgc ctt gag cag tcc 211  
 Gly Ile Val Pro Leu Arg Ala Arg Ile Ala Glu Arg Leu Glu Gln Ser  
 25 30 35

ggc cca act gtc agc cag act gtc gcc cgt atg gaa cgc gac ggt ctt 259  
 Gly Pro Thr Val Ser Gln Thr Val Ala Arg Met Glu Arg Asp Gly Leu  
 40 45 50

gtg cac gtc agc ccc gac cgc agc ctc gaa atg act cca gag gga cgt 307  
 Val His Val Ser Pro Asp Arg Ser Leu Glu Met Thr Pro Glu Gly Arg  
 55 60 65

tcc ctc gcc atc gcc gtg atg cgt aag cac cgc cta gca gaa cgc ctc 355  
 Ser Leu Ala Ile Ala Val Met Arg Lys His Arg Leu Ala Glu Arg Leu

70	75	80	85	
ctt acc gac atc atc ggc ttg gac atc cac aaa gtc cac gac gaa gca				403
Leu Thr Asp Ile Ile Gly Leu Asp Ile His Lys Val His Asp Glu Ala				
	90	95	100	
tgc cgc tgg gag cac gtg atg agt gat gag gtt gaa cgt cgc ctc gtt				451
Cys Arg Trp Glu His Val Met Ser Asp Glu Val Glu Arg Arg Leu Val				
	105	110	115	
gaa gtt ctt gac gat gtg cat cgc tcc cct ttc ggt aac cca att cct				499
Glu Val Leu Asp Asp Val His Arg Ser Pro Phe Gly Asn Pro Ile Pro				
	120	125	130	
ggc ctc ggc gaa atc ggt ttg gat caa gca gat gag cct gat tcc ggc				547
Gly Leu Gly Glu Ile Gly Leu Asp Gln Ala Asp Glu Pro Asp Ser Gly				
	135	140	145	
gtt cgt gcc atc gat				562
Val Arg Ala Ile Asp				
	150			
<210> 354				
<211> 154				
<212> PRT				
<213> Corynebacterium glutamicum				
<400> 354				
Val Lys Asp Leu Val Asp Thr Thr Glu Met Tyr Leu Arg Thr Ile Tyr				
1	5	10	15	
Glu Leu Glu Glu Glu Gly Ile Val Pro Leu Arg Ala Arg Ile Ala Glu				
	20	25	30	
Arg Leu Glu Gln Ser Gly Pro Thr Val Ser Gln Thr Val Ala Arg Met				
	35	40	45	
Glu Arg Asp Gly Leu Val His Val Ser Pro Asp Arg Ser Leu Glu Met				
	50	55	60	
Thr Pro Glu Gly Arg Ser Leu Ala Ile Ala Val Met Arg Lys His Arg				
	65	70	75	80
Leu Ala Glu Arg Leu Leu Thr Asp Ile Ile Gly Leu Asp Ile His Lys				
	85	90	95	
Val His Asp Glu Ala Cys Arg Trp Glu His Val Met Ser Asp Glu Val				
	100	105	110	
Glu Arg Arg Leu Val Glu Val Leu Asp Asp Val His Arg Ser Pro Phe				
	115	120	125	
Gly Asn Pro Ile Pro Gly Leu Gly Glu Ile Gly Leu Asp Gln Ala Asp				
	130	135	140	
Glu Pro Asp Ser Gly Val Arg Ala Ile Asp				
	145	150		

&lt;210&gt; 355

<400> 355																
cgtgttttaaa tctagaagtt taaaggggtga aaacagtgcca ttactttaagc accaatctgc																60
cataatttttt accccaacgc ataggcttaa cggtgtgaat																115
Val Lys Leu Thr Asp																5
1																
gcc	gcc	cgt	gaa	gct	gga	gta	ggg	tac	ggg	act	gct	tct	cgc	gca	att	163
Ala	Ala	Arg	Glu	Ala	Gly	Val	Gly	Tyr	Gly	Thr	Ala	Ser	Arg	Ala	Ile	
10 15 20																
tct	gga	cga	ggg	tcc	ggt	gat	gca	gca	acc	cgt	gac	aaa	gta	ctc	gcc	211
Ser	Gly	Arg	Gly	Ser	Val	Asp	Ala	Ala	Thr	Arg	Asp	Lys	Val	Leu	Ala	
25 30 35																
gcc	gcc	gag	aaa	ctt	ggg	tac	cga	acc	aac	gcc	atg	gct	cgt	gca	ctt	259
Ala	Ala	Glu	Lys	Leu	Gly	Tyr	Arg	Thr	Asn	Ala	Met	Ala	Arg	Ala	Leu	
40 45 50																
agg	gaa	aac	aag	acc	cgc	acc	ggt	ggc	ctg	atc	ggt	ccc	ggc	att	atc	307
Arg	Glu	Asn	Lys	Thr	Arg	Thr	Val	Gly	Leu	Ile	Val	Pro	Gly	Ile	Ile	
55 60 65																
aat	aag	ttc	tac	acc	gaa	tcc	gcc	act	gtc	ctc	caa	gat	gaa	tta	gac	355
Asn	Lys	Phe	Tyr	Thr	Glu	Ser	Ala	Thr	Val	Leu	Gln	Asp	Glu	Leu	Asp	
70 75 80 85																
aaa	tcc	gga	tac	caa	cta	ggt	ggt	tcc	aca	act	gga	aac	gac	gca	gaa	403
Lys	Ser	Gly	Tyr	Gln	Leu	Val	Val	Ser	Thr	Thr	Gly	Asn	Asp	Ala	Glu	
90 95 100																
aag	gaa	cgt	cga	gct	atc	gaa	tcc	atg	ctc	aac	cgc	cag	gta	gat	gca	451
Lys	Glu	Arg	Arg	Ala	Ile	Glu	Ser	Met	Leu	Asn	Arg	Gln	Val	Asp	Ala	
105 110 115																
gtg	gtg	cac	gct	cca	ggt	aat	ccc	caa	gcg	aag	ttt	cca	aag	ggc	ttc	499
Val	Val	His	Ala	Pro	Val	Asn	Pro	Gln	Ala	Lys	Phe	Pro	Lys	Gly	Phe	
120 125 130																
aaa	gtg	gtc	gag	ctt	aat	cgt	cgt	agc	gat	ctc	aac	cga	cct	act	gtg	547
Lys	Val	Val	Glu	Leu	Asn	Arg	Arg	Ser	Asp	Leu	Asn	Arg	Pro	Thr	Val	
135 140 145																
acc	agc	gat	gat	gcc	act	ggg	ttg	aag	gaa	ctt	gct	ctt	cat	att	ttg	595
Thr	Ser	Asp	Asp	Ala	Thr	Gly	Leu	Lys	Glu	Leu	Ala	Leu	His	Ile	Leu	
150 155 160 165																
gat	cag	gga	tac	cga	gat	ata	ggg	atc	att	gtc	ggg	cct	gct	gag	ctc	643
Asp	Gln	Gly	Tyr	Arg	Asp	Ile	Gly	Ile	Ile	Val	Gly	Pro	Ala	Glu	Leu	
170 175 180																
agc	acc	qcc	cga	qac	cgc	aaa	qcc	qga	ttc	atc	aac	qcc	ctc	qaa	acc	691

Ser	Thr	Ala	Arg	Asp	Arg	Lys	Ala	Gly	Phe	Ile	Asn	Ala	Leu	Glu	Thr		
			185					190					195				
gaa	gcc	aca	caa	cgc	gga	atc	cgc	gaa	gaa	cta	cga	ttc	cgg	gta	gtt	739	
Glu	Ala	Thr	Gln	Arg	Gly	Ile	Arg	Glu	Glu	Leu	Arg	Phe	Arg	Val	Val		
		200					205					210					
cac	tcc	cgc	tac	tcc	ccc	acc	ggc	ggt	tat	gaa	gca	ttc	gca	gaa	ttc	787	
His	Ser	Arg	Tyr	Ser	Pro	Thr	Gly	Gly	Tyr	Glu	Ala	Phe	Ala	Glu	Phe		
	215					220					225						
cgc	aat	gat	ctc	cct	caa	atc	gtg	gtg	ccc	ctg	agc	acg	caa	tta	act	835	
Arg	Asn	Asp	Leu	Pro	Gln	Ile	Val	Val	Pro	Leu	Ser	Thr	Gln	Leu	Thr		
230					235					240					245		
cta	gga	gtt	ctc	aaa	gca	acc	caa	gaa	aac	ggc	ata	aaa	ata	tcg	gat	883	
Leu	Gly	Val	Leu	Lys	Ala	Thr	Gln	Glu	Asn	Gly	Ile	Lys	Ile	Ser	Asp		
			250						255					260			
gac	ctg	tca	ctt	gct	tgt	tac	ggc	gtc	gcc	gaa	tgg	ctc	gca	gtg	tgg	931	
Asp	Leu	Ser	Leu	Ala	Cys	Tyr	Gly	Val	Ala	Glu	Trp	Leu	Ala	Val	Trp		
			265					270					275				
ggc	cct	ggc	atc	acc	gtt	ttc	gca	cca	gac	ctc	cca	gcc	atg	ggc	gcc	979	
Gly	Pro	Gly	Ile	Thr	Val	Phe	Ala	Pro	Asp	Leu	Pro	Ala	Met	Gly	Ala		
		280					285					290					
gca	gct	gcc	acg	cag	gtt	tta	acg	ott	ctc	gac	gcc	gcc	cca	ctc	ccc	1027	
Ala	Ala	Ala	Thr	Gln	Val	Leu	Thr	Leu	Leu	Asp	Ala	Ala	Pro	Leu	Pro		
		295				300					305						
gaa	aac	cac	tta	agc	att	ccg	ggg	cag	ctc	att	gtc	cgt	ggg	aca	act	1075	
Glu	Asn	His	Leu	Ser	Ile	Pro	Gly	Gln	Leu	Ile	Val	Arg	Gly	Thr	Thr		
310					315					320					325		
cca	aag	gtt	taa	agg	taga	ggc	gcaca	aat	aat	gaaa	aatt					1114	
Pro	Lys	Val															

&lt;210&gt; 356

&lt;211&gt; 328

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 356

Val	Lys	Leu	Thr	Asp	Ala	Ala	Arg	Glu	Ala	Gly	Val	Gly	Tyr	Gly	Thr		
1				5					10					15			
Ala	Ser	Arg	Ala	Ile	Ser	Gly	Arg	Gly	Ser	Val	Asp	Ala	Ala	Thr	Arg		
			20					25					30				
Asp	Lys	Val	Leu	Ala	Ala	Ala	Glu	Lys	Leu	Gly	Tyr	Arg	Thr	Asn	Ala		
		35					40					45					
Met	Ala	Arg	Ala	Leu	Arg	Glu	Asn	Lys	Thr	Arg	Thr	Val	Gly	Leu	Ile		
	50					55					60						
Val	Pro	Gly	Ile	Ile	Asn	Lys	Phe	Tyr	Thr	Glu	Ser	Ala	Thr	Val	Leu		
	65				70					75					80		

Gln Asp Glu Leu Asp Lys Ser Gly Tyr Gln Leu Val Val Ser Thr Thr  
                     85                    90                    95  
 Gly Asn Asp Ala Glu Lys Glu Arg Arg Ala Ile Glu Ser Met Leu Asn  
                     100                    105                    110  
 Arg Gln Val Asp Ala Val Val His Ala Pro Val Asn Pro Gln Ala Lys  
                     115                    120                    125  
 Phe Pro Lys Gly Phe Lys Val Val Glu Leu Asn Arg Arg Ser Asp Leu  
                     130                    135                    140  
 Asn Arg Pro Thr Val Thr Ser Asp Asp Ala Thr Gly Leu Lys Glu Leu  
                     145                    150                    155                    160  
 Ala Leu His Ile Leu Asp Gln Gly Tyr Arg Asp Ile Gly Ile Ile Val  
                     165                    170                    175  
 Gly Pro Ala Glu Leu Ser Thr Ala Arg Asp Arg Lys Ala Gly Phe Ile  
                     180                    185                    190  
 Asn Ala Leu Glu Thr Glu Ala Thr Gln Arg Gly Ile Arg Glu Glu Leu  
                     195                    200                    205  
 Arg Phe Arg Val Val His Ser Arg Tyr Ser Pro Thr Gly Gly Tyr Glu  
                     210                    215                    220  
 Ala Phe Ala Glu Phe Arg Asn Asp Leu Pro Gln Ile Val Val Pro Leu  
                     225                    230                    235                    240  
 Ser Thr Gln Leu Thr Leu Gly Val Leu Lys Ala Thr Gln Glu Asn Gly  
                     245                    250                    255  
 Ile Lys Ile Ser Asp Asp Leu Ser Leu Ala Cys Tyr Gly Val Ala Glu  
                     260                    265                    270  
 Trp Leu Ala Val Trp Gly Pro Gly Ile Thr Val Phe Ala Pro Asp Leu  
                     275                    280                    285  
 Pro Ala Met Gly Ala Ala Ala Ala Thr Gln Val Leu Thr Leu Leu Asp  
                     290                    295                    300  
 Ala Ala Pro Leu Pro Glu Asn His Leu Ser Ile Pro Gly Gln Leu Ile  
                     305                    310                    315                    320  
 Val Arg Gly Thr Thr Pro Lys Val  
                     325

&lt;210&gt; 357

&lt;211&gt; 1107

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1084)

&lt;223&gt; FRXA02763

&lt;400&gt; 357

cgtgttttaa tctagaagtt taaagggtga aaacagtcca ttacttaagc accaatctgc 60



cataattttt	accccaacgc	ataggcttaa	cggtgtgaat	gtg	aag	tta	act	gac	115
				Val	Lys	Leu	Thr	Asp	
				1				5	
gcc gcc cgt gaa gct gga gta ggt tac ggt act gct tct cgc gca att	163								
Ala Ala Arg Glu Ala Gly Val Gly Tyr Gly Thr Ala Ser Arg Ala Ile									
	10	15	20						
tct gga cga ggt tcc gtt gat gca gca acc cgt gac aaa gta ctc gcc	211								
Ser Gly Arg Gly Ser Val Asp Ala Ala Thr Arg Asp Lys Val Leu Ala									
	25	30	35						
gcc gcc gag aaa ctt ggg tac cga acc aac gcc atg gct cgt gca ctt	259								
Ala Ala Glu Lys Leu Gly Tyr Arg Thr Asn Ala Met Ala Arg Ala Leu									
	40	45	50						
agg gaa aac aag acc cgc acc gtt ggc ctg atc gtt ccc ggc att atc	307								
Arg Glu Asn Lys Thr Arg Thr Val Gly Leu Ile Val Pro Gly Ile Ile									
	55	60	65						
aat aag ttc tac acc gaa tcc gcc act gtc ctc caa gat gaa tta gac	355								
Asn Lys Phe Tyr Thr Glu Ser Ala Thr Val Leu Gln Asp Glu Leu Asp									
	70	75	80	85					
aaa tcc gga tac caa cta gtt gtt tcc aca act gga aac gac gca gaa	403								
Lys Ser Gly Tyr Gln Leu Val Val Ser Thr Thr Gly Asn Asp Ala Glu									
	90	95	100						
aag gaa cgt cga gct atc gaa tcc atg ctc aac cgc cag gta gat gca	451								
Lys Glu Arg Arg Ala Ile Glu Ser Met Leu Asn Arg Gln Val Asp Ala									
	105	110	115						
gtg gtg cac gct cca gtt aat ccc caa gcg aag ttt cca aag ggc ttc	499								
Val Val His Ala Pro Val Asn Pro Gln Ala Lys Phe Pro Lys Gly Phe									
	120	125	130						
aaa gtg gtc gag ctt aat cgt cgt agc gat ctc aac cga cct act gtg	547								
Lys Val Val Glu Leu Asn Arg Arg Ser Asp Leu Asn Arg Pro Thr Val									
	135	140	145						
acc agc gat gat gcc act ggt ttg aag gaa ctt gct ctt cat att ttg	595								
Thr Ser Asp Asp Ala Thr Gly Leu Lys Glu Leu Ala Leu His Ile Leu									
	150	155	160	165					
gat cag gga tac cga gat ata ggt atc att gtc ggt cct gct gag ctc	643								
Asp Gln Gly Tyr Arg Asp Ile Gly Ile Ile Val Gly Pro Ala Glu Leu									
	170	175	180						
agc acc gcc cga gac cgc aaa gcc gga ttc atc aac gcc ctc gaa acc	691								
Ser Thr Ala Arg Asp Arg Lys Ala Gly Phe Ile Asn Ala Leu Glu Thr									
	185	190	195						
gaa gcc aca caa cgc gga atc cgc gaa gaa cta cga ttc cgg gta gtt	739								
Glu Ala Thr Gln Arg Gly Ile Arg Glu Glu Leu Arg Phe Arg Val Val									
	200	205	210						
cac tcc cgc tac tcc ccc acc ggc ggt tat gaa gca ttc gca gaa ttc	787								
His Ser Arg Tyr Ser Pro Thr Gly Gly Tyr Glu Ala Phe Ala Glu Phe									
	215	220	225						

cgc aat gat ctc cct caa atc gtg gtg ccc ctg agc acg caa tta act 835  
 Arg Asn Asp Leu Pro Gln Ile Val Val Pro Leu Ser Thr Gln Leu Thr 245  
 230 235 240

cta gga gtt ctc aaa gca acc caa gaa aac ggc ata aaa ata tcg gat 883  
 Leu Gly Val Leu Lys Ala Thr Gln Glu Asn Gly Ile Lys Ile Ser Asp 260  
 250 255

gac ctg tca ctt gct tgt tac ggc gtc gcc gaa tgg ctc gca gtg tgg 931  
 Asp Leu Ser Leu Ala Cys Tyr Gly Val Ala Glu Trp Leu Ala Val Trp 275  
 265 270

ggc cct ggc atc acc gtt ttc gca cca gac ctc cca gcc atg ggc gcc 979  
 Gly Pro Gly Ile Thr Val Phe Ala Pro Asp Leu Pro Ala Met Gly Ala 290  
 280 285

gca gct gcc acg cag gtt tta acg ctt ctc gac gcc gcc cca ctc ccc 1027  
 Ala Ala Ala Thr Gln Val Leu Thr Leu Leu Asp Ala Ala Pro Leu Pro 305  
 295 300

gaa aac cac tta agc att ccg ggg cag ctc att gtg cgt ggg aca act 1075  
 Glu Asn His Leu Ser Ile Pro Gly Gln Leu Ile Val Arg Gly Thr Thr 325  
 310 315 320

cca aag gtt taaaggtaga ggcgacacaat aat 1107  
 Pro Lys Val

<210> 358

<211> 328

<212> PRT

<213> Corynebacterium glutamicum

<400> 358

Val Lys Leu Thr Asp Ala Ala Arg Glu Ala Gly Val Gly Tyr Gly Thr  
 1 5 10 15

Ala Ser Arg Ala Ile Ser Gly Arg Gly Ser Val Asp Ala Ala Thr Arg  
 20 25 30

Asp Lys Val Leu Ala Ala Ala Glu Lys Leu Gly Tyr Arg Thr Asn Ala  
 35 40 45

Met Ala Arg Ala Leu Arg Glu Asn Lys Thr Arg Thr Val Gly Leu Ile  
 50 55 60

Val Pro Gly Ile Ile Asn Lys Phe Tyr Thr Glu Ser Ala Thr Val Leu  
 65 70 75 80

Gln Asp Glu Leu Asp Lys Ser Gly Tyr Gln Leu Val Val Ser Thr Thr  
 85 90 95

Gly Asn Asp Ala Glu Lys Glu Arg Arg Ala Ile Glu Ser Met Leu Asn  
 100 105 110

Arg Gln Val Asp Ala Val Val His Ala Pro Val Asn Pro Gln Ala Lys  
 115 120 125

Phe Pro Lys Gly Phe Lys Val Val Glu Leu Asn Arg Arg Ser Asp Leu  
 130 135 140

Asn Arg Pro Thr Val Thr Ser Asp Asp Ala Thr Gly Leu Lys Glu Leu  
 145 150 155 160  
 Ala Leu His Ile Leu Asp Gln Gly Tyr Arg Asp Ile Gly Ile Ile Val  
 165 170 175  
 Gly Pro Ala Glu Leu Ser Thr Ala Arg Asp Arg Lys Ala Gly Phe Ile  
 180 185 190  
 Asn Ala Leu Glu Thr Glu Ala Thr Gln Arg Gly Ile Arg Glu Glu Leu  
 195 200 205  
 Arg Phe Arg Val Val His Ser Arg Tyr Ser Pro Thr Gly Gly Tyr Glu  
 210 215 220  
 Ala Phe Ala Glu Phe Arg Asn Asp Leu Pro Gln Ile Val Val Pro Leu  
 225 230 235 240  
 Ser Thr Gln Leu Thr Leu Gly Val Leu Lys Ala Thr Gln Glu Asn Gly  
 245 250 255  
 Ile Lys Ile Ser Asp Asp Leu Ser Leu Ala Cys Tyr Gly Val Ala Glu  
 260 265 270  
 Trp Leu Ala Val Trp Gly Pro Gly Ile Thr Val Phe Ala Pro Asp Leu  
 275 280 285  
 Pro Ala Met Gly Ala Ala Ala Ala Thr Gln Val Leu Thr Leu Leu Asp  
 290 295 300  
 Ala Ala Pro Leu Pro Glu Asn His Leu Ser Ile Pro Gly Gln Leu Ile  
 305 310 315 320  
 Val Arg Gly Thr Thr Pro Lys Val  
 325

<210> 359  
 <211> 759  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(759)  
 <223> RXS03200

<400> 359  
 gag aag ttg ctg cca ttc gcc aaa tcc acc ctt gac gcg gcg gag tct 48  
 Glu Lys Leu Leu Pro Phe Ala Lys Ser Thr Leu Asp Ala Ala Glu Ser  
 1 5 10 15  
 ttc ctc tcc cac gcc aag ggc gcc aac ggt tcg ctc act gga ccg ttg 96  
 Phe Leu Ser His Ala Lys Gly Ala Asn Gly Ser Leu Thr Gly Pro Leu  
 20 25 30  
 acc gta ggc atc atc ccc acg gcg gct cct tac att ttg ccg tca atg 144  
 Thr Val Gly Ile Ile Pro Thr Ala Ala Pro Tyr Ile Leu Pro Ser Met  
 35 40 45

ctg tcc atc gtg gat gaa gaa tat cca gat ctg gaa cct cac atc gtc 192  
 Leu Ser Ile Val Asp Glu Glu Tyr Pro Asp Leu Glu Pro His Ile Val  
 50 55 60

gag gac caa acc aag cat ctt ctc gcg ttg ctg cgc gac ggc gcc atc 240  
 Glu Asp Gln Thr Lys His Leu Leu Ala Leu Leu Arg Asp Gly Ala Ile  
 65 70 75 80

gac gtc gcc atg atg gcc ctg cct tct gag gca cca ggc atg aag gaa 288  
 Asp Val Ala Met Met Ala Leu Pro Ser Glu Ala Pro Gly Met Lys Glu  
 85 90 95

atc ccc ctc tac gac gaa gac ttt atc gtc gtt aca gct agc gat cac 336  
 Ile Pro Leu Tyr Asp Glu Asp Phe Ile Val Val Thr Ala Ser Asp His  
 100 105 110

ccc ttc gcc ggc cgc caa gac tta gaa cta tcc gcc tta gaa gac ctc 384  
 Pro Phe Ala Gly Arg Gln Asp Leu Glu Leu Ser Ala Leu Glu Asp Leu  
 115 120 125

gat ctg ctg ctt ctc gac gac gga cac tgc ctc cac gac caa att gtg 432  
 Asp Leu Leu Leu Leu Asp Asp Gly His Cys Leu His Asp Gln Ile Val  
 130 135 140

gac ctg tgc cgc cgc gga gac atc aac ccc att agc tcc act act gct 480  
 Asp Leu Cys Arg Arg Gly Asp Ile Asn Pro Ile Ser Ser Thr Thr Ala  
 145 150 155 160

gtc acc cgc gca tcc agc ctt acc acc gtc atg cag ctc gtc gtc gcc 528  
 Val Thr Arg Ala Ser Ser Leu Thr Thr Val Met Gln Leu Val Val Ala  
 165 170 175

ggc ctt gga tcc acc ttg gtc cca atc agc gca atc cca tgg gaa tgc 576  
 Gly Leu Gly Ser Thr Leu Val Pro Ile Ser Ala Ile Pro Trp Glu Cys  
 180 185 190

acc cga cca gga ctg gca aca gcc aac ttc aac tct gat gtc acc gca 624  
 Thr Arg Pro Gly Leu Ala Thr Ala Asn Phe Asn Ser Asp Val Thr Ala  
 195 200 205

aac cgc cgc att gga ttg gtg tac cgt tcc tct tct tct cgc gcc gaa 672  
 Asn Arg Arg Ile Gly Leu Val Tyr Arg Ser Ser Ser Ser Arg Ala Glu  
 210 215 220

gag ttc gaa cag ttt gca ctc att ttg cag cgc gct ttc caa gaa gcc 720  
 Glu Phe Glu Gln Phe Ala Leu Ile Leu Gln Arg Ala Phe Gln Glu Ala  
 225 230 235 240

gtc gcg ctt gct gcc tca act ggc atc acc ttg aag caa 759  
 Val Ala Leu Ala Ala Ser Thr Gly Ile Thr Leu Lys Gln  
 245 250

&lt;210&gt; 360

&lt;211&gt; 253

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 360

Glu Lys Leu Leu Pro Phe Ala Lys Ser Thr Leu Asp Ala Ala Glu Ser  
 1 5 10 15

Phe Leu Ser His Ala Lys Gly Ala Asn Gly Ser Leu Thr Gly Pro Leu  
                   20                                  25                                  30  
 Thr Val Gly Ile Ile Pro Thr Ala Ala Pro Tyr Ile Leu Pro Ser Met  
                   35                                  40                                  45  
 Leu Ser Ile Val Asp Glu Glu Tyr Pro Asp Leu Glu Pro His Ile Val  
                   50                                  55                                  60  
 Glu Asp Gln Thr Lys His Leu Leu Ala Leu Leu Arg Asp Gly Ala Ile  
                   65                                  70                                  75                                  80  
 Asp Val Ala Met Met Ala Leu Pro Ser Glu Ala Pro Gly Met Lys Glu  
                                   85                                  90                                  95  
 Ile Pro Leu Tyr Asp Glu Asp Phe Ile Val Val Thr Ala Ser Asp His  
                                   100                                  105                                  110  
 Pro Phe Ala Gly Arg Gln Asp Leu Glu Leu Ser Ala Leu Glu Asp Leu  
                   115                                  120                                  125  
 Asp Leu Leu Leu Leu Asp Asp Gly His Cys Leu His Asp Gln Ile Val  
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 Asp Leu Cys Arg Arg Gly Asp Ile Asn Pro Ile Ser Ser Thr Thr Ala  
                   145                                  150                                  155                                  160  
 Val Thr Arg Ala Ser Ser Leu Thr Thr Val Met Gln Leu Val Val Ala  
                                   165                                  170                                  175  
 Gly Leu Gly Ser Thr Leu Val Pro Ile Ser Ala Ile Pro Trp Glu Cys  
                                   180                                  185                                  190  
 Thr Arg Pro Gly Leu Ala Thr Ala Asn Phe Asn Ser Asp Val Thr Ala  
                   195                                  200                                  205  
 Asn Arg Arg Ile Gly Leu Val Tyr Arg Ser Ser Ser Ser Arg Ala Glu  
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 Glu Phe Glu Gln Phe Ala Leu Ile Leu Gln Arg Ala Phe Gln Glu Ala  
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